

ORIGIN		Query Match	99.8%;	Score 1387.8;	DB 6;	Length 1391;	
		Best Local Similarity	99.9%;	Pred. No. 0;			
		Matches 1389;	Conservative	0;	Mismatches	2;	Indels 0; Gaps 0;
Qy	1	GGGCGACCGGAA	CAGCAGT	TGGAGCTGGTCTCGTCTCCTCAGTCTGTGGGGGGCAGTA	60		
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Qy	181	TGGAAGTCTCTG	TCTCCC	CAGGAGGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCC	240		
Db	181	TGGAAGTCTCTG	TCTCCC	CAGGAGGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCC	240		
Qy	241	AACGGTCTCCCT	TCTTCC	TGTCGGGCTGTCCGATCCAGGATGAGGGGATTTTCCCGGTGCCAG	300		

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Qy	1381	CACATCTTGCA	1391			
Db	1381	CACATCTTGCA	1391			
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Best Local Similarity						
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Qy	121	GGCCCCAAGAACCCACCCAGCGGCTGGAACTGGAACCTGAACACAGGCGGACAGAAAGCT	180			
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Db 1381 CACATCTTGCA 1391

RESULT 3  
BC020669  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

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transcript variant 1, mRNA (cDNA clone MGC:22357 IMAGE:4718076),  
complete cds.  
BC020669  
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1 (bases 1 to 1436)  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shennen, C.W., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,  
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Sánchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1436)  
Straussberg, R.  
Direct Submission  
Submitted (03-JAN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapps-r@mail.nih.gov](mailto:cgapps-r@mail.nih.gov)  
Tissue Procurement: CLONTECH  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www.shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 37 Row: e Column: 17

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 26787960.

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Best Local Similarity 99.9%; Pred. No. 0;			
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ACCESSION  
AB036432.1 GI:6691625  
VERSION  
KEYWORDS  
SOURCE  
Homo sapiens RAGE mRNA for advanced glycation endproducts receptor,  
complete cds.  
Homo sapiens  
Homo sapiens (human)

1268 bp mRNA linear PRI 13-JAN-2000





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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Yonekura,H., Yamamoto,Y., Sakurai,S., Petrova,R.G., Abedin,Md.J.,
Li,H., Yasui,K., Takeuchi,M., Makita,Z., Takasawa,S., Okamoto,H.,
Watanabe,T. and Yamamoto,H.
TITLE Novel splice variants of the receptor for advanced glycation
end-products expressed in human vascular endothelial cells and
pericytes, and their putative roles in diabetes-induced vascular
injury
JOURNAL Biochem. J. 370 (Pt 3), 1097-1109 (2003)
MEDLINE 22510265
PUBMED 12495433
REFERENCE
AUTHORS Yonekura,H., Yamamoto,Y., Sakurai,S. and Yamamoto,H.
TITLE Direct Submission
Submitted (11-MAY-2001) Hideto Yonekura, Kanazawa University,
Graduate School of Medical Science; 13-1 Takara-machi, Kanazawa,
Ishikawa 920-8640, Japan (E-mail:hyone@med.kanazawa-u.ac.jp,
Tel:81-76-265-2182, Fax:81-76-234-4226)
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RESULT 6
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ACCESSION CO730900
VERSION CO730900.1 GI:42306010
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SOURCE Homo sapiens
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DB	387	TGGGAAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAGCGTGGTGTTCCTCAATAGGT 446
QY	423	GGGACATGTGTTCAGAGGAAGTACCTTCAGGACTCTTAGCTGGCACTTGATGG 482
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ACCESSION		AJ133822
VERSION		AJ133822.1 GI:4877290
KEYWORDS		RAGEsec gene; receptor for Advanced Glycation End Products; secreted isoform.
SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
REFERENCE		1 Malherbe, P., Richards, J.G., Gaillard, H., Thompson, A., Diener, C., Schuler, A. and Huber, G. CDNA cloning of a novel secreted isoform of the human receptor for advanced glycation end products and characterization of cells co-expressing cell-surface scavenger receptors and Swedish mutant amyloid precursor protein Brain Res. Mol. Brain Res. 71 (2), 159-170 (1999)
AUTHORS		99453317 10521570
TITLE		2 (bases 1 to 1250)
JOURNAL		Malherbe, P. Direct Submission Submitted (17-MAY-1999) Malherbe P., Pharma Division PRPN, F. Hoffmann-La Roche Ltd., Bldg. 69/333, CH-4070 Basel, SWITZERLAND
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Best Local Similarity 88.0%; Pred. No. 7.5e-254;
Matches 1221; Conservative 0; Mismatches 11; Indels 155; Gaps 3;
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## RESULT 10

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LOCUS
DEFINITION
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complete cds.
ACCESSION
M91212
VERSION
M91212.1 GI:163650
KEYWORDS
RAGE; cell surface receptor.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 1426)
Neeper,M., Schmidt,A.M., Brett,J., Yan,S.D., Wang,F., Pan,Y.C.,
Elliston,K., Stern,D. and Shaw,A.
Cloning and expression of a cell surface receptor for advanced
glycosylation end products of proteins
J Biol Chem. 267 (21), 14998-15004 (1992)
J2340547
MEDLINE
1378843
PUBMED
REFERENCE
2 (bases 1 to 1426)
Shaw,A.
Direct Submission
TITLE
Submitted (15-APR-1992) A. Shaw, Department of Cellular and
Molecular Biology, Merck Sharp and Dohme Research Laboratories,
West Point, PA 19486 USA
JOURNAL
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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/08633148  
; Patent No. 5864018  
; GENERAL INFORMATION:  
; APPLICANT: MORSE, MICHAEL J.  
; APPLICANT: NAGASHIMA, MARIKO  
; APPLICANT: HOLLANDER, DORIS A.  
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,148  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY ESQ., MATTHEW B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 014618-00560005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1023 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
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US-08-633-148-1

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; Sequence 5154, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
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## RESULT 3

US-08-633-148-3  
; Sequence 3, Application US/08633148  
; Patent No. 5864018  
; GENERAL INFORMATION:  
; APPLICANT: MORSE, MICHAEL J.  
; APPLICANT: NAGASHIMA, MARIKO  
; APPLICANT: HOLLANDER, DORIS A.  
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,148  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY ESQ., MATTHEW B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 014618-00560005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2422  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 957 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-633-148-3  
Query Match 99.0%; Score 332.8; DB 2; Length 957;  
Best Local Similarity 99.4%; Pred. No. 9.5e-93;  
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 1 GCTCAAAACATCACAGCCGGATTGGCGACCACTGCTGTAAGTGAAGGGGGCCCC 60  
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DB 61 AAGAAACACACCCAGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAG 120  
QY 121 GTCTGTCTCTCCCGAGGAGAGCCCTGGGACAGTGTGGCTGTGTCTCTTCCCAACGCG 180  
DB 121 GTCTGTCTCTCCCGAGGAGAGCCCTGGGACAGTGTGGCTGTGTCTCTTCCCAACGCG 180  
QY 181 TCCCTCTCTCTCCCGAGGAGAGCCCTGGGACAGTGTGGCTGTGTCTCTTCCCAACGCG 240  
DB 181 TCCCTCTCTCTCCCGAGGAGAGCCCTGGGACAGTGTGGCTGTGTCTCTTCCCAACGCG 240  
QY 241 ACAGGAATGGAAGAGACCAAGTCCCACTACCGAGTCCGTGTCTACAGATTCTCTGGG 300  
DB 241 ACAGGAATGGAAGAGACCAAGTCCCACTACCGAGTCCGTGTCTACAGATTCTCTGGG 300  
QY 301 AAGCCAGAAATTTAGATTCTGCCTCTGAATCTCAG 336  
DB 301 AAGCCAGAAATTTAGATTCTGCCTCTGAATCTCAG 336

RESULT 4  
US-09-638-649-4  
; Sequence 4, Application US/09638649  
; Patent No. 6563015  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED  
; TITLE OF INVENTION: GLYCAN ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 0575/62175  
; CURRENT APPLICATION NUMBER: US/09/638,649  
; CURRENT FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1391  
; TYPE: DNA  
; ORGANISM: Human  
US-09-638-649-4

Query Match 99.0%; Score 332.8; DB 4; Length 1391;  
Best Local Similarity 99.4%; Pred. No. 1.1e-92;  
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 60  
DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 126  
QY 61 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 120  
DB 127 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 186  
QY 121 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 180  
DB 187 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 246  
QY 181 TCCTCTTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 240  
DB 247 TCCTCTTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 306  
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCCTGCAAGGCAATG 336  
DB 367 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAGC 402

RESULT 5  
US-09-638-648-4  
; Sequence 4, Application US/09638648  
; Patent No. 6825164  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Yan, Shi Du  
; APPLICANT: Zlokovic, Berislav  
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID  
; TITLE OF INVENTION: ANGIOPATHY  
; FILE REFERENCE: 0575/62097  
; CURRENT APPLICATION NUMBER: US/09/638,648  
; CURRENT FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1391  
; TYPE: DNA  
; ORGANISM: Human

US-09-638-648-4

Query Match 99.0%; Score 332.8; DB 4; Length 1391;  
Best Local Similarity 99.4%; Pred. No. 1.1e-92;  
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 60  
DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 126  
QY 61 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 120  
DB 127 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 186  
QY 121 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 180  
DB 187 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 246  
QY 181 TCCTCTTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 240  
DB 247 TCCTCTTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 306  
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCCTGCAAGGCAATG 336  
DB 367 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAGC 402

RESULT 6

US-08-755-235-3  
; Sequence 3, Application US/08755235  
; Patent No. 6790443  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Wu, Jun  
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES  
; FILE REFERENCE: 0575/50159  
; CURRENT APPLICATION NUMBER: US/08/755,235  
; CURRENT FILING DATE: 1996-11-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1405  
; TYPE: DNA  
; ORGANISM: Human  
US-08-755-235-3

Query Match 99.0%; Score 332.8; DB 4; Length 1405;  
Best Local Similarity 99.4%; Pred. No. 1.1e-92;  
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 60  
DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 126  
QY 61 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 120  
DB 127 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 186  
QY 121 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 180  
DB 187 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 246  
QY 181 TCCTCTTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 240  
DB 247 TCCTCTTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 306  
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCCTTACCAAGTCTCTGGG 300

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Db 307 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCTCTGGG 366
QY 301 AAGCCAGAAATGTAGATTCTGCCTCTGAATCAGC 336
Db 367 AAGCCAGAAATGTAGATTCTGCCTCTGAATCAGC 402

RESULT 7
US-09-638-649-2
; Sequence 2, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Bos Taurus
US-09-638-649-2

Query Match 80.5%; Score 270.6; DB 4; Length 1426;
Best Local Similarity 90.4%; Pred. No. 1.7e-73;
Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 4 CAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTCTGAAGTGAAGGGGCCCCCAAG 63
Db 79 CAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTCTGAAGTGAAGGGGCCCCCAAG 138
QY 64 AAACACCCCGAGCGCTGGATGGAATGAACACAGCCGACAGAGCTTGAAGGTC 123
Db 139 AAACACCCCGAGCGCTGGATGGAATGAACACAGCCGACAGAGCTTGAAGGTC 198
QY 124 CTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGCTCC 183
Db 199 CTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGCTCC 255
QY 184 CTCTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGCTCC 243
Db 256 CTCTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGCTCC 315
QY 244 AGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCTCTGGGAAG 303
Db 316 CGAGCGGAAGGAGACCAAGTCTAACTACCGAGTCCGTGTCTATCAGATTCTCTGGGAAG 375
QY 304 CCAGAAATTTAGATTCTGCCTCTGAATCAGC 336
Db 376 CCAGAAATTTAGATTCTGCCTCTGAATCAGC 408

RESULT 9
US-08-755-235-1
; Sequence 1, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: DNA
; ORGANISM: Bovine
US-08-755-235-1

Query Match 80.5%; Score 270.6; DB 4; Length 1438;
Best Local Similarity 90.4%; Pred. No. 1.7e-73;
Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 4 CAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTCTGAAGTGAAGGGGCCCCCAAG 63
Db 79 CAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTCTGAAGTGAAGGGGCCCCCAAG 138
QY 64 AAACACCCCGAGCGCTGGATGGAATGAACACAGCCGACAGAGCTTGAAGGTC 123
Db 139 AAACACCCCGAGCGCTGGATGGAATGAACACAGCCGACAGAGCTTGAAGGTC 198
QY 124 CTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGCTCC 183
Db 199 CTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGCTCC 255
QY 184 CTCTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGCTCC 243
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Db 307 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCTCTGGG 366
QY 301 AAGCCAGAAATGTAGATTCTGCCTCTGAATCAGC 336
Db 367 AAGCCAGAAATGTAGATTCTGCCTCTGAATCAGC 402

RESULT 7
US-09-638-649-2
; Sequence 2, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Bos Taurus
US-09-638-649-2

Query Match 80.5%; Score 270.6; DB 4; Length 1426;
Best Local Similarity 90.4%; Pred. No. 1.7e-73;
Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 4 CAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTCTGAAGTGAAGGGGCCCCCAAG 63
Db 79 CAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTCTGAAGTGAAGGGGCCCCCAAG 138
QY 64 AAACACCCCGAGCGCTGGATGGAATGAACACAGCCGACAGAGCTTGAAGGTC 123
Db 139 AAACACCCCGAGCGCTGGATGGAATGAACACAGCCGACAGAGCTTGAAGGTC 198
QY 124 CTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGCTCC 183
Db 199 CTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGCTCC 255
QY 184 CTCTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGCTCC 243
Db 256 CTCTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGCTCC 315
QY 244 AGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCTCTGGGAAG 303
Db 316 CGAGCGGAAGGAGACCAAGTCTAACTACCGAGTCCGTGTCTATCAGATTCTCTGGGAAG 375
QY 304 CCAGAAATTTAGATTCTGCCTCTGAATCAGC 336
Db 376 CCAGAAATTTAGATTCTGCCTCTGAATCAGC 408

RESULT 8
US-09-638-648-2
; Sequence 2, Application US/09638648
; Patent No. 6825164
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; APPLICANT: Zlokovic, Berislav
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
; TITLE OF INVENTION: ANGIOPATHY
; FILE REFERENCE: 0575/62097
; CURRENT APPLICATION NUMBER: US/09/638,648
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
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OM nucleic - nucleic search, using sw model

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Perfect score: 1020  
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Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/PCUTS COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfileseq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1015	99.5	1023	2	US-08-633-148-1
2	1015	99.5	1215	4	US-09-949-016-5154
3	1009.8	99.0	1391	4	US-09-638-649-4
4	1009.8	99.0	1391	4	US-09-638-648-4
5	986.8	96.7	1405	4	US-08-755-235-3
6	945.8	92.7	957	2	US-08-633-148-3
7	746.4	73.2	1426	4	US-09-638-649-2
8	746.4	73.2	1426	4	US-09-638-648-2
9	717.6	70.4	1438	4	US-08-755-235-1
10	696.6	68.3	1347	4	US-09-638-648-6
11	696.6	68.3	1348	4	US-09-638-649-6
12	197	19.3	7080	4	US-09-949-016-16896
13	108.6	10.6	601	4	US-09-949-016-178939
14	93	9.1	601	4	US-09-949-016-178940
15	81	7.9	5816	4	US-09-949-016-16900
16	72.6	7.1	601	4	US-09-949-016-178938
17	40	3.9	601	4	US-09-949-016-178941
18	39.6	3.9	561	4	US-09-702-705-72
19	39.6	3.9	561	4	US-09-736-457-72
20	39.6	3.9	561	4	US-09-614-124B-72
21	39.6	3.9	561	4	US-09-671-325-72
22	39.6	3.9	561	4	US-09-589-184-72
23	39.6	3.9	561	4	US-09-658-824-72
24	39.6	3.9	2539	2	US-08-432-016-1
25	39.6	3.9	2539	2	US-08-684-594-1
26	39.6	3.9	2539	4	US-09-023-655-1496
27	39.6	3.9	2539	4	US-09-949-016-3677

ALIGNMENTS

RESULT 1  
US-08-633-148-1  
; Sequence 1, Application US/08633148  
; Patent No. 5864018  
; GENERAL INFORMATION:  
; APPLICANT: MORSE, MICHAEL J.  
; APPLICANT: NAGASHIMA, MARIKO  
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,148  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY ESQ., MATTHEW B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 014618-0056000US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1023 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-633-148-1

Best Match 99.5%; Score 1015; DB 2; Length 1023;  
Query Local Similarity 100.0%; Pred. No. 6e-271;  
Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAGCCGGAACAGCAGTTCGAGCCTGGGTGGTCTCAGTCTGTGGGGGCGAGTA 60  
DB 1 ATGGCAGCCGGAACAGCAGTTCGAGCCTGGGTGGTCTCAGTCTGTGGGGGCGAGTA 60

QY 61 GTAGGTGCTCAAAACATACAGCCCGATTGGAGCCACTGCTGCTGAAGTGAAGGG 120  
DB 61 GTAGGTGCTCAAAACATACAGCCCGATTGGAGCCACTGCTGCTGAAGTGAAGGG 120  
QY 121 GCGCCCAAGAAACACCCAGCGGCTGGAATGAACTGAACACAGCCGCGACAGAAGCT 180  
DB 121 GCGCCCAAGAAACACCCAGCGGCTGGAATGAACTGAACACAGCCGCGACAGAAGCT 180  
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QY 241 AACGGCTCCTCTTCTCCCGCTGTCGGATTCAGGATGAGGGATTTCCGGTGGCCAG 300  
DB 241 AACGGCTCCTCTTCTCCCGCTGTCGGATTCAGGATGAGGGATTTCCGGTGGCCAG 300  
QY 301 GCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTACCAAGTT 360  
DB 301 GCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTACCAAGTT 360  
QY 361 CTGGGAAGCCAGAAATTGATTTCTGCTCTGAACTCACGGCTGCTTCCCATAAG 420  
DB 361 CTGGGAAGCCAGAAATTGATTTCTGCTCTGAACTCACGGCTGCTTCCCATAAG 420  
QY 421 GTGGGACATGTGTGTCAGAGGAAGCTTACCCTGACGGGACTCTTAGCTGGCACTTGGAT 480  
DB 421 GTGGGACATGTGTGTCAGAGGAAGCTTACCCTGACGGGACTCTTAGCTGGCACTTGGAT 480  
QY 481 GGAAGCCCTGTGCTTAATGAAGAGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540  
DB 481 GGAAGCCCTGTGCTTAATGAAGAGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540  
QY 541 CTGTGACAGGGCTCTTCACTGACGTGCGAGCTAATGCTGACCCAGCCGCGGGAGCA 600  
DB 541 CTGTGACAGGGCTCTTCACTGACGTGCGAGCTAATGCTGACCCAGCCGCGGGAGCA 600  
QY 601 GATCCCGCTCCCACTTCTCTGCTGAGCTTACAGCCAGGGCTTCCCGGACACACCGGGCTTG 660  
DB 601 GATCCCGCTCCCACTTCTCTGCTGAGCTTACAGCCAGGGCTTCCCGGACACACCGGGCTTG 660  
QY 661 CGCACAGCCCAATCCAGCCCGCTGTCTGGAGCCCTGTGCTGAGAGGAGTCCAAATTG 720  
DB 661 CGCACAGCCCAATCCAGCCCGCTGTCTGGAGCCCTGTGCTGAGAGGAGTCCAAATTG 720  
QY 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTCTGTGGAAACCGTAACTGACCTCTGAA 780  
DB 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTCTGTGGAAACCGTAACTGACCTCTGAA 780  
QY 781 GTCCTGCCCAGCCCTCTCTCAAAATCCACTGGATGAAGGATGGTGTGCCCTTGGCCCTT 840  
DB 781 GTCCTGCCCAGCCCTCTCTCAAAATCCACTGGATGAAGGATGGTGTGCCCTTGGCCCTT 840  
QY 841 CCCCCAGCCCTGTGTGTATCTCTCTGATAGAGGCTCAGACACAGGGAACCTACAGC 900  
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QY 901 TGTGTGSCCAACCATTCAGCCAGCGGCCCCAGGAAAGCGTCTGTGACATCAGCATC 960  
DB 901 TGTGTGSCCAACCATTCAGCCAGCGGCCCCAGGAAAGCGTCTGTGACATCAGCATC 960  
QY 961 ATCGAACCCAGGAGGAGGGGCCCAACTGACGGCTCTGTGGAGGATCAGGGCTTG 1015  
DB 961 ATCGAACCCAGGAGGAGGGGCCCAACTGACGGCTCTGTGGAGGATCAGGGCTTG 1015

## RESULT 2

US-09-949-016-5154  
; Sequence 5154, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5154  
; LENGTH: 1215  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5154

Query Match 99.5%; Score 1015; DB 4; Length 1215;  
Best Local Similarity 100.0%; Pred. No. 6.5e-271;  
Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAGCGGAAACAGCAGTTGGAGCCCTGGGTGCTGCTCAGTCTGTGGGGGCACTA 60  
DB 1 ATGGCAGCGGAAACAGCAGTTGGAGCCCTGGGTGCTGCTCAGTCTGTGGGGGCACTA 60  
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DB 61 GTAGGTGCTCAAAAATCACAAGCCCGGATTTGGCAGCCACTGGTGTCTGAAGTGAAGGG 120  
QY 121 GCGCCCAAGAAACACCCAGCGGCTGGAATGAACTGAACACAGCCGCGACAGAAGCT 180  
DB 121 GCGCCCAAGAAACACCCAGCGGCTGGAATGAACTGAACACAGCCGCGACAGAAGCT 180  
QY 181 TGGAGGTGCTGCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGCTCTTCCC 240  
DB 181 TGGAGGTGCTGCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGCTCTTCCC 240  
QY 241 AACGGCTCCTCTTCTCCCGCTGTCGGATTCAGGATGAGGGATTTCCGGTGGCCAG 300  
DB 241 AACGGCTCCTCTTCTCCCGCTGTCGGATTCAGGATGAGGGATTTCCGGTGGCCAG 300  
QY 301 GCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTACCAAGTT 360  
DB 301 GCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTACCAAGTT 360  
QY 361 CTGTGGAAGCCAGAAATTGATTTCTGCTCTGAACTCACGGCTGCTTCCCATAAG 420  
DB 361 CTGTGGAAGCCAGAAATTGATTTCTGCTCTGAACTCACGGCTGCTTCCCATAAG 420  
QY 421 GTGGGACATGTGTGTCAGAGGAAGCTTACCCTGACGGGACTCTTAGCTGGCACTTGGAT 480  
DB 421 GTGGGACATGTGTGTCAGAGGAAGCTTACCCTGACGGGACTCTTAGCTGGCACTTGGAT 480  
QY 481 GGAAGCCCTGTGCTTCACTGACGTGCGAGCTAATGCTGACCCAGCCGCGGGAGCA 540  
DB 481 GGAAGCCCTGTGCTTCACTGACGTGCGAGCTAATGCTGACCCAGCCGCGGGAGCA 540  
QY 541 CTGTGACAGGGCTCTTCACTGACGTGCGAGCTAATGCTGACCCAGCCGCGGGAGCA 600  
DB 541 CTGTGACAGGGCTCTTCACTGACGTGCGAGCTAATGCTGACCCAGCCGCGGGAGCA 600  
QY 601 GATCCCGCTCCCACTTCTCTGCTGAGCTTACAGCCAGGGCTTCCCGGACACACCGGGCTTG 660  
DB 601 GATCCCGCTCCCACTTCTCTGCTGAGCTTACAGCCAGGGCTTCCCGGACACACCGGGCTTG 660  
QY 661 CGCACAGCCCAATCCAGCCCGCTGTCTGGAGCCCTGTGCTGAGAGGAGTCCAAATTG 720  
DB 661 CGCACAGCCCAATCCAGCCCGCTGTCTGGAGCCCTGTGCTGAGAGGAGTCCAAATTG 720  
QY 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTCTGTGGAAACCGTAACTGACCTCTGAA 780  
DB 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTCTGTGGAAACCGTAACTGACCTCTGAA 780



123 CCCCAGAAACACCCAGCGGTGGAATGGAACTGAACACAGGCCGGACAGAACTTG 182  
123 CCCCAGAAACACCCAGCGGTGGAATGGAACTGAACACAGGCCGGACAGAACTTG 182  
183 GAAGTCTCTGTCCTCCAGGAGAGGCCCTGGGACAGTGTGGCTGCTCTCCCAA 242  
183 GAAGTCTCTGTCCTCCAGGAGAGGCCCTGGGACAGTGTGGCTGCTCTCCCAA 242  
243 CGGCTCCCTCTCTCCGCTGTCGGGATCCAGGATGAGGGGATTTCCGGTGCAGC 302  
243 CGGCTCCCTCTCTCCGCTGTCGGGATCCAGGATGAGGGGATTTCCGGTGCAGC 302  
303 AATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGCTCTACCA 362  
303 AATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGCTCTACCA 362  
363 TGGGAAGCAGAAATTTGTAGATTTCTCCCTCTGAATCTCAAGGCTGCTCCAA 422  
363 TGGGAAGCAGAAATTTGTAGATTTCTCCCTCTGAATCTCAAGGCTGCTCCAA 422  
423 GGGGACATGTGTGTCAGAGGAGTACCTCGAGGACCTTAGCTGCACTTGGATGG 482  
423 GGGGACATGTGTGTCAGAGGAGTACCTCGAGGACCTTAGCTGCACTTGGATGG 482  
483 GAAGCCCTCTGCTGCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACAGGAC 542  
483 GAAGCCCTCTGCTGCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACAGGAC 542  
543 TGAGACAGGGCTCTTCACTGTCAGAGTAAATGGTGAACCCAGCCCGGGAGGAG 602  
543 TGAGACAGGGCTCTTCACTGTCAGAGTAAATGGTGAACCCAGCCCGGGAGGAG 602  
723 GGTGGAGCAGAAAGTGGAGCAGTAGCTCTCGTGGAAACCGTAAACCTGCTGAAGT 782  
723 GGTGGAGCAGAAAGTGGAGCAGTAGCTCTCGTGGAAACCGTAAACCTGCTGAAGT 782  
783 CCTGCGCAGCCCTCTCTCAATCCACTGGATGAAGGATGCTGCTTCCCTTCC 842  
783 CCTGCGCAGCCCTCTCTCAATCCACTGGATGAAGGATGCTGCTTCCCTTCC 842  
843 CCCCAGCCTGTGCTGATCTCTCTCAGATAGGGCTCAGGACAGGAAACCTACAGCTG 902  
843 CCCCAGCCTGTGCTGATCTCTCTCAGATAGGGCTCAGGACAGGAAACCTACAGCTG 902  
903 TGTGGCCACCCATTCAGCCAGCGGCCCGAGGAAAGCCGTGCTCAGCATCAGCAT 962  
903 TGTGGCCACCCATTCAGCCAGCGGCCCGAGGAAAGCCGTGCTCAGCATCAGCAT 962  
963 CGAACACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1015  
963 CGAACACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1015

RESULT 5

US-08-755-235-3  
; Sequence 3, Application US/08755235  
; Patent No. 6790443  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Wu, Jun  
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES  
; FILE REFERENCE: 0575/50159  
; CURRENT APPLICATION NUMBER: US/08/755,235

; CURRENT FILING DATE: 1996-11-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1405  
; TYPE: DNA  
; ORGANISM: Human  
US-08-755-235-3

Query Match 96.7%; Score 986.8; DB 4; Length 1405;  
Best Local Similarity 99.6%; Pred. No. 4.4e-263;  
Matches 1010; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 3 GGAGCCCGGAAACAGCAGATTGGAGCCTGGGTGCTGCTCCTCAGTCTGTGGGGGCGAGTAGT 62  
DB 3 GGAGCCCGGAAACAGCAGATTGGAGCCTGGGTGCTGCTCCTCAGTCTGTGGGGGCGAGTAGT 62  
QY 63 AGGTGCTCAAAACATCAGACCCCGGATTGGCGAGCCACTGGTGCTGAAGTGTAAAGGGGC 122  
DB 63 AGGTGCTCAAAACATCAGACCCCGGATTGGCGAGCCACTGGTGCTGAAGTGTAAAGGGGC 122  
QY 123 CCCCAGAAACACACCCAGCGGCTGGAATGGAAACTGAACACAGGCCGGACAGAAAGCTTG 182  
DB 123 CCCCAGAAACACACCCAGCGGCTGGAATGGAAACTGAACACAGGCCGGACAGAAAGCTTG 182  
QY 183 GAAGGTCTCTGCTCTCCCGAGGAGGAGGCCCTTGGGACAGTGTGGCTCGTGTCTTCCCAA 242  
DB 183 GAAGGTCTCTGCTCTCCCGAGGAGGAGGCCCTTGGGACAGTGTGGCTCGTGTCTTCCCAA 242  
QY 243 CGGCTCCCTCTTCTTCCGCTGTCGGGATCCAGGATGAGGGGATTTCCGGTGCAGGCG 302  
DB 243 CGGCTCCCTCTTCTTCCGCTGTCGGGATCCAGGATGAGGGGATTTCCGGTGCAGGCG 302  
QY 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGCTCAACAGATTCC 362  
DB 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGCTCAACAGATTCC 362  
QY 363 TGGGAAGCCAGAAATTTGTAGATTTCTGCTCTGAACTCAGCGCTGGTGTGTTCCCAATAAGT 422  
DB 363 TGGGAAGCCAGAAATTTGTAGATTTCTGCTCTGAACTCAGCGCTGGTGTGTTCCCAATAAGT 422  
QY 423 GGGGACATGTGTGTCAGAGGAGGAGTACCTGTCAGAGGACTTTAGTGGGACCTTGGATGG 482  
DB 423 GGGGACATGTGTGTCAGAGGAGGAGTACCTGTCAGAGGACTTTAGTGGGACCTTGGATGG 482  
QY 483 GAAGCCCTCTGCTGCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACAGGAGACCC 542  
DB 483 GAAGCCCTCTGCTGCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACAGGAGACCC 542  
QY 543 TGAGACAGGGCTCTTCACTGTCAGTCCGAGCTAATGTTGACCCAGCCCGGGAGGAGAG 602  
DB 543 TGAGACAGGGCTCTTCACTGTCAGTCCGAGCTAATGTTGACCCAGCCCGGGAGGAGAG 602  
QY 603 TCCCGTCCCACTTCTCTGTCAGTTCAGCCAGGCTTCCCGACACCCGGGCTTGGG 662  
DB 603 TCCCGTCCCACTTCTCTGTCAGTTCAGCCAGGCTTCCCGACACCCGGGCTTGGG 662  
QY 663 CACAGCCCCATCCAGCCCGGCTGTCGGAGGCTGTCCTCTGGAGGAGTCCAAATT-GG 721  
DB 663 CACAGCCCCATCCAGCCCGGCTGTCGGAGGCTGTCCTCTGGAGGAGTCCAAATTGGG 722  
QY 722 TGGTGGAGCCAGAAAGTGGAGCAGTAGCTCTCTGGTGAACCCGTAAACCTTGACCTGTGAAG 781  
DB 722 TGGTGGAGCCAGAAAGTGGAGCAGTAGCTCTCTGGTGAACCCGTAAACCTTGACCTGTGAAG 782  
QY 782 TCCCTGCCAGCCCTCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTGCCTTTC 841  
DB 782 TCCCTGCCAGCCCTCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTGCCTTTC 841  
QY 842 CCCCAGCCCTGTGCTGATCTCCCTCAGATAGGCGCTCAGGACAGGGAACCTACAGCT 901  
DB 842 CCCCAGCCCTGTGCTGATCTCCCTCAGATAGGCGCTCAGGACAGGGAACCTACAGCT 901



QY 902 GTGTGGCCACCATTCAGCCACGGGCCCCAGGAAACCGTGTGTGTCAGCATCAGCATCA 961  
Db 902 GTGTGGCCACCATTCAGCCACGGGCCCCAGGAAACCGTGTGTGTCAGCATCAGCATCA 961  
QY 962 TCGAACCCAGGAGGAGGGGCGCAACTCAGGCTCTGTGGGAGGATCAGGGCTGG 1015  
Db 962 TCGAACCCAGGAGGAGGGGCGCAACTCAGGCTCTGTGGGAGGATCAGGGCTGG 1015

## RESULT 6

US-08-633-148-3  
; Sequence 3, Application US/08633148  
; Patent No. 5864018  
; GENERAL INFORMATION:  
; APPLICANT: MORSE, MICHAEL J.  
; APPLICANT: NAGASHIMA, MARIKO  
; APPLICANT: HOLLANDER, DORIS A.  
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/633,148  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY ESQ., MATTHEW B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 014618-005600US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 957 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-633-148-3

Query Match 92.7%; Score 945.8; DB 2; Length 957;  
Best Local Similarity 99.8%; Pred. No. 8.4e-252;  
Matches 947; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 67 GCTCAAAACATCAGCCCGGATTGGCGAGCCCACTGGTGTGAAGTGTAAAGGGGCCCC 126  
Db 1 GCTCAAAACATCAGCCCGGATTGGCGAGCCCACTGGTGTGAAGTGTAAAGGGGCCCC 60  
QY 127 AAGAAACCCACCCAGCGGCTGGAAATGGAATGGAACACACAGCCCGGACAGAGCTTGAAG 186  
Db 61 AAGAAACCCACCCAGCGGCTGGAAATGGAATGGAACACACAGCCCGGACAGAGCTTGAAG 120  
QY 187 GTCTGTCTCCCGAGGAGAGGCCCCCTGGACAGTGTGGCTGTCTTCCCAACGGC 246  
Db 121 GTCTGTCTCCCGAGGAGAGGCCCCCTGGACAGTGTGGCTGTCTTCCCAACGGC 180  
QY 247 TCCTCTTCTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTTCGGTCCAGGCAATG 306  
Db 181 TCCTCTTCTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTTCGGTCCAGGCAATG 240  
QY 307 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTTACCAAGATTCCTGGG 366

Db 241 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTTACCAAGATTCCTGGG 300  
QY 367 AAGCCAGAAATTTAGATTCTGCTCTGAACCTCAGCGCTGGTGTTCCTCAATAAGAGTGGG 426  
Db 301 AAGCCAGAAATTTAGATTCTGCTCTGAACCTCAGCGCTGGTGTTCCTCAATAAGAGTGGG 360  
QY 427 ACATGTGTGTAGAGGGAAGCTACCTCTCAGAGGAGCTCTTAGCTGGGACCTTTGGATGGGAAG 486  
Db 361 ACATGTGTGTAGAGGGAAGCTACCTCTCAGAGGAGCTCTTAGCTGGGACCTTTGGATGGGAAG 420  
QY 487 CCCTGTGCTTAATCAGAGGAGGATATCTGTGAAGGAAACAGACACAGGAGACACCTGTAG 546  
Db 421 CCCTGTGCTTAATCAGAGGAGGATATCTGTGAAGGAAACAGACACAGGAGACACCTGTAG 480  
QY 547 ACAGGGCTCTTTCACACTGCGAGTCCGAGCTAAATGGTGACCCCGGCGGGGAGGAGATCCC 606  
Db 481 ACAGGGCTCTTTCACACTGCGAGTCCGAGCTAAATGGTGACCCCGGCGGGGAGGAGATCCC 540  
QY 607 CGTCCACCTTCTCTGTAGCTTACGCCAGGCTTTCCCGGACACCGGGGCTTTGGCGACA 666  
Db 541 CGTCCACCTTCTCTGTAGCTTACGCCAGGCTTTCCCGGACACCGGGGCTTTGGCGACA 600  
QY 667 GCGCCCATCCAGCCCGCTGTCTGGGAGCCTGTGCTCTGGAGGAGGTCCAAATTTGGTGGT 726  
Db 601 GCGCCCATCCAGCCCGCTGTCTGGGAGCCTGTGCTCTGGAGGAGGTCCAAATTTGGTGGT 660  
QY 727 GAGCCAGAAAGGTGGAGCAGTAGCTCTGTGTGGAACCGTAACCTGTGTGAAGTCCCT 786  
Db 661 GAGCCAGAAAGGTGGAGCAGTAGCTCTGTGTGGAACCGTAACCTGTGTGAAGTCCCT 720  
QY 787 GCGCAGCCCTCTCTCAATTCACATGGAATGAAGGATGGTGTGCTTGCCTTGCCTTCCCTCC 846  
Db 721 GCGCAGCCCTCTCTCAATTCACATGGAATGAAGGATGGTGTGCTTGCCTTGCCTTCCCTCC 780  
QY 847 AGCCCTGTCTGATCTCTCTGAGTAGGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 906  
Db 781 AGCCCTGTCTGATCTCTCTGAGTAGGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
QY 907 GCGCAGCCATTCAGCCACCGGCGCCAGGAAAGCGCTGTGTCTAGCATCAGCATCATCGAA 966  
Db 841 GCGCAGCCATTCAGCCACCGGCGCCAGGAAAGCGCTGTGTCTAGCATCAGCATCATCGAA 900  
QY 967 CCAGGCGAGGAGGCGCAACTGCGAGCTCTGTGGAGGATCAGGGCTGG 1015  
Db 901 CCAGGCGAGGAGGCGCAACTGCGAGCTCTGTGGAGGATCAGGGCTGG 949

## RESULT 7

US-09-638-649-2  
; Sequence 2, Application US/09638649  
; Patent No. 6563015  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED  
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 0575/62175  
; CURRENT APPLICATION NUMBER: US/09/638,649  
; CURRENT FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1426  
; TYPE: DNA  
; ORGANISM: Bos Taurus  
US-09-638-649-2

Query Match 73.2%; Score 746.4; DB 4; Length 1426;  
Best Local Similarity 84.1%; Pred. No. 1.5e-196;  
Matches 881; Conservative 0; Mismatches 131; Indels 36; Gaps 2;

[illegible]

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 17:18:58 ; Search time 877.54 Seconds  
(without alignments)  
9383.456 Million cell updates/sec

Title: US-10-091-019-1  
Perfect score: 1391  
Sequence: 1 999gcagccggaacagcagt.....aacacctgacacattcttga 1391

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1391	100.0	1391	6	ABQ79955 Human RAG
2	1389	99.9	1415	6	ABQ99597 Human cod
3	1387.8	99.8	1391	6	ABK10856 DNA encod
4	1387.8	99.8	1391	6	ABK41114 Human cdn
5	1387.8	99.8	1391	6	AAD36952 Human rec
6	1387.8	99.8	1391	10	AAD59952 Human RAG
7	1387.8	99.8	1391	10	ADG32021 Human DNA
8	1375.8	98.9	1582	4	AAS7444 Human lun
9	1373	98.7	1436	12	ADK00130 Human RAG
10	1331	95.7	1463	6	ABQ99598 Human cod
11	1303.8	93.7	1539	9	ACC59920 Human REM
12	1293.4	93.0	1678	9	ACC59907 Human REM
13	1265.6	91.0	1329	12	ADP19665 Human LP2
14	1250	89.9	1323	12	ADP19667 Human LP2
15	1242	89.3	1268	10	ADG33024 Human DNA
16	1233.8	88.7	1627	9	ACC59921 Human REM
17	1228	88.3	1384	12	ADP19659 Human LP2
18	1211.4	87.1	1217	10	ADP95563 Human NOV
19	1192	85.7	1294	12	ADP19669 Human LP2
20	1146.4	82.4	1226	10	ADP95565 Human NOV

21	1136	81.7	1146	13	ADS10302	Adel0302 Human the
22	1119	80.4	1173	10	ADP95567	Adel95567 Human NOV
23	1106	79.5	1291	12	ADP19655	Adp19655 Human LP2
24	1062	76.3	1223	6	ABV73151	ABV73151 Human sol
25	1062	76.3	1223	10	ADG37043	Adg37043 Receptor
26	1048	75.3	1339	12	ADP19661	Adp19661 Human LP2
27	1025.2	73.7	1761	12	ADK00128	Adk00128 Human RAG
28	1018	73.2	1023	2	AAV12394	AAV12394 Human sol
29	1018	73.2	1023	2	AAV06517	AAV06517 Human RAG
30	1013	72.8	1020	6	ABQ79956	Abq79956 Human sol
31	992	71.3	1194	12	ADP19657	Adp19657 Human LP2
32	992	71.3	1239	12	ADP19663	Adp19663 Human LP2
33	954	68.6	957	2	AAV06518	AAV06518 Human RAG
34	950.8	68.4	957	2	AAV12395	AAV12395 Human mat
35	944.8	67.9	1426	6	ABK10855	Abk10855 DNA encod
36	944.8	67.9	1426	6	AAD36951	Aad36951 Cow recep
37	944.8	67.9	1426	10	AAD59951	Aad59951 Bovine RA
38	944.8	67.9	1426	10	ADG32020	Adg32020 DNA encod
39	826.4	59.4	1347	6	ABK10858	Abk10858 DNA encod
40	826.4	59.4	1348	6	ABK10857	Abk10857 DNA encod
41	826.4	59.4	1348	6	AAD36953	Aad36953 Mouse rec
42	826.4	59.4	1348	10	AAD59953	Aad59953 Murine RA
43	820	59.0	1090	12	ADM80824	Adm80824 Human CAD
44	708.4	50.9	2057	12	ADK00123	Adk00123 Murine so
45	476.6	34.3	610	6	ABL65596	Ab165596 Lung canc

ALIGNMENTS

RESULT 1  
ABQ79955  
ID ABQ79955 standard; DNA; 1391 BP.

XX AC ABQ79955;

XX DT 23-DEC-2002 (first entry)

XX DE Human RAGE nucleotide sequence.

XX KW Receptor for Advanced Glycated end product; RAGE; recombinant; nootropic;  
XX KW antiarteriosclerotic; antidiabetic; cytosatic; nephrotropic; vasotropic;  
XX KW neuroprotective; antiinflammatory; gene therapy; human; ds.

XX OS Homo sapiens.

XX PN WO200270667-A2.

XX PD 12-SEP-2002.

XX PF 05-MAR-2002; 2002WO-US006881.

XX PR 05-MAR-2001; 2001US-0273418P.

XX PA (TRAN-) TRANSTECH PHARMA INC.

XX PI Harris R, Shen J, Shabbaz M;

XX XX WPI; 2002-713443/77.

XX XX High level expression of recombinant Receptors for Advanced Glycated end products (RAGE) proteins for treating increased levels of advanced glycosylation end products, comprises infecting cells with a high titer recombinant virus.

XX PS Claim 12; Fig 2A; 5lpp; English.

XX CC The invention relates to a method for high level expression of recombinant forms of the Receptor for Advanced Glycated end products (RAGE) or its fragments. The method involves (i) subcloning a nucleotide sequence encoding RAGE or its fragment into a virus; (ii) preparing a high titer stock of recombinant virus; and (iii) infecting host cells with the high titer recombinant virus under conditions such that

CC predetermined levels of RAGE or its fragment is produced, where the  
CC predetermined levels of RAGE comprises at least 25 mg recombinant protein  
CC per liter of culture. The method is useful for high level expression of  
CC recombinant RAGE polypeptide or its fragment which may be useful in  
CC preventing, treating or ameliorating diseases associated with increased  
CC levels of advanced glycosylation end products, such as atherosclerosis,  
CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's  
CC disease, inflammation, systemic lupus nephritis, inflammatory lupus  
CC nephritis, cancer or erectile dysfunction. The present sequence  
CC represents the nucleotide sequence of human RAGE as reported in GenBank  
CC /EMBL Accession no. XM004205  
XX  
SQ Sequence 1391 BP; 305 A; 408 C; 417 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 1391; DB 6; Length 1391;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACGCGGAAACAGCAGTTGGAGCTGGGTGCTGCTCCTCAGTCTGTGGGGGCGAGTA 60  
DB 1 GGGGACGCGGAAACAGCAGTTGGAGCTGGGTGCTGCTCCTCAGTCTGTGGGGGCGAGTA 60  
QY 61 GTAGTGTCTCAAAACATCAAGCCCGGATTGGGAGCCACTGGTGTGAAGTGTAAAGGG 120  
DB 61 GTAGTGTCTCAAAACATCAAGCCCGGATTGGGAGCCACTGGTGTGAAGTGTAAAGGG 120  
QY 121 GCGCCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCT 180  
DB 121 GCGCCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCT 180  
QY 181 TGAAGGTCTGTCTCCCAAGGAGGAGGCCCTCGGACAGTGTGGCTGTCTTCTTCCC 240  
DB 181 TGAAGGTCTGTCTCCCAAGGAGGAGGCCCTCGGACAGTGTGGCTGTCTTCTTCCC 240  
QY 241 AACGGTCTCTTCTTCCCGTGTGGGATCCAGGATCAGGAGATTTTCGGTGTCCAG 300  
DB 241 AACGGTCTCTTCTTCCCGTGTGGGATCCAGGATCAGGAGATTTTCGGTGTCCAG 300  
QY 301 GCATCAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTCTACACAGATT 360  
DB 301 GCATCAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTCTACACAGATT 360  
QY 361 CTTGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAG 420  
DB 361 CTTGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAG 420  
QY 421 GTGGGACATGTGTTCAGAGGAAGCTACCTGACGGGACTCTTAGCTGGGACATTGGAT 480  
DB 421 GTGGGACATGTGTTCAGAGGAAGCTACCTGACGGGACTCTTAGCTGGGACATTGGAT 480  
QY 481 GGGAGCCCTGTGTCTTAATGAGAGGAGTATCTGTGAAGAAACAGACACAGGAGACAC 540  
DB 481 GGGAGCCCTGTGTCTTAATGAGAGGAGTATCTGTGAAGAAACAGACACAGGAGACAC 540  
QY 541 CTTGAGACAGGGCTCTTCACTGCACTGCGAGCTAATGTTGACCCAGCCGCGGAGGA 600  
DB 541 CTTGAGACAGGGCTCTTCACTGCACTGCGAGCTAATGTTGACCCAGCCGCGGAGGA 600  
QY 601 GATCCCGTCCGACCTTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGCTTG 660  
DB 601 GATCCCGTCCGACCTTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGCTTG 660  
QY 661 CGCACAGCCCCCATCCAGCCCCGTGTCTGGAGCCCTGTGCTCTGGAGGAGTCCAAATTG 720  
DB 661 CGCACAGCCCCCATCCAGCCCCGTGTCTGGAGCCCTGTGCTCTGGAGGAGTCCAAATTG 720  
QY 721 GTGGTGGAGCCAGAAAGGTGAGCAGTAGCTCTCTGGTGGAAACCGTAAACCTGTGAA 780  
DB 721 GTGGTGGAGCCAGAAAGGTGAGCAGTAGCTCTCTGGTGGAAACCGTAAACCTGTGAA 780  
QY 781 GTCCCTGCCAGCCCTCTCTCTAAATCCACTGATGAAGATGGTGTGCCCTTGCCCTT 840  
DB 781 GTCCCTGCCAGCCCTCTCTCTAAATCCACTGATGAAGATGGTGTGCCCTTGCCCTT 840

QY 841 CCCCCCAGCCCTGTGTCTGATCTCTCCTGAGATAGGSCCTCAGGACCAGGAAACCTACAGC 900  
DB 841 CCCCCCAGCCCTGTGTCTGATCTCTCCTGAGATAGGSCCTCAGGACCAGGAAACCTACAGC 900  
QY 901 TGTGTGGCCACCCATTCCAGCCACGGGCCCAAGAAAGCCGTGTGTAGCATCAGCATC 960  
DB 901 TGTGTGGCCACCCATTCCAGCCACGGGCCCAAGAAAGCCGTGTGTAGCATCAGCATC 960  
QY 961 ATCGAACACAGGCGAGGAGGGGCCAACTGCAGGCTCTGTGGAGGATCAGGGCTGGGAAT 1020  
DB 961 ATCGAACACAGGCGAGGAGGGGCCAACTGCAGGCTCTGTGGAGGATCAGGGCTGGGAAT 1020  
QY 1021 CTAGCCCTGGCCCTGGGATCTCTGGGAGGCTTGGGACAGCCGCCCTGCTCATTTGGGGTC 1080  
DB 1021 CTAGCCCTGGCCCTGGGATCTCTGGGAGGCTTGGGACAGCCGCCCTGCTCATTTGGGGTC 1080  
QY 1081 ATCTTGTGCAAAAGGCGCAACCGCGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
DB 1081 ATCTTGTGCAAAAGGCGCAACCGCGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
QY 1141 GAAGAGGAGGCGTGCAGAACTGAATCAGTCGGAGGAACCTGAGGAGCGGAGAGTAGT 1200  
DB 1141 GAAGAGGAGGCGTGCAGAACTGAATCAGTCGGAGGAACCTGAGGAGCGGAGAGTAGT 1200  
QY 1201 ACTGAGAGGCGCTTGGGGGCCCAACAGACAGATCCCATCAGCTCCCTTTCTTTTTC 1260  
DB 1201 ACTGAGAGGCGCTTGGGGGCCCAACAGACAGATCCCATCAGCTCCCTTTCTTTTTC 1260  
QY 1261 CTTGAACTGTGTCTGGCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATAACC 1320  
DB 1261 CTTGAACTGTGTCTGGCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATAACC 1320  
QY 1321 CCACCTTGCAGAGCTTCTTCTACACAGAGGCCCCCAACATGATGATTAACACCTCA 1380  
DB 1321 CCACCTTGCAGAGCTTCTTCTACACAGAGGCCCCCAACATGATGATTAACACCTCA 1380  
QY 1381 CACATCTTGCA 1391  
DB 1381 CACATCTTGCA 1391  
RESULT 2  
ABQ99597  
ID ABQ99597 standard; cDNA; 1415 BP.  
XX  
AC ABQ99597;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
Human coding sequence SEQ ID 330.  
DE  
XX  
Human; expressed sequence tag; EST; chromosome 6p21.3;  
KW haematopoietic disorder; central nervous system disease; viral infection;  
KW peripheral nervous system disease; non-healing wound; infectious disease;  
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;  
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;  
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;  
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;  
KW immunostimulant; cerebroprotective; gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200259260-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 16-NOV-2001; 2001WO-US042950.  
XX  
PR 17-NOV-2000; 2000US-00714936.  
XX  
PA (HYSE-) HYSEQ INC.  
XX

PI	Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
PI	Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX	
DR	WPI; 2002-590824/63.
DR	N-PSDB; ABP65011.
XX	
PT	New isolated polynucleotide, useful in research, diagnostic or
PT	therapeutic methods, e.g. preventing or treating disorders involving
PT	aberrant protein expression or biological activity.
XX	
PS	Claim 1; SEQ ID NO 330; 394pp; English.
XX	
CC	The present invention relates to novel human coding sequences (ABQ9268-
CC	ABQ93608) and proteins (ABP64682-ABP65022). The sequences are useful in
CC	therapeutic, diagnostic and research methods. The polynucleotides may be
CC	used in the field of molecular biology as hybridisation probes, primers
CC	for PCR, for chromosome and gene mapping, for the recombinant production
CC	of protein, or in generation of anti-sense DNA or RNA. The
CC	polynucleotides are useful in diagnostics as expressed sequence tags
CC	(ESTs) for identifying expressed genes or for physical mapping of the
CC	human genome. The proteins may be used as molecular weight markers, or as
CC	nutritional sources or supplements. The proteins may be used to maintain
CC	and expand cell population in a totipotent or pluripotential state
CC	useful for re-engineering damaged or diseased tissues, transplantation,
CC	manufacture of bio-pharmaceuticals or the development of bio-sensors. The
CC	polynucleotides and proteins are useful for preventing, treating or
CC	ameliorating disorders involving aberrant protein expression or
CC	biological activity, e.g. haematopoietic disorders, central/peripheral
CC	nervous system diseases, mechanical and traumatic disorders, non-healing
CC	wounds, immune deficiencies and disorders, infectious diseases caused by
CC	viral, bacterial or fungal infection, autoimmune disorders, allergic
CC	reactions and conditions, coagulation disorders, or cancer. The
CC	polynucleotide sequences of the invention were assembled from ESTs
CC	isolated mainly by sequencing by hybridisation, and in some cases,
CC	sequences obtained from one or more public databases. Note: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 1415 BP; 313 A; 414 C; 425 G; 263 T; 0 U; 0 Other

Query Match	99.9%	Score 1389;	DB 6;	Length 1415;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1389;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	3	GGCAGCCGGACACGACAGTTGGAGCCTTGGTGCTCGTCTCAGTCTGTGGGGGGCAGTAGT	62	
DB	27	GGCAGCCGGACACGACAGTTGGAGCCTTGGTGCTCGTCTCAGTCTGTGGGGGGCAGTAGT	86	
QY	63	AGGTGCTCAAAACATCAGAGCCCGGATTGGCGAGCCACTGGTGCTGAAGTCTAAGGGGGC	122	
DB	87	AGGTGCTCAAAACATCAGAGCCCGGATTGGCGAGCCACTGGTGCTGAAGTCTAAGGGGGC	146	
QY	123	CCCCAAGAAACCCAGCCGGCTGGAACTGAACAACAGCCCGGACAGAACTTG	182	
DB	147	CCCCAAGAAACCCAGCCGGCTGGAACTGAACAACAGCCCGGACAGAACTTG	206	
QY	183	GAAGTCTCTCTCCCGAGGAGAGGCCCTTGGGACAGTGTGGCTGTGTCCTTCCCA	242	
DB	207	GAAGTCTCTCTCTCCCGAGGAGAGGCCCTTGGGACAGTGTGGCTGTGTCCTTCCCA	266	
QY	243	CGGCTCCCTCTTCTCCCGCTGTCGGATCCAGGATGAGGGGATTTTCGGTCCCAAGC	302	
DB	267	CGGCTCCCTCTTCTCCCGCTGTCGGATCCAGGATGAGGGGATTTTCGGTCCCAAGC	326	
QY	303	AATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGTTC	362	
DB	327	AATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGTTC	386	
QY	363	TGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAAGTCTACCGCTGGTGTTCCTAATAGGT	422	
DB	387	TGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAAGTCTACCGCTGGTGTTCCTAATAGGT	446	

RESULT 3  
ABK10856  
ID ABK10856 standard; cDNA; 1391 BP.  
XX



Db 1141 GAAGAGGAGCGTGCAGAACTGAATCACTCGAGGAACCTGAGGAGCGGAGAGTAGT 1200

Qy 1201 ACTGAGGGCCTTGGAGGGCCACAGACAGATCCATCCATGAGTCCCTTTCTTTTC 1260

Db 1201 ACTGAGGGCCTTGGAGGGCCACAGACAGATCCATCCATGAGTCCCTTTCTTTTC 1260

Qy 1261 CCTGAACTGTTTGGCCTCAGACCAACTCTCTCTGTATTAATCTCTCTCTGTATAAC 1320

Db 1261 CCTGAACTGTTTGGCCTCAGACCAACTCTCTCTGTATTAATCTCTCTCTGTATAAC 1320

Qy 1321 CCACCTTGCAAGCTTCTTCTACACAGAGCCGCCCAATGATGATTAAACACTGA 1380

Db 1321 CCACCTTGCAAGCTTCTTCTACACAGAGCCGCCCAATGATGATTAAACACTGA 1380

Qy 1381 CACATCTTGCA 1391

Db 1381 CACATCTTGCA 1391

RESULT 4

ABK84114

ID ABK84114 standard; cDNA; 1391 BP.

XX

AC ABK84114;

XX

DT 14-AUG-2002 (first entry)

XX

DE Human cDNA differentially expressed in granulocytic cells #685.

XX

KW Human; ss; granulocytic cell; DNA chip; bacterial infection;

KW viral infection; parasitic infection; protozoal infection;

KW fungal infection; sterile inflammatory disease; psoriasis;

KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

KW cardiac reperfusion injury; renal reperfusion injury; ARDS;

KW adult respiratory distress syndrome; inflammatory bowel disease;

KW Crohn's disease; ulcerative colitis; periodontal disease;

KW granulocyte activation; chronic inflammation; allergy.

XX

OS Homo sapiens.

XX

PN WO200228999-A2.

XX

PD 11-APR-2002.

XX

PF 03-OCT-2001; 2001WO-US030821.

XX

PR 03-OCT-2000; 2000US-0237189P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX

DR WPI; 2002-435328/46.

XX

PT Detecting granulocyte activation by detecting differential expression of

PT genes associated with granulocyte activation, which serves as diagnostic

PT markers that is useful for monitoring disease states and drug toxicity.

XX

PS Claim 1; SEQ ID NO 685; 114pp; English.

XX

CC The invention relates to detecting (M1) granulocyte (GC) activation

CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by

CC DNA chip analysis as given in the specification, and comparing the

CC expression level to an expression level in an unactivated GC, where

CC differential expression of Gs is indicative of GCA. Also included are

CC modulating (M2) GA by contacting GC with an agent that alters the

CC expression of at least one gene in Gs; (2) screening (M3) for an agent

CC capable of modulating GCA or an inflammation (especially chronic) in a

CC tissue, an allergic response in a subject, exposure of a subject to a

CC pathogen or sterile inflammatory disease using the gene expression

CC profile; (3) detecting (M4) an inflammation (especially chronic) in a

CC tissue, an allergic response in a subject, exposure of a subject to a

CC pathogen or sterile inflammatory disease, by detecting the level of

CC expression in a sample of the tissue of gene(s) from Gs, where the level

CC of expression of the gene is indicative of inflammation; (4) treating

CC (M5) an inflammation (especially chronic) or in a tissue, an allergic

CC response in a subject, exposure of a subject to a pathogen or sterile

CC inflammatory disease, by contacting a tissue having inflammation with an

CC agent that modulates the expression of gene(s) from Gs in the tissue. M1

CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful

CC for screening an agent capable of modulating GCA preferably in an

CC inflammation in a tissue; M4 is useful for detecting an inflammation

CC (especially chronic) in a tissue, an allergic response in a subject,

CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.

CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,

CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult

CC respiratory distress syndrome, inflammatory bowel disease, Crohn's

CC disease, ulcerative colitis, periodontal disease; also bacterial

CC infection, viral infection, parasitic infection, protozoal infection,

CC fungal infection and M5 is useful for treating one of the above

CC conditions. The present sequence represents a gene differentially

CC expressed in granulocytes. Note: the sequence data for this patent did

CC not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;

Query Match 99.8%; Score 1387.8; DB 6; Length 1391;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1389; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGCGGAGACAGACAGTTCGAGCCTGGGTGCTGCTCAGTCTGTGGGGGAGTA 60

Db 1 GGGGAGCGGAGACAGACAGTTCGAGCCTGGGTGCTGCTCAGTCTGTGGGGGAGTA 60

Qy 61 GTAGGTGCTCAAAAATACACAGCCCGATGGGAGCCACTGGTCTGAAGTCTAAGGGG 120

Db 61 GTAGGTGCTCAAAAATACACAGCCCGATGGGAGCCACTGGTCTGAAGTCTAAGGGG 120

Qy 121 GCGCCCAAGAAACACCCAGCGGCTTGGAAATGGAATCTGAACACAGCCCGGACAGAAGCT 180

Db 121 GCGCCCAAGAAACACCCAGCGGCTTGGAAATGGAATCTGAACACAGCCCGGACAGAAGCT 180

Qy 181 TGAAGGTCTCTCTCCCGAGGAGAGGCCCTCGGACAGTGTGGCTGTCTTCCCTCC 240

Db 181 TGAAGGTCTCTCTCTCCCGAGGAGAGGCCCTCGGACAGTGTGGCTGTCTTCCCTCC 240

Qy 241 AACGGCTCCTCTCTCTCCCGCTGTCGGATCCAGGATGAGGGATTTTCGGTGCCAG 300

Db 241 AACGGCTCCTCTCTCTCCCGCTGTCGGATCCAGGATGAGGGATTTTCGGTGCCAG 300

Qy 301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGTT 360

Db 301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGTT 360

Qy 361 CTGGGAGCCAGAAATTTAGATTCTGCTCTGAATCTCAGGCTGGTGTTCCTCAATAAG 420

Db 361 CTGGGAGCCAGAAATTTAGATTCTGCTCTGAATCTCAGGCTGGTGTTCCTCAATAAG 420

Qy 421 GTGGGAGCATGTGTTCAGAGGAGAGTACCTCGAGGGAGCTTTAGCTGGCACTTGGAT 480

Db 421 GTGGGAGCATGTGTTCAGAGGAGAGTACCTCGAGGGAGCTTTAGCTGGCACTTGGAT 480

Qy 481 GGGAGAGCCCTCGTCTTAATGAGAGGAGGATATCTGTGAAGGAAACAGACAGGAGACAC 540

Db 481 GGGAGAGCCCTCGTCTTAATGAGAGGAGGATATCTGTGAAGGAAACAGACAGGAGACAC 540

Qy 541 CTGTGAGAGAGGCTCTTCACTGTGAGTCTGAGTCTAATGGTGAACCCAGCCGGGAGGA 600

Db 541 CTGTGAGAGAGGCTCTTCACTGTGAGTCTAATGGTGAACCCAGCCGGGAGGA 600

Qy 601 GATCCCGTCCACACTTCTCTCTGAGCTTCAGCCCGAGGCTTCCCGACACACCGGCTTG 660

Db 601 GATCCCGTCCACACTTCTCTCTGAGCTTCAGCCCGAGGCTTCCCGACACACCGGCTTG 660





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QY 301 GCAATGACAGGATGGAAGGAGACCAAGTCCAACTACCGAGTCGGTGTCTTACCAGATT 360
Db 301 GCAATGACAGGATGGAAGGAGACCAAGTCCAACTACCGAGTCGGTGTCTTACCAGATT 360
QY 361 CCTGGGAAGCCAGAAATTTGTAGATTCTTCCCTCTGAACTCAGCGTCGGTGTTCCTCAATAAG 420
Db 361 CCTGGGAAGCCAGAAATTTGTAGATTCTTCCCTCTGAACTCAGCGTCGGTGTTCCTCAATAAG 420
QY 421 GTGGGACATGTGTGTGTCAGAGGAAGCTACCTCTCAGGGACTCTTAGCTGGCACTTTGGAT 480
Db 421 GTGGGACATGTGTGTGTCAGAGGAAGCTACCTCTCAGGGACTCTTAGCTGGCACTTTGGAT 480
QY 481 GGAAGCCCTGTGTCTTAATGAGAGGAGTATCTGTGAAGAAACAGACCAGAGACAC 540
Db 481 GGAAGCCCTGTGTCTTAATGAGAGGAGTATCTGTGAAGAAACAGACCAGAGACAC 540
QY 541 CCTGAGACAGGCTCTTCACTGTCAGTCGAGCTAATGTGTGACCCAGCCAGCCGGGAGGA 600
Db 541 CCTGAGACAGGCTCTTCACTGTCAGTCGAGCTAATGTGTGACCCAGCCAGCCGGGAGGA 600
QY 601 GATCCCGCTCCCACTTCTCTGTAGCTTCCAGCCAGGCTTCCCGACACCGGGCTTG 660
Db 601 GATCCCGCTCCCACTTCTCTGTAGCTTCCAGCCAGGCTTCCCGACACCGGGCTTG 660
QY 661 CGCACAGCCCCATCAGCCCCCTGTCTGGAGCTGTGCTCTGGAGAGGTCCTCAATTG 720
Db 661 CGCACAGCCCCATCAGCCCCCTGTCTGGAGCTGTGCTCTGGAGAGGTCCTCAATTG 720
QY 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGGTGGACCTGAACCTGACCTGTGA 780
Db 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGGTGGACCTGAACCTGACCTGTGA 780
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGGATGGTGTGCCCTTGGCCCTT 840
Db 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGGATGGTGTGCCCTTGGCCCTT 840
QY 841 CCCCCAGCCCTGTGTGATCTCTCTGATAGATAGGCTCTCAGACAGGGAACCTACAG 900
Db 841 CCCCCAGCCCTGTGTGATCTCTCTGATAGATAGGCTCTCAGACAGGGAACCTACAG 900
QY 901 TGTGTGGCCACCCATTCAGCCAGCGGCCCCAGGAAAGCCGTCTCAGCATCAGCATC 960
Db 901 TGTGTGGCCACCCATTCAGCCAGCGGCCCCAGGAAAGCCGTCTCAGCATCAGCATC 960
QY 961 ATCGAACCCAGCGGAGGAGGGCCCAACTGCAAGGCTCTGTGGAGGATCAGGGCTGGAACT 1020
Db 961 ATCGAACCCAGCGGAGGAGGGCCCAACTGCAAGGCTCTGTGGAGGATCAGGGCTGGAACT 1020
QY 1021 CTAGCCCTGGCCCTGGGATCTCTGGAGGCTCTGGGACAGCCGCTGTCTCATTTGGGTC 1080
Db 1021 CTAGCCCTGGCCCTGGGATCTCTGGAGGCTCTGGGACAGCCGCTGTCTCATTTGGGTC 1080
QY 1081 ATCTTGTGCAAGCGGCAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db 1081 ATCTTGTGCAAGCGGCAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 GAAGAGGAGGAGGCTGAGAACTGATCAGTCGAGGAACTCTGAGCGAGCGAGAGTAGT 1200
Db 1141 GAAGAGGAGGAGGCTGAGAACTGATCAGTCGAGGAACTCTGAGCGAGCGAGAGTAGT 1200
QY 1201 ACTGAGGAGGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
Db 1201 ACTGAGGAGGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
QY 1261 CTTGAGACTGTTTGGCCCTCAGACCACTCTCTCTGTATATCTCTCTCTCTCTCTATAAC 1320
Db 1261 CTTGAGACTGTTTGGCCCTCAGACCACTCTCTCTGTATATCTCTCTCTCTCTCTATAAC 1320
QY 1321 CCACCTTGCCAGCTTCTTCTTCAACCCAGAGGCCCCCAATGATGATTAACACCTGA 1380
Db 1321 CCACCTTGCCAGCTTCTTCTTCAACCCAGAGGCCCCCAATGATGATTAACACCTGA 1380
QY 1381 CACATCTTGA 1391
```

Db 1381 CACATCTTGA 1391

#### RESULT 6

AD59952 standard; DNA; 1391 BP.

AD59952;

18-DEC-2003 (first entry)

Human RAGE (receptor for advanced glycation end product) DNA.

Transgenic mouse; transgenic; nerve tissue specific promoter; nootropic; receptor for advanced glycation end product; RAGE; neurological disorder; Alzheimer's disease; amnesia; amyotrophic lateral sclerosis; neuroleptic; brain injury; cerebral senility; degenerative disorder; Down's syndrome; chronic peripheral neuropathy; cognitive disability; memory dysfunction; electric shock; Guillain-Barre syndrome; head trauma; mental retardation; Huntington's disease; learning disability; dyslexia; Tourette's syndrome; neuromuscular disorder; Parkinson's disease; myasthenia gravis; dementia; Pick's disease; human; gene; ds.

Homo sapiens.

Location/Qualifiers

1..1215

/tag= a

/product= "Human RAGE protein"

/note= "No start codon"

/partial

polyA\_signal

1368..1373

/tag= b

US6563015-B1.

13-MAY-2003.

14-AUG-2000; 2000US-00638649.

14-AUG-2000; 2000US-00638649.

(UYCO ) UNIV COLUMBIA NEW YORK.

Stern DM, Schmidt AM, Yan SD;

WPI; 2003-687217/65.

P-PSDB; AAE39510.

Transgenic mouse whose genome contain recombinant deoxyribonucleic acid sequence, comprises nerve tissue specific promoter encoding human receptor for advanced glycation end products, and mutant human amyloid precursor protein.

Disclosure; Col 6-7; 40pp; English.

The invention relates to a transgenic mouse whose genome contain a recombinant DNA sequence, comprising a nerve tissue specific promoter operatively linked to a DNA sequence, which encodes human receptor for advanced glycation end products (RAGE), and a mutant human amyloid precursor protein hAPP695, hAPP751, and hAPP770 bearing mutations linked to familial Alzheimer's disease in humans. The transgenic animal is used for evaluation of the potential therapeutic effect of an agent for treating Alzheimer's disease in a human. It is useful for screening of compounds, which would be useful in the treatment of neurological disorders in humans, e.g. amnesia, amyotrophic lateral sclerosis, a brain injury, cerebral senility, chronic peripheral neuropathy, a cognitive disability, a degenerative disorder associated with learning, Down's syndrome, dyslexia, electric shock induced amnesia or amnesia, Guillain-Barre syndrome, head trauma, Huntington's disease, a learning disability, a memory deficiency, memory loss, a mental illness, mental retardation, memory or cognitive dysfunction, multi-infarct dementia and senile

CC	dementia, myasthenia gravis, a neuromuscular disorder, Parkinson's
CC	disease, Pick's disease, a reduction in spatial memory retention,
CC	senility, or Tourette's syndrome. The present sequence is human RAGE DNA
XX	
SQ	Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;
	Query Match 99.8%; Score 1387.8; DB 10; Length 1391;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 1389; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 GGGGACGCGGACACAGCAGTTGGAGCTCGGCTGCTGCTCCTCAGTCTGTGGGGGACGTA 60
DB	1 GGGGACGCGGACACAGCAGTTGGAGCTCGGCTGCTGCTCCTCAGTCTGTGGGGGACGTA 60
QY	61 GTAGTGTCTCAAAACATCAGCCCGGATTGGGAGCCACTGGTGTGAAGTGAAGGG 120
DB	61 GTAGTGTCTCAAAACATCAGCCCGGATTGGGAGCCACTGGTGTGAAGTGAAGGG 120
QY	121 GCGCCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCCCGGACAGAAAGCT 180
DB	121 GCGCCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCCCGGACAGAAAGCT 180
QY	181 TGAAGGTCTGTCTCCCAAGGAGGAGCCCTCGGACAGTGTGCTGTCTCTTCCC 240
DB	181 TGAAGGTCTGTCTCCCAAGGAGGAGCCCTCGGACAGTGTGCTGTCTCTTCCC 240
QY	241 AACGGTCTCTCTCTCCGCTGTCGGATCCAGGATGAGGGATTTCCGGTGCAGG 300
DB	241 AACGGTCTCTCTCTCCGCTGTCGGATCCAGGATGAGGGATTTCCGGTGCAGG 300
QY	301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATT 360
DB	301 GCATGAACAGGATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATT 360
QY	361 CTGGGAAGCCGAAATTTAGATTCTGCTCTGAACTCACTCAGCGCTGGTGTCCCAATAAG 420
DB	361 CTGGGAAGCCGAAATTTAGATTCTGCTCTGAACTCACTCAGCGCTGGTGTCCCAATAAG 420
QY	421 GTGGGACATGTGTGTCAGAGGGAAGCTACCTGACGGGACTCTTAGCTGGCACTTGGAT 480
DB	421 GTGGGACATGTGTGTCAGAGGGAAGCTACCTGACGGGACTCTTAGCTGGCACTTGGAT 480
QY	481 GGGAAACCCCTGTGCTTAATGAGAAGGAGTATCTGTGAAGGAAACAGACCCAGGAGACAC 540
DB	481 GGGAAACCCCTGTGCTTAATGAGAAGGAGTATCTGTGAAGGAAACAGACCCAGGAGACAC 540
QY	541 CTGAGACAGGGCTCTTTCACATGTCAGTGTGAGCTAATGTGACCCACCCGCGGGAGGA 600
DB	541 CTGAGACAGGGCTCTTTCACATGTCAGTGTGAGCTAATGTGACCCACCCGCGGGAGGA 600
QY	601 GATCCCGTCCCACTTCTCTGCTAGCTTCAGCCAGGCTTCCCGACACACCGGCGCTTG 660
DB	601 GATCCCGTCCCACTTCTCTGCTAGCTTCAGCCAGGCTTCCCGACACACCGGCGCTTG 660
QY	661 CGCACAGCCCTTCCAGCCCTGTCTGGAGCTGTGCTCTGGAGGAGGTCCAATTG 720
DB	661 CGCACAGCCCTTCCAGCCCTGTCTGGAGCTGTGCTCTGGAGGAGGTCCAATTG 720
QY	721 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTGTGGTGGAAACCGTAACCCCTGACCTGAA 780
DB	721 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTGTGGTGGAAACCGTAACCCCTGACCTGAA 780
QY	781 GTCCTTGGCCAGCCCTCTCTCAAAATCCACTGATGAAGTGTGCTGCTTGGCCCTT 840
DB	781 GTCCTTGGCCAGCCCTCTCTCAAAATCCACTGATGAAGTGTGCTGCTTGGCCCTT 840
QY	841 CCCCCAGCCCTGTGTGATCTCTCTCTGATAGGCGCTCAGGACCCAGGAACTTACAGC 900
DB	841 CCCCCAGCCCTGTGTGATCTCTCTCTGATAGGCGCTCAGGACCCAGGAACTTACAGC 900
QY	901 TGTGTGGCCACCCATTCCAGCCACGGGCCCGGAGAAAGCGTCTGTACGATCAGCATC 960
DB	901 TGTGTGGCCACCCATTCCAGCCACGGGCCCGGAGAAAGCGTCTGTACGATCAGCATC 960

RESULT 7

ADG32021  
ID ADG32021 standard; DNA; 1391 BP.

XX ADG32021;  
XX AC  
XX DT 26-FEB-2004 (first entry)  
XX DE

Human DNA homologue of the lung-specific RAGE protein SeqID49.

human; tissue specific; targeted delivery; therapeutic complex; epilepsy;  
schizophrenia; bipolar disorder; Parkinson's disease; bacterial;  
fungal infection; asthma; cystic fibrosis; pulmonary oedema; diabetes;  
pancreatitis; endocrine tumour; pancreatic cancer; infarction;  
coronary heart disease; arrhythmia; neurotropic; neuroprotective;  
anti-parkinsonian; cerebroprotective; cytostatic; antibacterial;  
fungicidal; antiasthmatic; immunosuppressive; gene; ds.

OS Homo sapiens.

XX WO2003084469-A2.

XX 16-OCT-2003.

XX 31-MAR-2003; 2003WO-US010195.

XX 01-APR-2002; 2002US-0369452P.

XX (UTAH-) UTAH VENTURES II LP.

XX Roben PW, Stevens AC;

XX WPI; 2003-804234/75.

DR P-PSDB; ADG32004.

XX New brain-specific, heart-specific, lung-specific, and pancreas-specific  
therapeutic complexes, useful for treating or alleviating diseases that  
affect the brain, heart, lungs, or pancreas.

PS	XX	Example 4; SEQ ID NO 49; 127pp; English.	
CC	CC	This invention relates to novel tissue specific endothelial membrane proteins. Specifically, it relates to the targeted delivery of therapeutics to defined organs, tissues or cells using, for example, brain-, heart-, lung- or pancreas-specific complexes. Furthermore, these complexes can be used in smaller amounts than in conventional treatment such that there is reduced chance of associated toxicity and side effects. The present invention describes this therapeutic complex as comprising a ligand that binds to a tissue-specific luminally expressed protein, a therapeutic moiety and linker. As such, the therapeutic complexes are useful for treating or alleviating diseases that affect the brain (e.g. epilepsy, schizophrenia, bipolar disorder and Parkinson's disease), the lungs (e.g. bacterial or fungal infections, asthma, cystic fibrosis and pulmonary oedema), the pancreas (e.g. diabetes, pancreatitis, endocrine tumour and pancreatic cancer) or the heart (e.g. infarction, coronary heart disease and arrhythmia). Accordingly, these compositions exhibit neurotropic, neuroprotective, antiparkinsonian, cerebroprotective, cytostatic, antibacterial, fungicidal, antitachmic and immunosuppressive activities. This polynucleotide is the DNA sequence encoding a human homologue of a lung-specific luminally expressed protein, used in a therapeutic complex of the invention.	
XX	XX	Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;	
QY	QY	Query Match 99.8%; Score 1387.8; DB 10; Length 1391;	
DB	DB	Best Local Similarity 99.9%; Pred. No. 0;	
QY	QY	Matches 1399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
DB	DB	1 GGGGACGCGGAACAGCAGTGTGAGCTTGGCTGGTCTGGTCTCAGTCTGTGGGGGAGTA 60	661 CGCACAGCCCCCATCCAGCCCCCGTGTCTGGAGCCTGTGCTCTGGAGAGGTCCAATTG 720
QY	QY	1 GGGGACGCGGAACAGCAGTGTGAGCTTGGCTGGTCTCAGTCTGTGGGGGAGTA 60	661 CGCACAGCCCCCATCCAGCCCCCGTGTCTGGAGCCTGTGCTCTGGAGAGGTCCAATTG 720
DB	DB	61 GTAGTGTCTCAAAACATCAGCCCGGATTTGGGAGCCACTGGTGTGAAGTCTAAGGGG 120	721 GTGGTGGAGCCAGAGGTGGAGCAGTAGTCTCCTGGTGGAAACCGTAACCCCTGACCTGTGAA 780
QY	QY	61 GTAGTGTCTCAAAACATCAGCCCGGATTTGGGAGCCACTGGTGTGAAGTCTAAGGGG 120	721 GTGGTGGAGCCAGAGGTGGAGCAGTAGTCTCCTGGTGGAAACCGTAACCCCTGACCTGTGAA 780
DB	DB	121 GCGCCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCCCGGACAGAAGCT 180	781 GTCCCTGGCCAGCCCTCTCCTCAAAATCCACTGGATGAAGGATGGTGTGCCCTTGGCCCTT 840
QY	QY	121 GCGCCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCCCGGACAGAAGCT 180	781 GTCCCTGGCCAGCCCTCTCCTCAAAATCCACTGGATGAAGGATGGTGTGCCCTTGGCCCTT 840
DB	DB	181 TGGAGGTCTGTCTCCAGGAGAGAGCCCTCGGACAGTGTGCTGTCTCTCC 240	841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCCTCAGGACAGGGAACCTACAGC 900
QY	QY	181 TGGAGGTCTGTCTCCAGGAGAGAGCCCTCGGACAGTGTGCTGTCTCTCC 240	841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCCTCAGGACAGGGAACCTACAGC 900
DB	DB	241 AACGGTCTCTCTCTCCGCTGTGGATCCAGATGAGGGGATTTTCGGTCCAG 300	901 TGTGTGGCCACCATTTCCAGCCACGCGGCCCACTGGTGTGGAGGATCGAGCATCAGCATC 960
QY	QY	241 AACGGTCTCTCTCTCCGCTGTGGATCCAGATGAGGGGATTTTCGGTCCAG 300	901 TGTGTGGCCACCATTTCCAGCCACGCGGCCCACTGGTGTGGAGGATCGAGCATCAGCATC 960
DB	DB	301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTACCAAGATT 360	961 ATCGAACACAGGCGAGGAGGGGGCCAACTGAGGCTCTGTGGAGGATCAGGGCTGGGAAT 1020
QY	QY	301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTACCAAGATT 360	961 ATCGAACACAGGCGAGGAGGGGGCCAACTGAGGCTCTGTGGAGGATCAGGGCTGGGAAT 1020
DB	DB	361 CTGGAAGCAGCAAAATTGATATTCTGCTCTGAACTCACTACCGCTGGTGTCCCAATAAG 420	1021 CTAGCCCTGGCCCTGGGGATCTCTGGAGGCTTGGGACAGCCGCCCTGTCTATTGGGGTC 1080
QY	QY	361 CTGGAAGCAGCAAAATTGATATTCTGCTCTGAACTCACTACCGCTGGTGTCCCAATAAG 420	1021 CTAGCCCTGGCCCTGGGGATCTCTGGAGGCTTGGGACAGCCGCCCTGTCTATTGGGGTC 1080
DB	DB	421 GTGGGACATGTGTCTCAGAGGAAGTACCTCCGAGGGACTTTAGCTGGCACTTGGAT 480	1081 ATCTTGTGCAAGCGGCAACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY	QY	421 GTGGGACATGTGTCTCAGAGGAAGTACCTCCGAGGGACTTTAGCTGGCACTTGGAT 480	1081 ATCTTGTGCAAGCGGCAACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB	DB	481 GGGAGCCCTGTGTCTAATGAGAGGGAGTATCTGTGAAGGAAACAGACAGGAGACAC 540	1141 GAAGAGGAGGAGCTGCAGAACTGAATCAGTGGAGGAACTTGAAGGAGGAGGAGGAGTGT 1200
QY	QY	481 GGGAGCCCTGTGTCTAATGAGAGGGAGTATCTGTGAAGGAAACAGACAGGAGACAC 540	1141 GAAGAGGAGGAGCTGCAGAACTGAATCAGTGGAGGAACTTGAAGGAGGAGGAGTGT 1200
DB	DB	541 CTGAGACAGGGCTCTTCACTGCACTGCACTCGAGTAAATGGTACCCAGCCCGGGAGGA 600	1201 ACTGAGGAGGCTTGAAGGGGCCCAACAGAGATCCCAATCATCAGTCTCTTTCTTTTTC 1260
QY	QY	541 CTGAGACAGGGCTCTTCACTGCACTGCACTCGAGTAAATGGTACCCAGCCCGGGAGGA 600	1201 ACTGAGGAGGCTTGAAGGGGCCCAACAGAGATCCCAATCATCAGTCTCTTTCTTTTTC 1260
DB	DB	601 GATCCCGTCCCACTTCTCTGTAGCTTCCAGCCAGGGCTTCCCGACACCGGGCTTG 660	1261 CTTGAACTGTCTGGCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACC 1320
QY	QY	601 GATCCCGTCCCACTTCTCTGTAGCTTCCAGCCAGGGCTTCCCGACACCGGGCTTG 660	1261 CTTGAACTGTCTGGCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACC 1320
DB	DB		1321 CCACCTTGGCAAGCTTTCTTTTACACACAGAGCCCCCAATGATGATTAACACCTGA 1380
			1321 CCACCTTGGCAAGCTTTCTTTTACACACAGAGCCCCCAATGATGATTAACACCTGA 1380
			1381 CACATCTTGCA 1391
			1381 CACATCTTGCA 1391
			RESULT 8
			AAH57444
			ID AAH57444 standard; cDNA; 1582 BP.
			XX AAH57444;
			AC AAH57444;
			XX 10-SEP-2001 (first entry)
			XX Human lung cell specific cDNA sequence SEQ ID NO:284.
			DE Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
			XX liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
			XX metabolic disease; developmental disease; cytostatic; immunomodulatory;
			XX neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
			OS Homo sapiens.
			XX WO200132927-A2.
			XX 10-MAY-2001.
			PD



KW amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;  
 KW chronic inflammatory disease; osteoarthritis; irritable bowel disease;  
 KW multiple sclerosis; psoriasis; ss.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1436  
 FT /\*tag= a  
 FT /product= "RAGE"  
 XX  
 PN WO2004016229-A2.  
 XX  
 XX 26-FEB-2004.  
 PD  
 XX  
 PF 18-AUG-2003; 2003WO-US025996.  
 XX  
 XX 16-AUG-2002; 2002US-0404205P.  
 PR  
 XX (AMHP ) WYETH.  
 PA  
 XX Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FM;  
 PI Feldmann M, Foxwell BJM, Feldman JL;  
 PI  
 XX WPI; 2004-192067/18.  
 DR P-PSDB; ADK00129.  
 DR  
 XX New fusion protein comprising a Receptor for Advanced Glycation End  
 PT Product Ligand Binding Element (RAGE-LBE) and an immunoglobulin element,  
 PT useful for preparing a composition for treating e.g., Alzheimer's  
 PT disease.  
 PT  
 XX Disclosure; SEQ ID NO 44; 100pp; English.  
 PS  
 XX The present invention relates to a new fusion protein comprises a  
 CC Receptor for Advanced Glycation End Product Ligand Binding Element (RAGE-  
 CC LBE) and an immunoglobulin element. The fusion protein is useful for  
 CC preparing a composition for treating RAGE-associated disorder such as  
 CC amyloidosis, cancer, Crohn's disease, diabetes, complications of  
 CC diabetes, prion-related disorders, vasculitis, nephropathies,  
 CC retinopathies and/or neuropathies; Alzheimer's disease, chronic  
 CC inflammatory disease e.g., rheumatoid arthritis, osteoarthritis,  
 CC irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute  
 CC inflammatory disease e.g., sepsis, or cardiovascular disease, e.g.,  
 CC atherosclerosis or restenosis. The present sequence represents human RAGE  
 CC protein encoding sequence.  
 XX  
 SQ Sequence 1436 BP; 340 A; 411 C; 422 G; 263 T; 0 U; 0 Other;

Query Match 98.7%; Score 1373; DB 12; Length 1436;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 3 GGAGCGGGAACAGCAGTGGAGCCCTGGGTGCTGCTCAGTCTGTGGGGGCACTAGT 62  
 DB 22 GGAGCGGGAACAGCAGTGGAGCCCTGGGTGCTGCTCAGTCTGTGGGGGCACTAGT 81  
 QY 63 AGGTGCTCAAAACATCACAGCCCGGATGGCGAGCCACTGGTCTCAAGTGTAAAGGGGC 122  
 DB 82 AGGTGCTCAAAACATCACAGCCCGGATGGCGAGCCACTGGTCTCAAGTGTAAAGGGGC 141  
 QY 123 CCCCAAGAAACACCCAGCGGTGGAATGGAACCTGAACACAGGCGGACAGAGCTTG 182  
 DB 142 CCCCAAGAAACACCCAGCGGTGGAATGGAACCTGAACACAGGCGGACAGAGCTTG 201  
 QY 183 GAAGGTCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGCTGTGTCTTCCCAA 242  
 DB 202 GAAGGTCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGCTGTGTCTTCCCAA 261  
 QY 243 CGGCTCCCTTCTTCCGCTGTCCGATCCAGGATGAGGGGATTTCCGGTCCAGGC 302  
 DB 262 CGGCTCCCTTCTTCCGCTGTCCGATCCAGGATGAGGGGATTTCCGGTCCAGGC 321

QY 303 AATGAACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACCAGATTCC 362  
 DB 322 AATGAACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACCAGATTCC 381  
 QY 363 TGGGAAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTACGGCTGGTGTCCCAATAGGT 422  
 DB 382 TGGGAAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTACGGCTGGTGTCCCAATAGGT 441  
 QY 423 GGGGACATGTGTGTCAGAGGGAAGCTACCTCGCAGGAGCTCTTTAGCTGGCACTTGGATGG 482  
 DB 442 GGGGACATGTGTGTCAGAGGGAAGCTACCTCGCAGGAGCTCTTTAGCTGGCACTTGGATGG 501  
 QY 483 GAAAGCCCTGGTGCCTTAATGAGAAAGGAGTATCTGTGAAGGAACAGACAGGAGACACC 542  
 DB 502 GAAAGCCCTGGTGCCTTAATGAGAAAGGAGTATCTGTGAAGGAACAGACAGGAGACACC 561  
 QY 543 TGAGACAGGGCTCTTTCACACTGCGAGTGGAGCTTAATGTTGACCCAGCCCGGGGAGAGA 602  
 DB 562 TGAGACAGGGCTCTTTCACACTGCGAGTGGAGCTTAATGTTGACCCAGCCCGGGGAGAGA 621  
 QY 603 TCCCCGTCCACCTTCTCTGTAGCTTTCAGCCCGAGCCCTTCCCGGACACCGGGCCTTGGC 662  
 DB 622 TCCCCGTCCACCTTCTCTGTAGCTTTCAGCCCGAGCCCTTCCCGGACACCGGGCCTTGGC 681  
 QY 663 CACAGCCCCCATCCAGCCCGGTGTCTGGAGCCTGTGCCTCTCTGGAGAGGTCCAAATGGT 722  
 DB 682 CACAGCCCCCATCCAGCCCGGTGTCTGGAGCCTGTGCCTCTCTGGAGAGGTCCAAATGGT 741  
 QY 723 GGTGGAGCAGAAAGGTGGAGCAGTACTCTCTGTGTGAACCGTAAACCTGTGAGT 782  
 DB 742 GGTGGAGCAGAAAGGTGGAGCAGTACTCTCTGTGTGAACCGTAAACCTGTGAGT 801  
 QY 783 CCTGCCCCAGCCCTCTCTCAATCACTGGATGAAGATGGTGTGCCCCCTTGCCTTCC 842  
 DB 802 CCTGCCCCAGCCCTCTCTCAATCACTGGATGAAGATGGTGTGCCCCCTTGCCTTCC 861  
 QY 843 CCCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGGCCTCAGGACCCAGGGAACCTACAGCTG 902  
 DB 862 CCCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGGCCTCAGGACCCAGGGAACCTACAGCTG 921  
 QY 903 TGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAACCGTGTCTGAGCATCAGCATCAT 962  
 DB 922 TGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAACCGTGTCTGAGCATCAGCATCAT 981  
 QY 963 CGAACCCAGCGAGGAGGGGCCAACTCGAGCTCTGTGGAGGATCAGGGCTGGGAACTCT 1022  
 DB 982 CGAACCCAGCGAGGAGGGGCCAACTCGAGCTCTGTGGAGGATCAGGGCTGGGAACTCT 1041  
 QY 1023 AGCCCTGGCCCTTGGGGATCTCTGGAGCCCTTGGGACAGCCGCCCTGCTCATTTGGGGTTCAT 1082  
 DB 1042 AGCCCTGGCCCTTGGGGATCTCTGGAGCCCTTGGGACAGCCGCCCTGCTCATTTGGGGTTCAT 1101  
 QY 1083 CTTTGTGCAAAAGCGCGCAACGCGGAGGAGAGAGAGAGGCCCCAGAAAACAGGAGGA 1142  
 DB 1102 CTTTGTGCAAAAGCGCGCAACGCGGAGGAGAGAGAGAGGCCCCAGAAAACAGGAGGA 1161  
 QY 1143 AGAGGAGGAGCGTGCAGAACTGAATCAGTCGGAGGAACCTGAGGCGAGGAGTAGTATAC 1202  
 DB 1162 AGAGGAGGAGCGTGCAGAACTGAATCAGTCGGAGGAACCTGAGGCGAGGAGTAGTATAC 1221  
 QY 1203 TGGAGGGCCTTGGAGGGGCCACAGACAGATCCCATCCATCAGCTCCCTTTTCTTTTCCC 1262  
 DB 1222 TGGAGGGCCTTGGAGGGGCCACAGACAGATCCCATCCATCAGCTCCCTTTTCTTTTCCC 1281  
 QY 1263 TTGAATCTGTCTGGCCCTCAGACCAACTCTCTCTGTATATCTCTCTCTCTGTATAACCCC 1322  
 DB 1282 TTGAATCTGTCTGGCCCTCAGACCAACTCTCTCTGTATATCTCTCTCTCTGTATAACCCC 1341  
 QY 1323 ACCTTGCCCAAGCTTTCTCTTACAACAGAGCCCCCAGCAATGATGATTAAACACCTTGACA 1382  
 DB 1342 ACCTTGCCCAAGCTTTCTCTTACAACAGAG-CCCCCAGCAATGATGATTAAACACCTTGACA 1400

QY 1383 CATCT 1387  
Db 1401 CATCT 1405

RESULT 10  
ABQ99598  
ID ABQ99598 standard; cDNA; 1463 BP.  
XX  
AC ABQ99598;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Human coding sequence SEQ ID 331.  
XX  
XX Human; expressed sequence tag; EST; chromosome 6p21.3;  
KW haematopoietic disorder; central nervous system disease; viral infection;  
KW peripheral nervous system disease; non-healing wound; infectious disease;  
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;  
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;  
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;  
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;  
KW immunostimulant; cerebroprotective; gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200259260-A2.  
XX  
XX 01-AUG-2002.  
XX  
XX 16-NOV-2001; 2001WO-US042950.  
XX  
XX 17-NOV-2000; 2000US-00714936.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;  
XX Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
XX WPI; 2002-590824/63.  
XX N-PSDB; ABP65012.  
XX  
XX New isolated polynucleotide, useful in research, diagnostic or  
XX therapeutic methods, e.g. preventing or treating disorders involving  
XX aberrant protein expression or biological activity.  
XX  
XX Claim 1; SEQ ID NO 331; 394pp; English.  
XX  
XX The present invention relates to novel human coding sequences (ABQ99268-  
XX ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in  
XX therapeutic, diagnostic and research methods. The polynucleotides may be  
XX used in the field of molecular biology as hybridisation probes, primers  
XX for PCR, for chromosome and gene mapping, for the recombinant production  
XX of protein, or in generation of anti-sense DNA or RNA. The  
XX polynucleotides are useful in diagnostics as expressed sequence tags  
XX (ESTs) for identifying expressed genes or for physical mapping of the  
XX human genome. The proteins may be used as molecular weight markers, or as  
XX nutritional sources or supplements. The proteins may be used to maintain  
XX and expand cell population in a totipotent or pluripotent state.  
XX useful for re-engineering damaged or diseased tissues, transplantation,  
XX manufacture of bio-pharmaceuticals or the development of bio-sensors. The  
XX polynucleotides and proteins are useful for preventing, treating or  
XX ameliorating disorders involving aberrant protein expression or  
XX biological activity, e.g. haematopoietic disorders, central/peripheral  
XX nervous system diseases, mechanical and traumatic disorders, non-healing  
XX wounds, immune deficiencies and disorders, infectious diseases caused by  
XX viral, bacterial or fungal infection, autoimmune disorders, allergic  
XX reactions and conditions, coagulation disorders, or cancer. The  
XX polynucleotide sequences of the invention were assembled from ESTs  
XX isolated mainly by sequencing by hybridisation, and in some cases,  
XX sequences obtained from one or more public databases. Note: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1463 BP; 332 A; 420 C; 443 G; 268 T; 0 U; 0 Other;  
Query Match 95.7%; Score 1331; DB 6; Length 1463;  
Best Local Similarity 96.7%; Pred. No. 0;  
Matches 1389; Conservative 0; Mismatches 0; Indels 48; Gaps 1;  
QY 3 GGAGCCGGGAACAGCAGATTGGAGCCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTAGT 62  
Db 27 GGCAGCCGGGAACAGCAGATTGGAGCCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTAGT 86  
QY 63 AGGTGCTCAAAACATCACAGCCCGATTGGCGAGCCACTGGTGTCTGAAGTAAAGGGGC 122  
Db 87 AGGTGCTCAAAACATCACAGCCCGATTGGCGAGCCACTGGTGTCTGAAGTAAAGGGGC 146  
QY 123 CCCAAGAAACACCCAGCCGCTGGATGGAACCTGAACACAGGCGCGACAGAGCTTG 182  
Db 147 CCCAAGAAACACCCAGCCGCTGGATGGAACCTGAACACAGGCGCGACAGAGCTTG 206  
QY 183 GAAGGTCTCTCTCTCCAGGAGGAGGCCCTCGGACAGTGTGGTCTGCTCTCTCCCAA 242  
Db 207 GAAGGTCTCTCTCTCCAGGAGGAGGCCCTCGGACAGTGTGGTCTGCTCTCTCCCAA 266  
QY 243 CGGCTCCCTCTCTCTCCGCTGTCTGGATCCAGATGAGGGGATTTCCGCTGCCAGGC 302  
Db 267 CGGCTCCCTCTCTCTCCGCTGTCTGGATCCAGATGAGGGGATTTCCGCTGCCAGGC 326  
QY 303 AATGACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAATCC 362  
Db 327 AATGACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAATCC 386  
QY 363 TGGGAAGCCAGAAATTTAGATTCTGCTCTCTGAACTCACGGTGTGTCTCCAAATA 418  
Db 387 TGGGAAGCCAGAAATTTAGATTCTGCTCTCTGAACTCACGGTGTGTCTCCAAATA 446  
QY 419 -----AGTGGGACATGTGT 434  
Db 447 AGTGGGAAGAAAGCAGGAGAAAGTAGAAAACGGCCCTGTGAACAGGAGGTGGGACATGT 506  
QY 435 GTGAGGGAAGCTACCTCGCAGGAGCTTTAGCTGGCACTTGGATGGGAAGCCCTGT 494  
Db 507 GTGAGGGAAGCTACCTCGCAGGAGCTTTAGCTGGCACTTGGATGGGAAGCCCTGT 566  
QY 495 GCCTAATGAGAGGAGGATCTGTGAAGGAACAGACACAGGAGACACCTTGACAGGGCT 554  
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QY 555 CTTTCACTGCACTGCGAGCTTAATGTTGACCCAGCCCGGGGAGGAGATCCCGTCCCAC 614  
Db 627 CTTTCACTGCACTGCGAGCTTAATGTTGACCCAGCCCGGGGAGGAGATCCCGTCCCAC 686  
QY 615 CTTTCTCTGTAGCTTTCAGCCAGGCTTTCCCGGACACCGGGCTTTGCGCACAGGCCCAT 674  
Db 687 CTTTCTCTGTAGCTTTCAGCCAGGCTTTCCCGGACACCGGGCTTTGCGCACAGGCCCAT 746  
QY 675 CCAGCCCGCTGTCTGGGAGCCTGTGCTCTTGGAGGAGTCCAATTGGTGGAGCCAGA 734  
Db 747 CCAGCCCGCTGTCTGGGAGCCTGTGCTCTTGGAGGAGTCCAATTGGTGGAGCCAGA 806  
QY 735 AGGTGAGCAGTAGCTCTGTGGGAACCGTAACCTGACCTGTGAAGTCCCTGCCAGCC 794  
Db 807 AGGTGAGCAGTAGCTCTGTGGGAACCGTAACCTGACCTGTGAAGTCCCTGCCAGCC 866  
QY 795 CTCTCTCAATCCACTGATGAAGGATGTGTGCTGCTTCCCTTCCCTCCAGGCCCTGT 854  
Db 867 CTCTCTCAATCCACTGATGAAGGATGTGTGCTGCTTCCCTTCCCTCCAGGCCCTGT 926  
QY 855 GCTGATCTCTCTGAGATAGGCGCTCAGGACACAGGGAACCTACAGTGTGTGGCCACCA 914  
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QY 915 TTCCAGCCACCGGGCCCCAGGAAGCCGTGCTGTACGATCAGCATCATCGACAGGCCA 974





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QY 371 CAGAAATTTCTAGATTTCTGCTCTGAACTCACGGCTGGTGTCCCAATAAGGTGGGACAT 430
Db 505 CAGAAATTTCTAGATTTCTGCTCTGAACTCACGGCTGGTGTCCCAATAAGGTGGGACAT 564
QY 431 GTGTGTCTAGAGGAAGCTACCTCTGCAGGAGCTCTTAGCTGGCACTTGGATGGGAAGCCCC 490
Db 565 GTGTGTCTAGAGGAAGCTACCTCTGCAGGAGCTCTTAGCTGGCACTTGGATGGGAAGCCCC 624
QY 491 TGGTGCCTTAATGAGAGGAGTATCTGTGAAGACAGACACAGGAGACACCTGTGAGACAG 550
Db 625 TGGTGCCTTAATGAGAGGAGTATCTGTGAAGAAACAGACACAGGAGACACCTGTGAGACAG 684
QY 551 GGCTCTTTCACACTGACAGTCCGAGCTAATGGTGAACCCAGCCGGGGAGGAGATCCCGCTC 610
Db 685 GGCTCTTTCACACTGACAGTCCGAGCTAATGGTGAACCCAGCCGGGGAGGAGATCCCGCTC 744
QY 611 CCACCTTCTCTGTAGCTTACGCCAGCCAGGCTTCCCGCAACACGGGGCTTGGCGACAGCCC 670
Db 745 CCACCTTCTCTGTAGCTTACGCCAGCCAGGCTTCCCGCAACACGGGGCTTGGCGACAGCCC 804
QY 671 CCATCCAGCCCGGTGTCG-----GAGCCTGTGCTCTGAGGAGGTCCAAATG 720
Db 805 CCATCCAGCCCGGTGTCGCGGTGAGCATGAGCCCTGTGCTCTGAGGAGGTCCAAATG 864
QY 721 GTGGTGGAGCCAGAAAGGTGGAGCAGTAGCTCTGTGGTGAACCGTAAACCTGTGTGAA 780
Db 865 GTGGTGGAGCCAGAAAGGTGGAGCAGTAGCTCTGTGGTGAACCGTAAACCTGTGTGAA 924
QY 781 GTCCCTGCCAGCCCTCTCTCTAAATCCATCTGATGAAGATGGTGTGCCCTTGGCCCTT 840
Db 925 GTCCCTGCCAGCCCTCTCTCTAAATCCATCTGATGAAGATGGTGTGCCCTTGGCCCTT 984
QY 841 CCCCCAGCCCTGTGTGATCTCTCTGATAGTAGGCTCAGGACAGGAACTTACACG 900
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QY 961 ATCGAAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Db 1105 ATCGAAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1164
QY 1021 CTAGCCCTGGCCCTGGGATCTCTGGAGGCTTGGGACAGCCGCTGTCTCATTTGGGTC 1080
Db 1165 CTAGCCCTGGCCCTGGGATCTCTGGAGGCTTGGGACAGCCGCTGTCTCATTTGGGTC 1224
QY 1081 ATCTTGTGCAAGGCGGCAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db 1225 ATCTTGTGCAAGGCGGCAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1284
QY 1141 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Db 1285 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1344
QY 1201 ACTGGAGGCTTGGGGGCCCCACACAGATCCCATCCATCAGCTCCCTTTCTTTTC 1260
Db 1345 ACTGGAGGCTTGGGGGCCCCACACAGATCCCATCCATCAGCTCCCTTTCTTTTC 1404
QY 1261 CCTTGAATGTTCTGGCCCTCAGACCAACTCTCTCTGTATATCTCTCTCTCTGTATAACC 1320
Db 1405 CCTTGAATGTTCTGGCCCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATAACC 1464
QY 1321 CCACCTTGGCAGCTTCTTCTTACAAACAGAGGCCCCCCTCAATGATGATTAACACCTGA 1380
Db 1465 CCACCTTGGCAGCTTCTTCTTACAAACAGAGGCCCCCCTCAATGATGATTAACACCTGA 1524
QY 1381 CACATCTTGA 1391
Db 1525 CACATCTCGA 1535
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RESULT 12
ACC59907
ID ACC59907 standard; cDNA; 1678 BP.
XX
AC ACC59907;
XX
DT 07-JUL-2003 (first entry)
XX
XX Human REMAP-20 encoding cDNA SEQ ID NO:56.
XX
XX Human; receptor and membrane-associated protein; REMAP; cytostatic;
XX anti-atherosclerotic; anticonvulsant; nootropic; neuroprotective;
XX cerbroprotective; anti-HIV; anti-allergic; anti-inflammatory; cancer;
XX thymolametic; gene therapy; cell proliferative disorder; atherosclerosis;
XX neurological disorder; epilepsy; Huntington's disease; stroke; AIDS;
XX immune disorder; inflammatory disorder; allergy; developmental disorder;
XX hypothyroidism; Cushing's syndrome; infection; gene; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 108..1373
XX /*tag= a
XX /*product= "REMAP-20"
XX
XX WO2003025130-A2.
XX
XX 27-MAR-2003.
XX
XX 12-SEP-2002; 2002WO-US029220.
XX
XX 14-SEP-2001; 2001US-0322157P.
XX 28-SEP-2001; 2001US-0326029P.
XX 05-OCT-2001; 2001US-0327380P.
XX 12-OCT-2001; 2001US-0329198P.
XX 19-OCT-2001; 2001US-0343742P.
XX 02-NOV-2001; 2001US-0343906P.
XX 02-NOV-2001; 2001US-0343980P.
XX 16-NOV-2001; 2001US-0332426P.
XX 13-MAR-2002; 2002US-0364339P.
XX 15-MAR-2002; 2002US-0364494P.
XX 29-MAR-2002; 2002US-0369248P.
XX
XX (INCV-) INCYTE GENOMICS INC.
XX
XX Warren BA, Gietzen KJ, Lal PG, Xu Y, Tran UK, Lee S;
XX Borowsky ML, Becha SD, Sanjanwala MM, Thangavelu K, Tang YT;
XX Honchell CD, Yue H, Elliott VS, Richardson TW, Azimzai Y, Chawla NK;
XX Baughn MR, Lu DAM, Nguyen DB, Kalafus DP, Sapperstein SK;
XX Ramkumar J, Lehr-Mason PM, Griffin JA, Duggan BM, Lee SY;
XX Zeburjadian Y, Hafalia AJA, Gururajan R, Swarnakar A, Lee EA;
XX Marquis JP, Khare R, Emerling BM, Jiang X, Jackson AA;
XX
XX WPI; 2003-354596/33.
XX
XX P-PSDB; ABR43188.
XX
XX New human receptors and membrane-associated proteins (REMAP), useful for
XX diagnosing, treating and preventing diseases or conditions associated
XX with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or
XX infections.
XX
XX Claim 5; Page 230-231; 241pp; English.
XX
XX ACC59888 to ACC59923 encode the human receptor and membrane-associated
XX proteins given in ABR43169 to ABR43204 and designated REMAP-1 to REMAP-36
XX (i). (I) have cytostatic, anti-atherosclerotic, anticonvulsant,
XX nootropic, neuroprotective, cerbroprotective, anti-HIV, anti-allergic,
XX anti-inflammatory and thymolametic activities, and can be used in gene
XX therapy. The REMAP polypeptides and polynucleotides are useful in
XX diagnosing, treating and preventing diseases or conditions associated
XX with the decreased expression or overexpression of REMAP, such as cell
XX proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
```

CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, CC allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) CC disorders, or infections. They are also useful in assessing the effects CC of exogenous compounds on the expression of nucleic acid and amino acid CC sequences of REMAP. The REMAPs or their fragments are useful in screening CC compounds for effectiveness as agonist or antagonist of the polypeptides, CC or in altering the expression of the target polynucleotide and compounds CC that specifically bind to or modulate the activity of the polypeptide XX  
SQ Sequence 1678 BP; 471 A; 438 C; 480 G; 289 T; 0 U; 0 Other;

Query Match 93.08; Score 1293.4; DB 9; Length 1678;  
Best Local Similarity 96.94; Pred. No. 0;  
Matches 1346; Conservative 0; Mismatches 1; Indels 42; Gaps 1;

QY 3 GGCAGCGCGAAGCAGCTTGGAGCTTGGGCTGCTGCTCAGTCTGTGGGGGCGAGTAGT 62  
DB 203 GGCAGCGCGAAGCAGCTTGGAGCTTGGGCTGCTGCTCAGTCTGTGGGGGCGAGTAGT 262

QY 63 AGTGTCTCAAAAATCAACAGCCCGGATTTGGCGAGCCACTGGTCTGAAAGTGAAGGGGC 122  
DB 263 AGTGTCTCAAAAATCAACAGCCCGGATTTGGCGAGCCACTGGTCTGAAAGTGAAGGGGC 322

QY 123 CCCAAGAACACCCAGCGCTGGATGGAATGGAATCAACAGCCCGGAGAGCTTG 182  
DB 323 CCCAAGAACACCCAGCGCTGGATGGAATGGAATCAACAGCTTGGAATGGAATCAACAGCTTG 358

QY 183 GAAGGCTCTGCTCTCCAGCGAGAGGCGCCCTGGGACAGTGGCTGCTGCTCTCCCAA 242  
DB 359 -----GGAGAGGCGCCCTGGGACAGTGGCTGCTGCTCTCCCAA 400

QY 243 CGGCTCCCTCTTCCGCTGTCGGGATCCAGGATGAGGGGATTTCCGGTGCCAGGC 302  
DB 401 CGGCTCCCTCTTCCGCTGTCGGGATCCAGGATGAGGGGATTTCCGGTGCCAGGC 460

QY 303 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGCTACAGATTC 362  
DB 461 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGCTACAGATTC 520

QY 363 TGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTCAGCGCTGGTGTCCCAATAAGGT 422  
DB 521 TGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTCAGCGCTGGTGTCCCAATAAGGT 580

QY 423 GGGACATGTGTCTCAGAGGAAGTACCCCTGAGGGACTCTTGTAGCTGGCCTTGGATGG 482  
DB 581 GGGACATGTGTCTCAGAGGAAGTACCCCTGAGGGACTCTTGTAGCTGGCCTTGGATGG 640

QY 483 GAAGCCCTGGTCCCTAATGAGAAGGGAGTATCTGTGAAGGAACAGACAGGAGACACC 542  
DB 641 GAAGCCCTGGTCCCTAATGAGAAGGGAGTATCTGTGAAGGAACAGACAGGAGACACC 700

QY 543 TGAGACAGGGCTCTTCACTCAGCTCGGAGCTAATGGTACCCAGCCCGGGGAGAGA 602  
DB 701 TGAGACAGGGCTCTTCACTCAGCTCGGAGCTAATGGTACCCAGCCCGGGGAGAGA 760

QY 603 TCCCGCTCCACCTCTCTCTGTAGCTTACGCCAGGCTTTCCCGGACAGCCGGGCTTTGG 662  
DB 761 TCCCGCTCCACCTCTCTCTGTAGCTTACGCCAGGCTTTCCCGGACAGCCGGGCTTTGG 820

QY 663 CACAGCCCTCCATCAGCCCGCTGTCTGGAGAGCTGTGCTCTGTGGAGAGTCCAATGGT 722  
DB 821 CACAGCCCTCCATCAGCCCGCTGTCTGGAGAGCTGTGCTCTGTGGAGAGTCCAATGGT 880

QY 723 GGTGGAGCCAGAGGTGGAGCTAGTCTCTGTGGAAACCGTAACCTGACCTGTCAAGT 782  
DB 881 GGTGGAGCCAGAGGTGGAGCTAGTCTCTGTGGAAACCGTAACCTGACCTGTCAAGT 940

QY 783 CCCTGCCAGCCCTCTCTCAAAATCAACTGGAATGAAGATGGTGTGCCCTTGGCCCTTCC 842  
DB 941 CCCTGCCAGCCCTCTCTCAAAATCAACTGGAATGAAGATGGTGTGCCCTTGGCCCTTCC 1000

QY 843 CCCAGCCCTGTGCTGATCTCTCTCAGATAGGGCTTCAGGACCAAGGAACTTACAGCTG 902  
DB 902

DB 1001 CCCAGCCCTGTGCTGATCTCTCTGAGATAGGGCTCTAGGACCAAGGAACTTACAGTG 1060  
QY 903 TGTGGCCACCCATTCCAGCCACGGGGCCCGAGGAAAGCCGTGCTGTGAGCATCAGCATCAT 962  
DB 1061 TGTGGCCACCCATTCCAGCCACGGGGCCCGAGGAAAGCCGTGCTGTGAGCATCAGCATCAT 1120  
QY 963 CGAACAGCGGAGGAGGGGCCAACTCAGAGCTCTGTGGAGGATCAGGGCTGGGAACTCT 1022  
DB 1121 CGAACAGCGGAGGAGGGGCCAACTCAGAGCTCTGTGGAGGATCAGGGCTGGGAACTCT 1180

QY 1023 AGCCCTGGCCCTGGGGATCTTGGGAGGCTTGGGAGCAGCGCCCTGCTCATTGGGGTCTAT 1082  
DB 1181 AGCCCTGGCCCTGGGGATCTTGGGAGGCTTGGGAGCAGCGCCCTGCTCATTGGGGTCTAT 1240

QY 1083 CTTTGTGGCAAAAGCGCGCAACGCCGAGGAGAGAGAGGCGCCCGAGAAACCCAGGAGGA 1142  
DB 1241 CTTTGTGGCAAAAGCGCGCAACGCCGAGGAGAGAGAGGCGCCCGAGAAACCCAGGAGGA 1300

QY 1143 AGAGGAGGAGCTGTGAGAACTGAATCAGTTCGAGGAACTCTGAGGAGGCGAGAGTAGTAC 1202  
DB 1301 AGAGGAGGAGCTGTGAGAACTGAATCAGTTCGAGGAACTCTGAGGAGGCGAGAGTAGTAC 1360

QY 1203 TGGAGGCGCTTGGGGGCGCCACAGACAGATCCCATCATCAGCTCCCTTTCTTTTCCC 1262  
DB 1361 TGGAGGCGCTTGGGGGCGCCACAGACAGATCCCATCATCAGCTCCCTTTCTTTTCCC 1420

QY 1263 TTGAAGCTGTTGGCCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACCCC 1322  
DB 1421 TTGAAGCTGTTGGCCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACCCC 1480

QY 1323 ACCTTGCCAAAGCTTTCTTCTAACCAAGGCGCCCAACCAATGATGATTAACACCTGACA 1382  
DB 1481 ACCTTGCCAAAGCTTTCTTCTAACCAAGGCGCCCAACCAATGATGATTAACACCTGACA 1540

QY 1383 CATCTTGA 1391  
DB 1541 CATCTTGA 1549

RESULT 13  
ADP19665  
ID ADP19665 standard; cDNA; 1329 BP.  
XX  
AC ADP19665;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human LP2005 encoding cDNA SEQ ID NO:11.  
XX  
KW human; LP2005; antidiabetic; neuroprotective; nootropic;  
KW antiinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;  
KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;  
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
KW systemic lupus erythematosus; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 46..1206  
FT /tag= b  
FT /product= "LP2005"  
FT /note= "the present sequence only seems to encodes amino  
FT acids 1 to 386 of the LP2005 protein"  
FT sig\_peptide 46..114  
FT /tag= a  
FT mat\_peptide 115..1203  
FT /tag= c  
XX  
PN WO2004044126-A2.  
XX 27-MAY-2004.  
XX

PF	05-NOV-2003; 2003WO-US032734.	QY	183	GAAGTCTCTCTCCAGGAGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAA	242
XX					
PR	14-NOV-2002; 2002US-0426253P.	Db	228	GAAGTCTCTCTCCAGGAGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAA	287
XX	(ELIL ) LILLY & CO ELI.				
PA	Na S, Perkins DR;	QY	243	CGGCTCCCTCTTCCGCTGTCCGATCAGAGTGGGGATTTCCGGTGCAGGC	302
XX					
PI	WPI; 2004-411705/38.	Db	288	CGGCTCCCTCTTCCGCTGTCCGATCAGAGTGGGGATTTCCGGTGCAGGC	347
DR	P-PSDB; ADP19666.	QY	303	RATGAACAGGAAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTACCAATCC	362
XX					
PT	New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or	Db	348	AATGAACAGGAAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTACCAATCC	407
PT	LP2003) for diagnosing or treating disorders associated with aberrant	QY	363	TGGGAAGCCAGAAAATTGTAGATTCTGCTCTGAACTCAGCGTGTGTTCCTAATAGT	422
PT	levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome	Db	408	TGGGAAGCCAGAAAATTGTAGATTCTGCTCTGAACTCAGCGTGTGTTCCTAATAGT	467
XX	identification.				
PS	Claim 1; SEQ ID NO 11; 11lpp; English.	QY	423	GGGACATGTGTGTGTCAGAGGGAAGTACCTGACGGGACTCTTAGCTGGCACTTGATGG	482
XX	The present sequence encodes human LP2005, which is used in the	Db	468	GGGACATGTGTGTGTCAGAGGGAAGTACCTGACGGGACTCTTAGCTGGCACTTGATGG	527
CC	exemplification of the present invention. The present invention	QY	483	GAAGCCCTGTGTGCTTAATGAGAGGAGTATCTGTGAAGAAACAGACAGGAGACACC	542
CC	describes: (1) an isolated nucleic acid (I) comprising DNA having at	Db	528	GAAGCCCTGTGTGCTTAATGAGAGGAGTATCTGTGAAGAAACAGACAGGAGACACC	587
CC	least 95% sequence identity to a polynucleotide selected from the group	QY	543	TGAGACAGGGCTCTTCACTGACGTCCGAGCTAATGTGTGACCCAGGCCCGGGAGGA	602
CC	consisting of: (a) a polynucleotide having a nucleotide sequence as shown	Db	588	TGAGACAGGGCTCTTCACTGACGTCCGAGCTAATGTGTGACCCAGGCCCGGGAGGA	647
CC	in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a	QY	603	TCCCGTCCACCTTCTCTGTAGCTTACGCCAGCCCTTCCCGACACCCGGGCTTGGG	662
CC	polypeptide or mature form of a polypeptide having the amino acid	Db	648	TCCCGTCCACCTTCTCTGTAGCTTACGCCAGCCCTTCCCGACACCCGGGCTTGGG	707
CC	sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide	QY	663	CACAGCCCATCCAGCCCGTGTCTGGAGGCTGTGCTCTGGAGGAGTCCAATTGTG	722
CC	fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide	Db	708	CACAGCCCATCCAGCCCGTGTCTGGAGGCTGTGCTCTGGAGGAGTCCAATTGTG	767
CC	having a nucleotide sequence which is complementary to the nucleotide	QY	723	GGTGGAGCCAGAAAGTGGAGCAGTAGTCTCTGGTGGAAACCGTAAACCTGTGAAGT	782
CC	sequence of a polynucleotide as in (a), (b) or (c); (2) a vector	Db	768	GGTGGAGCCAGAAAGTGGAGCAGTAGTCTCTGGTGGAAACCGTAAACCTGTGAAGT	827
CC	comprising (1); (3) a host cell comprising the vector; (4) producing an	QY	783	CCCTGCCAGCCCTCTCTCAATCCATGAGTGAAGTGTGTGCTTCCCTCCCTCC	842
CC	LP polypeptide; (5) an isolated polypeptide produced by the above method	Db	828	CCCTGCCAGCCCTCTCTCAATCCATGAGTGAAGTGTGTGCTTCCCTCCCTCC	887
CC	and comprising an amino acid sequence comprising about 95% sequence	QY	843	CCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGGACCAAGGAACTTACAGCTG	902
CC	identity to a sequence of amino acid residues comprising LP2001, LP2003,	Db	888	CCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGGACCAAGGAACTTACAGCTG	947
CC	LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric	QY	903	TGTGGCCACCCATTCCAGCCAGGGGCCCCAGGAAAGCCGTGTGTGATCAGCATCAT	962
CC	molecule comprising an LP polypeptide fused to a heterologous amino acid	Db	948	TGTGGCCACCCATTCCAGCCAGGGGCCCCAGGAAAGCCGTGTGTGATCAGCATCAT	1007
CC	sequence; (7) an antibody which specifically binds to an LP polypeptide	QY	963	CGAACAGCGGAGGAGGGGCCAACTGCAAGCTCTGTGGAGGATCAGGCTGGGACTCT	1022
CC	described above; (8) a composition (C) comprising a therapeutic amount of	Db	1008	CGAACAGCGGAGGAGGGGCCAACTGCAAGCTCTGTGGAGGATCAGGCTGGGAACTCT	1067
CC	an active agent selected from an LP polypeptide, an agonist to an LP	QY	1023	AGCCCTGGCCCTGGGGATCTCTGGAGGCTCTGGGACAGCGCCCTCTCATTTGGGGTCTAT	1082
CC	polypeptide, an antagonist to an LP polypeptide, an LP polypeptide	Db	1068	AGCCCTGGCCCTGGGGATCTCTGGAGGCTCTGGGACAGCGCCCTCTCATTTGGGGTCTAT	1127
CC	antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a	QY	1083	CTTTGTGGCAAAAGCGCGCAACGCCGAGGAGAAAGGCCCCAGAGAAAACAGAGAGA	1142
CC	polynucleotide in combination with a pharmaceutical carrier; and (9)	Db	1128	CTTTGTGGCAAAAGCGCGCAACGCCGAGGAGAAAGGCCCCAGAGAAAACAGAGAGA	1183
CC	diagnosing or treating a mammal suffering from a disease, condition or	QY	1143	AGAGGAGGAGCGTGCAGAACTGAATCAGTCGGAGGAACTCTGAGGAGGAGGAGTAGTAC	1202
CC	disorder associated with aberrant levels of an LP-polypeptide. (C) has	Db	1184	AGAGGAGGAGCGTGCAGAACTGAATCAGTCGGAGGAACTCTGAGGAGGAGGAGTAGTAC	1243
CC	antidiabetic, neuroprotective, nootropic, antiinflammatory,	QY	1203	TGAGGGGCTTGGAGGGGCCCAACAGACAGATCCCATCAGCTCCCTTTTCTTTTCCC	1262
CC	antirheumatic, antiarthritic, vulnary, cytostatic, immunosuppressive,	Db	1244	TGAGGGGCTTGGAGGGGCCCAACAGACAGATCCCATCAGCTCCCTTTTCTTTTCCC	1303
CC	nephrotropic and dermatological activities, and can be used in gene				
CC	therapy. The compositions (C) and methods are useful for diagnosing or				
CC	treating disorders associated with aberrant levels of an LP polypeptide,				
CC	such as diabetes and its complications, Alzheimer's disease,				
CC	inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple				
CC	sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They				
CC	may also be used for chromosome identification. The LP polypeptide can				
CC	also be used in manufacturing a medicament for the treatment of the above				
CC	mentioned diseases, conditions or disorders associated with aberrant				
CC	levels of the LP polypeptide.				
XX					
SQ	Sequence 1329 BP; 289 A; 379 C; 424 G; 235 T; 0 U; 2 Other;				
	Query Match 91.0%; Score 1265.6; DB 12; Length 1329;				
	Best Local Similarity 99.6%; Pred. No. 0;				
	Matches 1279; Conservative 1; Mismatches 0; Indels 4; Gaps 1;				
QY	3 GGAGCCGGACAGCAGTGGACCTGGGCTGTGGTCTCAGTCTGTGGGGGCGAGTAGT	62			
Db	48 GGAGCCGGAAACAGCAGTGGAGCCCTGGGCTGTGGTCTCAGTCTGTGGGGGCGAGTAGT	107			
QY	63 AGTGTCTCAAAACATCACACCCCGGATTTGGCGAGCCACTGGTGTCTGAAAGTGAAGGGGC	122			
Db	108 AGTGTCTCAAAACATCACACCCCGGATTTGGCGAGCCACTGGTGTCTGAAAGTGAAGGGGC	167			
QY	123 CCCCAAGAAACACCCAGCGGCTGGAAATGGAATCTGAACACAGGCGCGGACAGAGCTTG	192			
Db	168 CCCCAAGAAACACCCAGCGGCTGGAAATGGAATCTGAACACAGGCGCGGACAGAGCTTG	227			

QY 1263 TTGAACTGTTCTGGCCTCAGACCA 1286  
 Db 1304 TTGAACTGTTCTGGCCTCAGACCR 1327

RESULT 14  
 ADP19667  
 ID ADP19667 standard; cDNA; 1323 BP.  
 AC ADP19667;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human LP2006 encoding cDNA SEQ ID NO:13.  
 XX  
 KW human; LP2006; antidiabetic; neuroprotective; nootropic;  
 KW antiinflammatory; antirheumatic; antiarthritic; vulnery; cytosstatic;  
 KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;  
 KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
 KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
 KW systemic lupus erythematosus; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX

Key Location/Qualifiers  
 CDS 46..414  
 /\*tag= b  
 /product= "LP2006"  
 /note= "the present sequence only seems to encodes amino  
 acids 1 to 122 of the LP2006 protein"  
 sig\_peptide 46..114  
 /\*tag= a  
 mat\_peptide 115..411  
 /\*tag= c  
 WO2004044126-A2.  
 27-MAY-2004.  
 05-NOV-2003; 2003WO-US032734.  
 14-NOV-2002; 2002US-0426253P.  
 PR (ELIL ) LILLY & CO ELI.  
 PA Na S, Perkins DR;  
 PI WPI; 2004-411705/38.  
 XX P-PSDB; ADP19668.  
 DR  
 XX  
 PT New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or  
 PT LP2003) for diagnosing or treating disorders associated with aberrant  
 PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome  
 PT identification.  
 PT  
 XX  
 PS Claim 1; SEQ ID NO 13; 111pp; English.  
 XX  
 CC The present sequence encodes human LP2006, which is used in the  
 CC exemplification of the present invention. The present invention  
 CC describes: (1) an isolated nucleic acid (1) comprising DNA having at  
 CC least 95% sequence identity to a polynucleotide selected from the group  
 CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown  
 CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a  
 CC polypeptide or mature form of a polypeptide having the amino acid  
 CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide  
 CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide  
 CC having a nucleotide sequence which is complementary to the nucleotide  
 CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector  
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an  
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method  
 CC and comprising an amino acid sequence comprising about 95% sequence  
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,  
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric

molecule comprising an LP polypeptide fused to a heterologous amino acid  
 sequence; (7) an antibody which specifically binds to an LP polypeptide  
 described above; (8) a composition (C) comprising a therapeutic amount of  
 an active agent selected from an LP polypeptide, an agonist to an LP  
 polypeptide, an antagonist to an LP polypeptide, an LP polypeptide  
 antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a  
 polynucleotide in combination with a pharmaceutical carrier; and (9)  
 diagnosing or treating a mammal suffering from a disease, condition or  
 disorder associated with aberrant levels of an LP-polypeptide. (C) has  
 antidiabetic, neuroprotective, nootropic, antiinflammatory,  
 antirheumatic, antiarthritic, vulnery, cytosstatic, immunosuppressive,  
 nephrotropic and dermatological activities, and can be used in gene  
 therapy. The compositions (C) and methods are useful for diagnosing or  
 treating disorders associated with aberrant levels of an LP polypeptide,  
 such as diabetes and its complications, Alzheimer's disease,  
 inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple  
 sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
 may also be used for chromosome identification. The LP polypeptide can  
 also be used in manufacturing a medicament for the treatment of the above  
 -mentioned diseases, conditions or disorders associated with aberrant  
 levels of the LP polypeptide.  
 CC  
 XX  
 SQ Sequence 1323 BP; 292 A; 375 C; 423 G; 231 T; 0 U; 2 Other;

Query Match 89.9%; Score 1250; DB 12; Length 1323;  
 Best Local Similarity 99.0%; Pred. No.:0;  
 Matches 1273; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 3 GGCAGCCGGAACAGCAGTGGAGCTGGGTGCTGCTCAGTCTCTGGGGGGCAGTAGT 62  
 Db 48 GGCAGCCGGAACAGCAGTGGAGCTGGGTGCTGCTCAGTCTCTGGGGGGCAGTAGT 107  
 QY 63 AGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGC 122  
 Db 108 AGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGC 167  
 QY 123 CCCCAGAAACCCACCCAGCGGCTGGAATGGAACCTGAACACAGGCCGACAGAGCTTG 182  
 Db 168 CCCCAGAAACCCACCCAGCGGCTGGAATGGAACCTGAACACAGGCCGACAGAGCTTG 227  
 QY 183 GAAGTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCTCTCCCA 242  
 Db 228 GAAGTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCTCTCCCA 287  
 QY 243 CGGCTCCCTCTTCTCCCGGCTGTGGGATCCAGATGAGGGGATTTCCGGTCCAGGC 302  
 Db 288 CGGCTCCCTCTTCTCCCGGCTGTGGGATCCAGATGAGGGGATTTCCGGTCCAGGC 347  
 QY 303 ATGAAACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTACAGATTCC 362  
 Db 348 AATGAACAGGAATGGAAGAGACCAAGTCCAACTACCGA-----AGATTCC 394  
 QY 363 TGGGAGCCAGAAATGTAGATTCTGCCCTCTGAACCTCAGGGCTGGTGTCCCAATAAGGT 422  
 Db 395 TGGGAGCCAGAAATGTAGATTCTGCCCTCTGAACCTCAGGGCTGGTGTCCCAATAAGGT 454  
 QY 423 GGGGACATGTGTCTCAGAGGGAAGCTACCTTCAGGGGACTCTTAGCTGGCACTTGGATGG 482  
 Db 455 GGGGACATGTGTCTCAGAGGGAAGCTACCTTCAGGGGACTCTTAGCTGGCACTTGGATGG 514  
 QY 483 GAAGCCCTCTGGTCTTAATGAGAGGAGTATCTGTGAAGGAACACACAGCAGGACACCC 542  
 Db 515 GAAGCCCTCTGGTCTTAATGAGAGGAGTATCTGTGAAGGAACACACAGCAGGACACCC 574  
 QY 543 TGAGCAGGGCTCTTACACTGCAGTCCGAGGCTAATGGTGACCCAGCCCGGGGAGGAGA 602  
 Db 575 TGAGCAGGGCTCTTACACTGCAGTCCGAGGCTAATGGTGACCCAGCCCGGGGAGGAGA 634  
 QY 603 TCCCCCTCCACCTCTCTCTGTAGTTCAGCCAGGCTTCCCGGACACCGGGCTTGGC 662  
 Db 635 TCCCCCTCCACCTCTCTCTGTAGTTCAGCCAGGCTTCCCGGACACCGGGCTTGGC 694  
 QY 663 CACAGCCCCCATCCAGCCCCCGTGTCTGGAGGCTGTGCTCTGGAGGAGGTCCAATTGGT 722

Db 695 CACAGCCCCCATCCAGCCCCGCTCTGGAGAGCCCTGTGCCTCTGGAGAGGTCCAAATGGT 754  
Qy 723 GGTGGAGCCAGAGGTGGAGCAGTAGCTCTGTGTGGAACCGTAACCTGACCTGTGAAGT 782  
Db 755 GGTGGAGCCAGAGGTGGAGCAGTAGCTCTGTGTGGAACCGTAACCTGACCTGTGAAGT 814  
Qy 783 CCTGTGCCAGCCCTCTCCTCAAAATCCACTGATGAAGAGTGGTGTGCCCTTGGCCCTTCC 842  
Db 815 CCTGTGCCAGCCCTCTCCTCAAAATCCACTGATGAAGAGTGGTGTGCCCTTGGCCCTTCC 874  
Qy 843 CCCAGCCCTGTCTGATCCTCCCTGAGATPAGGSCCTCAGGACCAAGGAACTTACAGCTG 902  
Db 875 CCCAGCCCTGTCTGATCCTCCCTGAGATPAGGSCCTCAGGACCAAGGAACTTACAGCTG 934  
Qy 903 TGTGGCCACCCATTCAGCACAGGCCCCCAGGAAAGCCGTGCTGTGAGCATCAGCATCAT 962  
Db 935 TGTGGCCACCCATTCAGCACAGGCCCCCAGGAAAGCCGTGCTGTGAGCATCAGCATCAT 994  
Qy 963 CGAACAGGCGAGGAGGGGCAACTGCAGGCTCTGTGGAGGATCAGGCTGGGAACTCT 1022  
Db 995 CGAACAGGCGAGGAGGGGCAACTGCAGGCTCTGTGGAGGATCAGGCTGGGAACTCT 1054  
Qy 1023 AGCCCTGGCCCTGGGATCTGGAGGCTCTGGAGGCTTGGGACAGCGCCCTCTCATTTGGGCTCAT 1082  
Db 1055 AGCCCTGGCCCTGGGATCTGGAGGCTCTGGAGGCTTGGGACAGCGCCCTCTCATTTGGGCTCAT 1114  
Qy 1083 CTGTGTGCAAGGCGGCAAGCCCGAGAGAGGAGAGAGGCCCCAGAAACCCAGAGGA 1142  
Db 1115 CTGTGTGCAAGGCGGCAAGCCCGAGAGAGGAGAGAGGCCCCAGAAACCCAGAGGA 1174  
Qy 1143 AGAGGAGGAGCGTGCAGAACTGAATCAGTCCGAGGAACTTGAGGAGGCGAGAGTAGTAC 1202  
Db 1175 AGAGGAGGAGCGTGCAGAACTGAATCAGTCCGAGGAACTTGAGGAGGCGAGAGTAGTAC 1234  
Qy 1203 TGGAGGCGCTTGAGGGGCCCCACAGACAGATCCCATCAGCTCCCTTTCTTTTCCC 1262  
Db 1235 TGGAGGCGCTTGAGGGGCCCCACAGACAGATCCCATCAGCTCCCTTTCTTTTCCC 1294  
Qy 1263 TTGAATGTCTGGCTCAGACCAAC 1288  
Db 1295 TTGAATGTCTGGCTCAGACCAAC 1320

RESULT 15

ADG33024  
ID ADG33024 standard; DNA; 1268 BP.

XX AC ADG33024;

XX XX 26-FEB-2004 (first entry)

XX DE Human DNA differentially expressed in patients with SLE SeqID348.

XX KW human; ds; autoimmune; chronic inflammatory disease; SLE;  
KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;  
KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;  
KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;  
KW diverticulitis; primary biliary sclerosis.

XX OS Homo sapiens.

XX PN WO2003090694-A2.

XX XX 06-NOV-2003.

XX PF 24-APR-2003; 2003WO-US013015.

XX PR 24-APR-2002; 2002US-00131827.

XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX PI Wohlgemuth J, Fry K, Woodward R, Ly N;

XX WPI; 2003-877243/81.  
XX Diagnosing or monitoring autoimmune and chronic inflammatory diseases,  
PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative  
PT colitis, psoriasis and asthma by detecting the expression level of one or  
PT more genes.  
XX Claim 18; SEQ ID NO 348; 877pp; English.  
PS  
XX This invention relates to novel methods for diagnosing and monitoring  
CC autoimmune and chronic inflammatory diseases. Specifically, it refers to  
CC the identification of genes that have a clinical utility as diagnostic  
CC tools for the management of, in particular, patients with systemic lupus  
CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the  
CC present invention describes a method for determining the levels of  
CC multiple differentially expressed genes of a patient, in a concerted  
CC manner, in order to achieve an improved diagnostic assay with sensitivity  
CC and specificity for the disease in question. As such, these genes are  
CC useful for the diagnosis of various other inflammatory disorders  
CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,  
CC ankylosing spondylitis, ulcerative colitis, primary sclerosing  
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.  
CC This polynucleotide is a DNA sequence representing human mRNA that is  
CC differentially expressed in patients with SLE, used in an exemplification  
CC of the invention.

SQ Sequence 1268 BP; 280 A; 361 C; 410 G; 217 T; 0 U; 0 Other;

Query Match 89.3%; Score 1242; DB 10; Length 1268;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCACGCCGAACAGCAGTTGGAGCTGGGTGCTGCTCCTCAGTCTGTGGGGGCGAGTAGT 62  
Db 27 GGCACGCCGAACAGCAGTTGGAGCTGGGTGCTGCTCCTCAGTCTGTGGGGGCGAGTAGT 86  
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Qy	723	GGTGGAGCAGAAAGGTGGAGCAGTAGTCTCTGTGTGGAAACCGTAACCTTGACCTGTGAAGT	782
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1387.8	99.8	1391	4	US-09-638-648-4
3	1348.2	96.9	1405	4	US-08-755-235-3
4	1213	87.2	1215	4	US-09-949-016-5154
5	1018	73.2	1023	2	US-08-633-148-1
6	950.8	68.4	957	2	US-08-633-148-3
7	944.8	67.9	1426	4	US-09-638-649-2
8	944.8	67.9	1426	4	US-09-638-648-2
9	901.4	64.8	1438	4	US-08-755-235-1
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18	42.6	3.1	1614	4	US-09-616-289-45
19	41.4	3.0	247781	4	US-09-949-016-14193
20	41	2.9	169998	3	US-09-676-6108-24
21	41	2.9	197496	4	US-09-877-177A-10
22	40	2.9	601	4	US-09-949-016-178941
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24	39.6	2.8	561	4	US-09-702-705-72
25	39.6	2.8	561	4	US-09-736-457-72
26	39.6	2.8	561	4	US-09-614-124B-72
27	39.6	2.8	561	4	US-09-671-325-72

28	39.6	2.8	561	4	US-09-589-184-72	Sequence 72, Appl
29	39.6	2.8	561	4	US-09-588-824-72	Sequence 72, Appl
30	39.6	2.8	2539	2	US-08-432-016-1	Sequence 1, Appli
31	39.6	2.8	2539	2	US-08-684-594-1	Sequence 1, Appli
32	39.6	2.8	2539	4	US-09-023-655-1496	Sequence 1496, Ap
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41	39.2	2.8	6108	4	US-09-949-016-12213	Sequence 12213, A
42	38.4	2.8	22218	4	US-09-949-016-14240	Sequence 14240, A
43	38	2.7	1416	4	US-09-902-540-4687	Sequence 4687, Ap
44	38	2.7	3991	3	US-08-506-296B-3	Sequence 3, Appli
45	38	2.7	28558	4	US-09-902-540-1231	Sequence 1231, Ap

ALIGNMENTS

RESULT 1

US-09-638-649-4  
; Sequence 4, Application US/09638649  
; Patent No. 6563015  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND  
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND  
; FILE REFERENCE: 0575/62175  
; CURRENT APPLICATION NUMBER: US/09/638,649  
; CURRENT FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1391  
; TYPE: DNA  
; ORGANISM: Human  
US-09-638-649-4

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Best Local Similarity		99.9%;	Pred. No. 0;		
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				Indels	0;
				Gaps	0;
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DB	61	GTAGTGTCTCAAAACATCATCAGCCCGGATTCGGAGCCACTGGTCTGAAGTCTAAGGGG	120		
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DB	121	GGCCCCAAGAAACACCCAGCGGCTGGAACTGAAACTGAACACAGCCGCGACAGAGCT	180		
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DB	181	TGGAAGTCTCTGTCTCTCCAGGAGGAGGCCCTTCGGAGCAGTGTGGCTCGTGTCTTCCC	240		
QY	241	AACGGTCTCTCTCTCTCCGGCTGTGGGATTCAGGATGAGGGGATTTTCGGTCCGAG	300		
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RESULT 3
US-08-755-235-3
; Sequence 3, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Human
US-08-755-235-3

Query Match          96.9%;   Score 1348.2;   DB 4;   Length 1405;
Best Local Similarity 99.6%;   Pred. No. 0;
Matches 1383;   Conservative 0;   Mismatches 3;   Indels 3;   Gaps 3;

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Qy			
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Db			
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QY 121 G C C C C A G A A A C C A C C C C A G C G G C T G G A A T G G A A A C T G A A C A C A C A G C C C G G A C A G A G C T 180  
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Db 181 T G G A G G T C C T G T C T C C C C A G G A G A G A G C C C C T G G A C A G T G T G C T C G T G C T C C T T C C C 240  
QY 241 A A C G G T C C C C T C T C C T C C G G C T G T C G G A T C C A G G A T G A G G G A T T T T C C G G T G C C A G 300  
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QY 901 T G T G T G G C C A C C A T T C C A G C C A G C G G C C C C A G A A G C C G T C T C A G C A T C A G C A T C 960  
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RESULT 2

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; Sequence 351, Application US/10115635  
; Publication No. US20040137434A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Wang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and  
; FILE REFERENCE: 797CON  
; CURRENT APPLICATION NUMBER: US/10/115,635  
; CURRENT FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: 09/714,936  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 362  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 351  
; LENGTH: 1415  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(1239)  
US-10-115-635-351

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 603 TCCCTGCTCCACCTCTTCTGTAGCTTTCAGCCAGGCTTTCCTCCGACACCGGCTTGG 662  
Db 627 TCCCTGCTCCACCTCTTCTGTAGCTTTCAGCCAGGCTTTCCTCCGACACCGGCTTGG 686  
Qy 663 CACAGCCCTGCTGATCCTCCCTGAGATGAGGCTTTCCTCTGGAGAGTCCAAATGGT 722  
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Qy 783 CCTGCTCCAGCTCTCTCTCAATCACTGATGAAGATGGTGTGCTTCCCTTCCCTTCC 842  
Db 807 CCTGCTCCAGCTCTCTCTCAATCACTGATGAAGATGGTGTGCTTCCCTTCCCTTCC 866  
Qy 843 CCCCAGCTGTGCTGATCCTCCCTGAGATGAGGCTTTCAGGACAGGGAACCTTACAGCTG 902  
Db 867 CCCCAGCTGTGCTGATCCTCCCTGAGATGAGGCTTTCAGGACAGGGAACCTTACAGCTG 926  
Qy 903 TGTGGCCACCCATTCAGCCACCGGGCCCAAGAAAGCGTGTGTGAGCATCAGATCAT 962  
Db 927 TGTGGCCACCCATTCAGCCACCGGGCCCAAGAAAGCGTGTGTGAGCATCAGATCAT 986  
Qy 963 CGAACAGCGAGAGGGCCAACTGAGCTCTGTGGGAGGATCAGGCTGGGAACTCT 1022  
Db 987 CGAACAGCGAGAGGGCCAACTGAGCTCTGTGGGAGGATCAGGCTGGGAACTCT 1046  
Qy 1023 AGCCCTGGCCCTGGGATCCTGGAGGCTTGGGACAGCGCCCTGCTCATTTGGGGTCA 1082  
Db 1047 AGCCCTGGCCCTGGGATCCTGGAGGCTTGGGACAGCGCCCTGCTCATTTGGGGTCA 1106  
Qy 1083 CTTGTGGCAAGCGCGCAACCGCCAGAGAGAGAGAGGCGCCCAAGAAACAGAGGA 1142  
Db 1107 CTTGTGGCAAGCGCGCAACCGCCAGAGAGAGAGAGGCGCCCAAGAAACAGAGGA 1166  
Qy 1143 AGAGGAGGAGCTGCAGAACTGAATCAGTCGGAGGAACCTTGGGAGGCGAGAGTAGTAC 1202  
Db 1167 AGAGGAGGAGCTGCAGAACTGAATCAGTCGGAGGAACCTTGGGAGGCGAGAGTAGTAC 1226  
Qy 1203 TGGAGGGCTTGAAGGGCCCAACAGACAGATCCCATCAGCTCCCTTTTCTTTTCCC 1262  
Db 1227 TGGAGGGCTTGAAGGGCCCAACAGACAGATCCCATCAGCTCCCTTTTCTTTTCCC 1286  
Qy 1263 TTGAACGTGTGCTGCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATATACCC 1322  
Db 1287 TTGAACGTGTGCTGCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATATACCC 1346  
Qy 1323 ACCTTGGCAGCTTCTTCTACACAGAGGCGCCCAACATGATGATTAACACCTGACA 1382  
Db 1347 ACCTTGGCAGCTTCTTCTTACACAGAGGCGCCCAACATGATGATTAACACCTGACA 1406

Qy 1383 CATCTTGCA 1391  
Db 1407 CATCTTGCA 1415

## RESULT 3

US-08-905-709-3  
; Sequence 3, Application US/08905709  
; Publication No. US20010039256A1  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David  
; APPLICANT: Schmidt, Ann M.  
; TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED  
; TITLE OF INVENTION: ATHEROSCLEROSIS USING (SRAE) SOLUBLE RECEPTOR FOR  
; TITLE OF INVENTION: ADVANCED GLYCATION ENDPRODUCTS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/905,709  
; FILING DATE: 05-AUG-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/52876  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0526  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1405 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-905-709-3

Query Match 96.9%; Score 1348.2; DB 8; Length 1405;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1383; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 GGGGAGCGCGGACAGCAGCTTGGAGCCTGGGTCTGCTCAGTCTGTGGGGGGCAGTA 60  
Db 1 GGGGAGCGCGGACAGCAGCTTGGAGCCTGGGTCTGCTCAGTCTGTGGGGGGCAGTA 60  
Qy 61 GTAGGTGCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGGTGTGAAGTGTAAAGGG 120  
Db 61 GTAGGTGCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGGTGTGAAGTGTAAAGGG 120  
Qy 121 GCGCCCAAGAAACACCCCGAGGGCTTGAATGGAACCTGAACACAGCCCGGACAGAGCT 180  
Db 121 GCGCCCAAGAAACACCCCGAGGGCTTGAATGGAACCTGAACACAGCCCGGACAGAGCT 180  
Qy 181 TGAAGGTCTGTCTCCCGAGGAGAGCCCTTGGGACAGTGTGCTGTGCTTCCC 240  
Db 181 TGAAGGTCTGTCTCCCGAGGAGAGCCCTTGGGACAGTGTGCTGTGCTTCCC 240  
Qy 241 AACGGCTCTCTTCTTCCCTGCTGCGGATTCAGGATGAGGGGATTTTCCGGTGCAG 300  
Db 241 AACGGCTCTCTTCTTCCCTGCTGCGGATTCAGGATGAGGGGATTTTCCGGTGCAG 300





QY 1020 TCTAGCCCTGCGCTTGGGATCTCTGGAGGCTTGGGACAGCCCTGCTGCTCAATTGGGGT 1079  
Db 1020 TCTAGCCCTGCGCTTGGGATCTCTGGAGGCTTGGGACAGCCCTGCTGCTCAATTGGGGT 1079  
QY 1080 CATCTTGGCAAGGGGGGCAACCCGAGGAGGAGAGAGAGGCCCCAGAAAACCAAGGA 1139  
Db 1080 CATCTTGGCAAGGGGGGCAACCCGAGGAGGAGAGAGAGG--AGGCCCCAGAAAACCAAGGA 1138  
QY 1140 GGAAGAGGAGGAGGCTGCAGAACTGAATCAGTGGGAGGAACTTGAGGAGGAGGAGTAG 1199  
Db 1139 GGAAGAGGAGGAGGCTGCAGAACTGAATCAGTGGGAGGAACTTGAGGAGGAGGAGTAG 1198  
QY 1200 TACTGGAGGCGCTTGGAGGGCCCAACAGACATCCCATCAGCTCCCTTTCTTTTTT 1259  
Db 1199 TACTGGAGGCGCTTGGAGGGGCCCAACAGACATCCCATCAGCTCCCTTTCTTTTTT 1258  
QY 1260 CCCTTGAACCTGCTGCGCTCAGACCACTCTCTCTGTATATCTCTCTCTGTATAAC 1319  
Db 1259 CCCTTGAACCTGCTGCGCTCAGACCACTCTCTCTGTATATCTCTCTCTGTATAAC 1318  
QY 1320 CCACCTTGGCAAGCTTTCTTACAAACAGAGAGGCCCCCAACAATGATTAACAACCTG 1379  
Db 1319 CCACCTTGGCAAGCTTTCTTACAAACAGAGAGGCCCCCAACAATGATTAACAACCTG 1378  
QY 1380 ACACATCTT 1388  
Db 1379 ACACATCTT 1387

## RESULT 6

US-10-115-635-352  
; Sequence 352, Application US/10115635  
; Publication No. US20040137434A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyang  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and  
; FILE OF INVENTION: Polypeptides  
; FILE REFERENCE: 797CON  
; CURRENT APPLICATION NUMBER: US/10/115,635  
; CURRENT FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: 09/714,936  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 362  
; SOFTWARE: pt FL genes Version 2.0  
; SEQ ID NO 352  
; LENGTH: 1463  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(1287)  
US-10-115-635-352

Query Match 95.7%; Score 1331; DB 18; Length 1463;  
Best Local Similarity 96.7%; Pred. No. 0;  
Matches 1389; Conservative 0; Mismatches 0; Indels 48; Gaps 1;

QY 3 GCAGCCGGAACAGAGTTGGAGCCCTGGGTGCTTCAGTCTGTGGGGGAGTAGT 62  
Db 27 GCAGCCGGAACAGAGTTGGAGCCCTGGGTGCTTCAGTCTGTGGGGGAGTAGT 86  
QY 63 AGGTGCTCAAAACATCACAGCCCGGATTTGGGAGCCACTGGTCTGAAAGTGAAGGGGCG 122

Db 87 AGGTGCTCAAAACATCACAGCCCGGATTTGGGAGCCACTGGTCTGAAAGTGAAGGGGCG 146  
QY 123 CCCAAGAAACCAACCCAGCGGCTGGAATGGAACCTGAACACAGGCCGACAGAGCTTG 182  
Db 147 CCCAAGAAACCAACCCAGCGGCTGGAATGGAACCTGAACACAGGCCGACAGAGCTTG 206  
QY 183 GAAGTCTCTGCTCTCCACGAGGAGGCGCTTGGGACAGTGTGGTCTGCTCTCTTCCCAA 242  
Db 207 GAAGTCTCTGCTCTCCACGAGGAGGCGCTTGGGACAGTGTGGTCTGCTCTCTTCCCAA 266  
QY 243 CGGCTCCCTCTCTCTCCGCTGTCGGGATCCAGATGAGGGGATTTTCCGGTGCACGCG 302  
Db 267 CGGCTCCCTCTCTCTCCGCTGTCGGGATCCAGATGAGGGGATTTTCCGGTGCACGCG 326  
QY 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTC 362  
Db 327 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTC 386  
QY 363 TGGGAAGCCAGAAATTTAGATTCTGCTCTCAACTCAGGCTGTGTTCCTCAATA--- 418  
Db 387 TGGGAAGCCAGAAATTTAGATTCTGCTCTCAACTCAGGCTGTGTTCCTCAATAAGGT 446  
QY 419 -----AGTGGGACATGTGT 434  
Db 447 AGTGAAGAAAGCAGGAGAGTAGAAACGGCCCTGTGAACAGGAGGTGGGACATGTGT 506  
QY 435 GTCAGAGGAGTACCTTCAGGAGACTTTAGCTGGGACACTTGGATGGGAGCCCTGGT 494  
Db 507 GTCAGAGGAGTACCTTCAGGAGACTTTAGCTGGGACACTTGGATGGGAGCCCTGGT 566  
QY 495 GCCTAATGAGAGGAGTATCTGCAAGGAAACAGACAGGAGACACCTTGAGACAGGCT 554  
Db 567 GCCTAATGAGAGGAGTATCTGCAAGGAAACAGACAGGAGACACCTTGAGACAGGCT 626  
QY 555 CTTCACTGCACTCGGAGCTAATGGTCAACCCAGCCCGGGAGGAGATCCCGTCCAC 614  
Db 627 CTTCACTGCACTCGGAGCTAATGGTCAACCCAGCCCGGGAGGAGATCCCGTCCAC 686  
QY 615 CTTCTCTGTAGCTTCAGCCAGGCTTCCCGGACACCGGGCTTGGCAGAGCCCTCAT 674  
Db 687 CTTCTCTGTAGCTTCAGCCAGGCTTCCCGGACACCGGGCTTGGCAGAGCCCTCAT 746  
QY 675 CCAGCCCGTGTCTGGGAGCTTGCCTCTGGAGAGGTCCAATTTGGTGGAGCCAGA 734  
Db 747 CCAGCCCGTGTCTGGGAGCTTGCCTCTGGAGAGGTCCAATTTGGTGGAGCCAGA 806  
QY 735 AGTGGAGCAGTAGCTCTGTGGAAACCGTAAACCTTGACCTGTGAAGTCCCTGCCAGCC 794  
Db 807 AGTGGAGCAGTAGCTCTGTGGAAACCGTAAACCTTGACCTGTGAAGTCCCTGCCAGCC 866  
QY 795 CTCTCTCAAAATCCAATGGAAGGATGGTGGCTTGGCCCTTCCCGCCAGCCCTGT 854  
Db 867 CTCTCTCAAAATCCAATGGAAGGATGGTGGCTTGGCCCTTCCCGCCAGCCCTGT 926  
QY 855 GCTGATCTCTCTGAGATPAGGCTCAGGACAGGGAACCTTACAGCTGTGTGGCCACCCA 914  
Db 927 GCTGATCTCTCTGAGATPAGGCTCAGGACAGGGAACCTTACAGCTGTGTGGCCACCCA 986  
QY 915 TTCCAGCCAGCGGCCCGGAGGAGGCGCTGTGTCAGCATCAGCATCATCGAACAGGCGA 974  
Db 987 TTCCAGCCAGCGGCCCGGAGGAGGCGCTGTGTCAGCATCAGCATCATCGAACAGGCGA 1046  
QY 975 GGAGGGGCCAACTGCAGGCTCTGTGGGAGGATCAGGCTGGGAACTCTAGCCCTGGCCCT 1034  
Db 1047 GGAGGGGCCAACTGCAGGCTCTGTGGGAGGATCAGGCTGGGAACTCTAGCCCTGGCCCT 1106  
QY 1035 GGGGATCTTGGGAGGCTTGGGAGCAGCGCCCTGCTCATTTGGGGTCACTTTGTGGCAAG 1094  
Db 1107 GGGGATCTTGGGAGGCTTGGGAGCAGCGCCCTGCTCATTTGGGGTCACTTTGTGGCAAG 1166  
QY 1095 GCGCAACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1154



QY 843 CCCAGCCCTGTGTGATCTCTCCCTGAGATAGGSCCTCAGGACCCAGGAACTTACAGCTG 902  
DB 845 CCCAGCCCTGTGTGATCTCTCCCTGAGATAGGSCCTCAGGACCCAGGAACTTACAGCTG 904  
QY 903 TGTGGCCACCATTCACAGCAGCGGCCCCAGGAAAGCCGTGTGTGATCATCATCATCAT 962  
DB 905 TGTGGCCACCATTCACAGCAGCGGCCCCAGGAAAGCCGTGTGTGATCATCATCATCAT 964  
QY 963 CGAACAGGCGAGGAGGCGCACTGACAGCTCTGTGGGAGGATCAGGCTGGGAATCT 1022  
DB 965 CGAACAGGCGAGGAGGCGCACTGACAGCTCTGTGGGAGGATCAGGCTGGGAATCT 1024  
QY 1023 AGCCCTGGCCCTGGGATCTCTGGGAGGCTTGGGACAGCGCCCTGTCTCATTTGGGTCTAT 1082  
DB 1025 AGCCCTGGCCCTGGGATCTCTGGGAGGCTTGGGACAGCGCCCTGTCTCATTTGGGTCTAT 1084  
QY 1083 CTTGTGCAAAAGCGGCAACCGCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1142  
DB 1085 CTTGTGCAAAAGCGGCAACCGCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1144  
QY 1143 AGAGGAGGCGTGCAGAACTGATCAGTCGAGGAGACCTGAGGCGAGGAGAGTAGTAC 1202  
DB 1145 AGAGGAGGCGTGCAGAACTGATCAGTCGAGGAGACCTGAGGCGAGGAGAGTAGTAC 1204  
QY 1203 TGGAGGCGCTTGA 1215  
DB 1205 TGGAGGCGCTTGA 1217

RESULT 8

US-10-309-290-97  
; Sequence 97, Application US/10309290  
; Publication No. US20040023241A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsbrook II, John P.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Chillakuru, Rajeev A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Gould-Rothberg, Bonnie E.  
; APPLICANT: Jeffers, Michael E.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Li, Li  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Murphey, Ryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Peyman, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Starling, Gary  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Voss, Edward Z.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-502A  
; CURRENT APPLICATION NUMBER: US/10/309,290  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/336,600  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,285  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/341,346  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/341,477

; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/341,540  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/342,592  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/344,297  
; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/344,903  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/373,288  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 60/380,981  
; PRIOR FILING DATE: 2002-05-15  
; Remaining prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: Curasequlst version 0.1  
; SEQ ID NO 97  
; LENGTH: 1226  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(1194)  
US-10-309-290-97

Query Match 82.4%; Score 1146.4; DB 17; Length 1226;  
Best Local Similarity 96.5%; Pred. No. 0;  
Matches 1199; Conservative 0; Mismatches 1; Indels 42; Gaps 1;

QY 3 GCAGCCGGAACAGCAGATTGGAGCTGGGTGCTGTGCTCAGTCTGTGGGGGCGAGTAGT 62  
DB 27 GCAGCCGGAACAGCAGATTGGAACTGGGTGCTGTGCTCAGTCTGTGGGGGCGAGTAGT 86  
QY 63 AGGTGCTCAAAACATCAGAGCCCGGATTTGGCGAGCACTGGTGTGAAGTGAAGGGGC 122  
DB 87 AGGTGCTCAAAACATCAGAGCCCGGATTTGGCGAGCACTGGTGTGAAGTGAAGGGGC 146  
QY 123 CCCCAAGAAACCCAGCCAGCGGCTGGAATGGAATCTGAACACAGGCGCGACAGAAGCTTG 182  
DB 147 CCCCAAGAAACCCAGCCAGCGGCTGGAATGGAATCTGGAATGGAATCTGGAATGGA 182  
QY 183 GAAGTCTGTCTCTCCAGGAGGAGGCGCCCTGGGACAGTGTGGTGTGCTTCCCAA 242  
DB 183 -----GGGAGGAGGCGCCCTGGGACAGTGTGGTGTGCTTCCCAA 224  
QY 243 CGGCTCCCTCTCTCCGCTGTGGATCCAGATCAGGAGGATTTCCGCTGCGAGC 302  
DB 225 CGGCTCCCTCTCTCCGCTGTGGATCCAGATCAGGAGGATTTCCGCTGCGAGC 284  
QY 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 362  
DB 285 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 344  
QY 363 TGGGAAGCCAGAAATTTAGATTCTGCTGTGAATCTACGCTGTGTTCCTCAATAGGT 422  
DB 345 TGGGAAGCCAGAAATTTAGATTCTGCTGTGAATCTACGCTGTGTTCCTCAATAGGT 404  
QY 423 GGGGACATGTGTCTCAGAGGAGGAGTACCTTCAGGAGGACTCTTAGCTGGCACTTGGATGG 482  
DB 405 GGGGACATGTGTCTCAGAGGAGGAGTACCTTCAGGAGGACTCTTAGCTGGCACTTGGATGG 464  
QY 483 GAAAGCCCTGTGTCTAATGAAAGGAGATCTGTGAAGGAAACAGACAGGAGACACCC 542  
DB 465 GAAAGCCCTGTGTCTAATGAAAGGAGATCTGTGAAGGAAACAGACAGGAGACACCC 524  
QY 543 TGAGACAGGCTCTTTTCACTGAGTCCGAGCTAATGTGACCCCGAGGAGGAGGAG 602  
DB 525 TGAGACAGGCTCTTTTCACTGAGTCCGAGCTAATGTGACCCCGAGGAGGAGGAG 584  
QY 603 TCCCGTCCCACTTCTCTCTGTAGCTTCAGGCGGCTTCCCGACACCCGCGCTTGG 662  
DB 585 TCCCGTCCCACTTCTCTCTGTAGCTTCAGGCGGCTTCCCGACACCCGCGCTTGG 644

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QY 663 CACAGCCCCCATCCAGCCCGTGTCTGGAGGCTGTGCTCTCGAGGAGGTCCAATTGGT 722
Db 645 CACAGCCCCCATCCAGCCCGTGTCTGGAGGCTGTGCTCTCGAGGAGGTCCAATTGGT 704
QY 723 GGTGGAGCCAGAGGTGGAGCAGTCTCTGCTGGACCGTAACCGTGAACCTGACCTGTGAAGT 782
Db 705 GGTGGAGCCAGAGGTGGAGCAGTCTCTGCTGGACCGTAACCGTGAACCTGACCTGTGAAGT 764
QY 783 CCCTGCCAGCCCTCTCTCCAAATCCATGCGATGAAGGATGGTGTGCCCTTGGCCCTTCC 842
Db 765 CCCTGCCAGCCCTCTCTCCAAATCCATGCGATGAAGGATGGTGTGCCCTTGGCCCTTCC 824
QY 843 CCCAGCCCTGTCTGATCTCTCTGATATGAGGCTCAGGACCGAGGAACTTACAGCTG 902
Db 825 CCCAGCCCTGTCTGATCTCTCTGATATGAGGCTCAGGACCGAGGAACTTACAGCTG 884
QY 903 TGTGGCCACCCATTCAGCCAGCCGCGCCCGAGGAAAGCGTGTCTGATCAGCATCAGCATCAT 962
Db 885 TGTGGCCACCCATTCAGCCAGCCGCGCCCGAGGAAAGCGTGTCTGATCAGCATCAGCATCAT 944
QY 963 CGAACCCAGGCGAGGAGGCGCAACTGCAGGCTCTGTGGAGGATCAGGGCTGGGAACTCT 1022
Db 945 CGAACCCAGGCGAGGAGGCGCAACTGCAGGCTCTGTGGAGGATCAGGGCTGGGAACTCT 1004
QY 1023 AGCCCTGGCCCTGGGATCTCTGGAGGCTGTGGGACAGCCGCTCTCATTTGGGTCTAT 1082
Db 1005 AGCCCTGGCCCTGGGATCTCTGGAGGCTGTGGGACAGCCGCTCTCATTTGGGTCTAT 1064
QY 1083 CTTGTGGCAAGGCGCAAGCGCGAGGAGGAGGAGGCGCCCGAGGAAACCCAGGAGGA 1142
Db 1065 CTTGTGGCAAGGCGCAAGCGCGAGGAGGAGGAGGAGGCGCCCGAGGAAACCCAGGAGGA 1124
QY 1143 AGAGGAGGAGCGTGCAGAACTGAATCAGTCCGAGGAACTTGAGGCGAGGAGTAGTAC 1202
Db 1125 AGAGGAGGAGCGTGCAGAACTGAATCAGTCCGAGGAACTTGAGGCGAGGAGTAGTAC 1184
QY 1203 TGAGGGCTTGAGGGGCCACAGACAGATCCCATCATCAG 1244
Db 1185 TGAGGGCTTGAGGGGCCACAGACAGATCCCATCATCAG 1226
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RESULT 9

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US-10-309-290-99
; Sequence 99, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Hailong
; APPLICANT: Zhong, Mei
```

```
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD:
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 99
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1170)
; US-10-309-290-99
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Query Match 80.4%; Score 1119; DB 17; Length 1173;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1171; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

QY 3 GGCAGCCGGAACAGCAGTTGGAGCCCTGGGCTGTGCTCCTCAGTCTCTGGGGGCGAGTAGT 62
Db 3 GGCAGCCGGAACAGCAGTTGGAGCCCTGGGCTGTGCTCCTCAGTCTCTGGGGGCGAGTAGT 62
QY 63 AGGTGCTCAAAACATCAGAGCCCGGATTCGCGAGCCACCTGCTGCTGAAGTGTAAAGGGGC 122
Db 63 AGGTGCTCAAAACATCAGAGCCCGGATTCGCGAGCCACCTGCTGCTGAAGTGTAAAGGGGC 122
QY 123 CCCCAGAAACCAACCCAGCGCTGGAATGGAACTGAAACACAGGCCCGGACAGAAAGCTTG 182
Db 123 CCCCAGAAACCAACCCAGCGCTGGAATGGAACTGAAATGGAACCT----- 158
QY 183 GAAGTCTCTGCTCTCCCGAGGAGGAGGCGCCCTGGGACAGTGTGGCTGCTGCTCTCCCAA 242
Db 159 -----GGGAGGAGGAGGCGCCCTGGGACAGTGTGGCTGCTGCTCTCCCAA 200
QY 243 CGGCTCCCTCTTCTCCCGGCTGTCCGGATCCAGGATGAGGGGATTTTCGGTGCCAGGC 302
Db 201 CGGCTCCCTCTTCTCCCGGCTGTCCGGATCCAGGATGAGGGGATTTTCGGTGCCAGGC 260
QY 303 AATGAACAGGAATGGAAGAGGAGACCAAGTCCAACTAACCGAGTCCGTGTACCAAGTTCC 362
Db 261 AATGAACAGGAATGGAAGAGGAGACCAAGTCCAACTAACCGAGTCCGTGTACCAAGTTCC 320
QY 363 TGGGAGCCAGAAATGTAGATTCTGCTCTGAACTCAGCGCTGGTGTCCCAATAGGT 422
Db 321 TGGGAGCCAGAAATGTAGATTCTGCTCTGAACTCAGCGCTGGTGTTCCTCAATAGGT 380
QY 423 GGGGACATGTGTGTCAGAGGAGGAGTACCTCTGAGGAGCTTTAGCTGGCACTTGGATGG 482
Db 381 GGGGACATGTGTGTCAGAGGAGGAGTACCTCTGAGGAGCTTTAGCTGGCACTTGGATGG 440
QY 483 GAAGCCCTGGTGCCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACCGAGGAGACCC 542
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Db 441 GAAGCCCTGGTCTTAATGAGAGGAGTATCTGTGAAGAAACAGACACAGGAGACACCC 500
Qy 543 TGAGACAGGCTCTTACACTGAGTGGAGCTAATGGTACCCAGCCCGGGGAGGAGA 602
Db 501 TGAGACAGGCTCTTACACTGAGTGGAGCTAATGGTACCCAGCCCGGGGAGGAGA 560
Qy 603 TCCCGCTCCCACTCTCTCTGTAGCTTACAGCCAGGCTTCCCGACACCGGCGCTTGG 662
Db 561 TCCCGCTCCCACTCTCTCTGTAGCTTACAGCCAGGCTTCCCGACACCGGCGCTTGG 620
Qy 663 CACAGCCCCCATCAGCCCGCTGTCTGGAGCTGTGCTCTCTGGAGAGTCCAAATGGT 722
Db 621 CACAGCCCCCATCAGCCCGCTGTCTGGAGCTGTGCTCTCTGGAGAGTCCAAATGGT 680
Qy 723 GGTGGAGCCAGAGGTGGAGCAGTGTCTCTGTGGACCGTAAACCTGACCTGTGAAGT 782
Db 681 GGTGGAGCCAGAGGTGGAGCAGTGTCTCTGTGGACCGTAAACCTGACCTGTGAAGT 740
Qy 783 CCTGGCCAGCCCTCTCTCTCAAAATCCACTGGATGAAGAGTGTGTGCTTGCCTTCC 842
Db 741 CCTGGCCAGCCCTCTCTCTCAAAATCCACTGGATGAAGAGTGTGTGCTTGCCTTCC 800
Qy 843 CCCAGCCCTGTGTGATCTCTCTCTGAGATAGGCTCTCAGGACAGGGAACCTTACAGCTG 902
Db 801 CCCAGCCCTGTGTGATCTCTCTCTGAGATAGGCTCTCAGGACAGGGAACCTTACAGCTG 860
Qy 903 TGTGGCCACCCATTCAGCCACAGGCGCCAGGAAAGCCGTGTCTCAGCATCAGCATCAT 962
Db 861 TGTGGCCACCCATTCAGCCACAGGCGCCAGGAAAGCCGTGTCTCAGCATCAGCATCAT 920
Qy 963 CGAACAGGCGAGGAGGGGCAACTGCAGGCTCTGTGGAGGATCAGGGCTGGGAACTCT 1022
Db 921 CGAACAGGCGAGGAGGGGCAACTGCAGGCTCTGTGGAGGATCAGGGCTGGGAACTCT 980
Qy 1023 AGCCCTGGCCCTGGGATCTCTGGAGGCTTGGGAGCAGCCGCTCTCTCTTGGGTCAT 1082
Db 981 AGCCCTGGCCCTGGGATCTCTGGAGGCTTGGGAGCAGCCGCTCTCTCTTGGGTCAT 1040
Qy 1083 CTTGTGCAAGGCGGCAAGCGCGAGGAGAGGAGGAGGCGCCAGAGAAACCCAGGAGGA 1142
Db 1041 CTTGTGCAAGGCGGCAAGCGCGAGGAGAGGAGGAGGCGCCAGAGAAACCCAGGAGGA 1100
Qy 1143 AGAGGAGGAGCGTGCAAGACTGAATCAGTCGGAGGAACTCTGAGCAGGCGAGAGTAGTAC 1202
Db 1101 AGAGGAGGAGCGTGCAAGACTGAATCAGTCGGAGGAACTCTGAGCAGGCGAGAGTAGTAC 1160
Qy 1203 TGGAGGCGCTTGA 1215
Db 1161 TGGAGGCGCTTGA 1173
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## RESULT 10

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US-10-472-507A-1
; Sequence 1, Application US/10472507A
; Publication No. US20050033017A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Hiroshi
; APPLICANT: Yamamoto, Hideto
; APPLICANT: Yamamoto, Yasuhiko
; APPLICANT: Sakurai, Shigeru
; APPLICANT: Watanabe, Takuo
; TITLE OF INVENTION: Soluble Rage Protein
; FILE REFERENCE: 026350-089
; CURRENT APPLICATION NUMBER: US/10/472, 507A
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: PCT/JP02, 02623
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: JP 2001-78409
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: JP 2001-243114
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: JP 2002-48182
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; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25) ... (1068)
US-10-472-507A-1
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Query Match 76.3%; Score 1062; DB 19; Length 1223;

Best Local Similarity 92.4%; Pred. No. 6.9e-303;

Matches 1147; Conservative 0; Mismatches 50; Indels 45; Gaps 1;

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Qy 3 GGAGCCGGAAACAGCAGTTGGAGCTTGGGTGTGTTCTCAGTCTGTGGGGGCGAGTAGT 62
Db 27 GGAGCCGGAAACAGCAGTTGGAGCTTGGGTGTGTTCTCAGTCTGTGGGGGCGAGTAGT 86
Qy 63 AGGTGCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGTGTCTGAGTGTAAAGGGGC 122
Db 87 AGGTGCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGTGTCTGAGTGTAAAGGGGC 146
Qy 123 CCCCAGAAACACACCCCGGCTGGAATGGAATCTGAAACACAGCCCGGACAGAAAGCTTG 182
Db 147 CCCCAGAAACACACCCCGGCTGGAATGGAATCTGAAACACAGCCCGGACAGAAAGCTTG 206
Qy 183 GAAAGTCTCTCTCTCCAGGAGGAGGCGCTTGGGACAGTGTGGCTGTCTTCCCAA 242
Db 207 GAAAGTCTCTCTCTCCAGGAGGAGGCGCTTGGGACAGTGTGGCTGTCTTCCCAA 266
Qy 243 CGGCTCCCTCTCTCTCCGCTGTCCGATCCAGATGAGGGGATTTCCGCTGCCAGGC 302
Db 267 CGGCTCCCTCTCTCTCCGCTGTCCGATCCAGATGAGGGGATTTCCGCTGCCAGGC 326
Qy 303 AATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATTCC 362
Db 327 AATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATTCC 386
Qy 363 TGGAGCCAGAAATGTAGATTCTGCTGTGAATCTCAGGCTGTGTCTCCCAATAAGT 422
Db 387 TGGAGCCAGAAATGTAGATTCTGCTGTGAATCTCAGGCTGTGTCTCCCAATAAGT 446
Qy 423 GGGGACATGTGTCTCAGAGGGAAGCTACCTGACGGAGTACCTGACGGAGTCTTAGCTTGGATGG 482
Db 447 GGGGACATGTGTCTCAGAGGGAAGTACCTGACGGAGTCTTAGCTTGGATGG 506
Qy 483 GAAAGCCCTGTGCTTAAATGAAAGGAGTATCTGTGAAGGAACAGACAGGAGACACCC 542
Db 507 GAAAGCCCTGTGCTTAAATGAAAGGAGTATCTGTGAAGGAACAGACAGGAGACACCC 566
Qy 543 TGAGACAGGCTCTTCACTGAGTGGAGCTAATGGTGAACCCAGCCCGGGGAGGAGA 602
Db 567 TGAGACAGGCTCTTCACTGAGTGGAGCTAATGGTGAACCCAGCCCGGGGAGGAGA 626
Qy 603 TCCCGCTCCCACTCTCTCTGTAGCTTACAGCCAGGCTTCCCGACACCCGGGCTTGG 662
Db 627 TCCCGCTCCCACTCTCTCTGTAGCTTACAGCCAGGCTTCCCGACACCCGGGCTTGG 686
Qy 663 CACAGCCCCCATCAGCCCGCTGTCTGGAGCTGTGCTCTGTGGAGAGTCCAAATGGT 722
Db 687 CACAGCCCCCATCAGCCCGCTGTCTGGAGCTGTGCTCTGTGGAGAGTCCAAATGGT 746
Qy 723 GGTGGAGCCAGAGGTGGAGCAGTAGCTCTGTGGTGAACCGTAAACCTGACCTGTGAAGT 782
Db 747 GGTGGAGCCAGAGGTGGAGCAGTAGCTCTGTGGTGAACCGTAAACCTGACCTGTGAAGT 806
Qy 783 CCTCTCCAGCCCTCTCTCTCAAAATCCACTGGATGAAGAGTGTGTGCCCTTGTGCCCTTCC 842
Db 807 CCTCTCCAGCCCTCTCTCTCAAAATCCACTGGATGAAGAGTGTGTGCCCTTGTGCCCTTCC 866
Qy 843 CCCCAGCCCTGTGTGTGATCTCTCCCTGAGATAGGGGCTCAGGACAGGGAACCTACAGCTG 902
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[illegible]

## RESULT 11

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US-10-091-019-2
; Sequence 2, Application US/10091019
; Publication No. US20030166063A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Shen, Jane M.
; APPLICANT: Shahbaz, Manouchehr M.
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins
; FILE REFERENCE: 41305-270555
; CURRENT APPLICATION NUMBER: US/10/091,019
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/273,418
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1020)
; OTHER INFORMATION:
US-10-091-019-2

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	Query Match	72.8%;	Score 1013;	DB 16;	Length 1020;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-288;		
	Matches 1013;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	3	GGCAGCCGGAAACACAGCTTGGAGCCTGGGTGCTGGTCTCAGTCTGTGGGGGGCAGTAGT	62		
DB	3	GGCAGCCGGAAACACAGCTTGGAGCCTGGGTGCTGGTCTCAGTCTGTGGGGGGCAGTAGT	62		
QY	63	AGGTGCTCAAAAACATCAACAGCCCGGATTTGGGAGCCCACTGGTGTCTGAAGTGTATAAGGGGGC	122		
DB	63	AGGTGCTCAAAAACATCAACAGCCCGGATTTGGGAGCCCACTGGTGTCTGAAGTGTATAAGGGGGC	122		
QY	123	CCCCAAGAAACACCCAGCGGGCTTGGAAATGGAACACTGAAACACAGGCCGCGACAGAAAGCTTG	182		
DB	123	CCCCAAGAAACACCCAGCGGGCTTGGAAATGGAACACTGAAACACAGGCCGCGACAGAAAGCTTG	182		
QY	183	GAAGGTCTGTCTCTCCACAGGAGAGAGCCCTCTGGACAGTGTGGCTCGTGTCTTCTCCAA	242		
DB	183	GAAGGTCTGTCTCTCCACAGGAGAGAGCCCTCTGGACAGTGTGGCTCGTGTCTTCTCCAA	242		

Qy	243	CGGCTCCCTCTTCTTCCGCTGTCCGATCCAGATGAGGGATTTTCCGTCGCCAGC	302
Db	243	CGGCTCCCTCTTCTTCCGCTGTCCGATCCAGATGAGGGATTTTCCGTCGCCAGC	302
Qy	303	AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATCC	362
Db	303	AATGAACAGGANATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATCC	362
Qy	363	TGGGAAGCCAGAAATTTAGATTCTGCCTCTGAACTCAGCGTGTGTGTCTCCAAATAAGT	422
Db	363	TGGGAAGCCAGAAATTTAGATTCTGCCTCTGAACTCAGCGTGTGTGTCTCCAAATAAGT	422
Qy	423	GGGACATGTGTGTACAGAGGAAGTACCTGTCAGGAGTCTTACCTGGCACTTGGATGG	482
Db	423	GGGACATGTGTGTACAGAGGAAGTACCTGTCAGGAGTCTTACCTGGCACTTGGATGG	482
Qy	483	GAAGCCCTGTGTGCTTAATGAGAAGGAGTATCTGTGAAGGAACAGACAGGAGACACCC	542
Db	483	GAAGCCCTGTGTGCTTAATGAGAAGGAGTATCTGTGAAGGAACAGACAGGAGACACCC	542
Qy	543	TGAGACAGGGCTCTTCACTGCACTCGAGTCCGAGCTAATGTGTAGCCCCCGGGAGGAGA	602
Db	543	TGAGACAGGGCTCTTCACTGCACTCGAGTCCGAGCTAATGTGTAGCCCCCGGGAGGAGA	602
Qy	603	TCCCGCTCCACTTCTCTGTAGTTTCAGCCAGGCTTCCCGACACCGGGGCTTGG	662
Db	603	TCCCGCTCCACTTCTCTGTAGTTTCAGCCAGGCTTCCCGACACCGGGGCTTGG	662
Qy	663	CACAGCCCCCATCAGCCCCGTGTCTGGAGCTGTGCTCTGTGAGGAGGTCCAAATGT	722
Db	663	CACAGCCCCCATCAGCCCCGTGTCTGGAGCTGTGCTCTGTGAGGAGGTCCAAATGT	722
Qy	723	GGTGGAGCCAGAAAGGTGGAGCAGTAGCTCTCTGGTGGAAACCGGTAAACCTGTGAAGT	782
Db	723	GGTGGAGCCAGAAAGGTGGAGCAGTAGCTCTCTGGTGGAAACCGGTAAACCTGTGAAGT	782
Qy	783	CCCTGCCAGCCCTCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTCCGCCCTTCC	842
Db	783	CCCTGCCAGCCCTCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTCCGCCCTTCC	842
Qy	843	CCCCAGCCCTGTGTGATCTCTCCCTGATATGGGCTTCAGACACAGGGAACCTACAGCTG	902
Db	843	CCCCAGCCCTGTGTGATCTCTCCCTGATATGGGCTTCAGACACAGGGAACCTACAGCTG	902
Qy	903	TGTGGCCACCATTCACAGCCACGGGCCACGAAAGCCGTGTCTGACGATCAGGATCAT	962
Db	903	TGTGGCCACCATTCACAGCCACGGGCCACGAAAGCCGTGTCTGACGATCAGGATCAT	962
Qy	963	CGAACAGGGCAGGAGGGGCCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGG	1015
Db	963	CGAACAGGGCAGGAGGGGCCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGG	1015

## RESULT 12

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US-08-905-709-1
Sequence 1, Application US/08905709
Publication No. US20010039256A1
GENERAL INFORMATION:
APPLICANT: Stern, David
APPLICANT: Schmidt, Ann M.
TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED
TITLE OF INVENTION: ATHEROSCLEROSIS USING (SRAGE) SOLUBLE RECEPTOR FOR
TITLE OF INVENTION: ADVANCED GLYCATION ENDPRODUCTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,709  
FILING DATE: 05-AUG-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/52876  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1438 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-905-709-1

Query Match 64.8%; Score 901.4; DB 8; Length 1438;  
Best Local Similarity 82.4%; Pred. No. 1.9e-255;  
Matches 1177; Conservative 0; Mismatches 191; Indels 61; Gaps 10;

QY 3 GGCGAGCGGAAACAGCAGTGGAGCCCTGGGCTGGTCTCAGTCTGGGGGGCAGTAGT 62  
DB 12 GGCGAGCGGAGGAGTGGTGGAGCCCTGGATGCTAGTCTCAGTCTGGGGGGGACGTAC 71  
QY 63 AGGTGCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGGTCTCAAGTGTAAAGGGGC 122  
DB 72 GGGGACCAAAACATCACAGCCCGATCGGAAGCCACTGGTCTGAACTGCAAGGAGC 131  
QY 123 CCCCAAGAAACACCCAGCGGTGGAATGGAACCTGAACACAGGCCGACAGAACTTG 182  
DB 132 CCCCAAGAAACACCCAGCAGCTGGAATGGAACCTGAACACAGGCCGACAGAACTTG 191  
QY 183 GAAGTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGGTCTGCTCCCTCCCA 242  
DB 192 GAAGTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGGTCTGCTCCCTCCCA 248  
QY 243 CGGCTCCCTCTCTCCCGAGTCTCGGATTCAGGATGAGGGATTTTCGGTGCACAGC 302  
DB 249 CGGCTCCCTCTCTCCCGAGTCTCGGATTCAGGATGAGGGATTTTCGGTGCACAGC 308  
QY 303 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTCTACCAATTC 362  
DB 309 AACGAGCCGAGCGGAAAGAGAGACCAAGTCTAACTACCGAGTCCGAGTCTATCAGATTCC 368  
QY 363 TGGGAAGCCAGAAATGTAGATTCTCCCTCTGAACCTCAGGCTGGGTGTTCCCAATAAGT 422  
DB 369 TGGGAAGCCAGAAATGTAGATTCTCCCTCTGAACCTCAGGCTGGGTGTTCCCAATAAGT 428  
QY 423 GGGGACATGTGTCTCAGGAGGAGTACCTCTCAGGAGTCTTTAGTGGCACTTTGATGG 482  
DB 429 GGGGACATGTGTCTCAGGAGGAGTACCTCTCAGGAGTCTTTAGTGGCACTTTGATGG 488  
QY 483 GAAGCCCTGTGGTCCCTAATGAGAGGAGTATCTGTAAGAGAACACAGCAGAGACACC 542  
DB 489 GAA-ACTCTGATTCCTGATGGCAAGAGAGTGTCAAGTGAAGAGAGACCAAGAGACACC 547  
QY 543 TGAGACAGGCTCTTCACACTGCGAGTCAATGAGTGAACCCAGCCCGGGAGGAGA 602  
DB 548 AAGACAGAGGCTTTTCACTCTCAATTCGAGAGTGTGGTGAACCCAGCTCGGGAGGAGC 607  
QY 603 TCCCGTCCCACTCTCTCTGTAGTTCAGCCAGGCTTCCCGACACCCGGGCTTTGGG 662  
DB 608 TCTCCACCCCACTCTCTCTGTAGTTCACCCCTGGCCCTTCCCGCGCGCGAGCCCTGCA 667  
QY 663 CACAGCCCCCATCCAGCCCGGTCTG----- 689

DB 668 CACGGCCCCCATCCAGCTCAGGCTCAGCAGCCAGGCTGGGGAGGGGCCCAACGT 727  
QY 690 GGAGCCTGTGCTCTGGAGGAGGTCAATTTGTTGGTGGAGCCAGAGGTGGAGCAGTAGC 749  
DB 728 GGACGCTGTGCACACTGAAGAGTCAAGTT- GTGGTAGAGCCAGAGAGGGGAGCAGTAGC 786  
QY 750 TCTGTGTGAACCGTAACCCCTGACCTGTGAAGTCCCTGCCAGCCCTCTCTCAAAATCCA 809  
DB 787 TCTGTGTGTACTGTGACCTTGACCTGTGAAGCCCGCCAGCCCTCAATCAATCCA 846  
QY 810 CTGGATGAAGAGTGTGTCCTTCCCTCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCT 869  
DB 847 CTGGATCAAGAGTGTGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 906  
QY 870 GATAGGCTCAGGACCAAGGAACTTACAGCTGTGTGGCCACCCATTCAGCCACGGGCC 929  
DB 907 GGTAGGCTCAGGACCAAGGAACTTACAGCTGTGTGGCCACCCATTCAGCCACGGGCC 966  
QY 930 CCAGGAAAGCCGTGTGTCTCAGCATCAGCATCATCGAAACAGGAGGAGGGGCCAACTGC 989  
DB 967 GGAGGAGAGCCGTGTGTCTCAGCATCAGCATCATCGAAACAGGAGGAGGGGAGCTGC 1026  
QY 990 AGGCTCTGTGGAGAGTCAAGGCTGGGAACTCTAGCCCTGGCCCTGGGAGTCTTGGGAGG 1049  
DB 1027 AGGCTCTGTGGAAGGCGCGGGCTGGAAC-CTAGCCCTGACCCCTGGGATCTTGGGAGG 1085  
QY 1050 CTTGGGAGCAGCCGCTCTCATTTGGGGTCTATTTGTGGC---AAAGCGCGCAACGCC 1105  
DB 1086 CTTGGGAGCAGTCGCGCTCTCATTTGGGGTCTATTTGTGGC---AAAGCGCGCAACGCC 1145  
QY 1106 GAGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1162  
DB 1146 AAGGACAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1205  
QY 1163 TGAATCAGTTCGAGGAACTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1222  
DB 1206 TGAACCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1265  
QY 1223 ACAGACAGATCCATCCATCAGTCCCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1282  
DB 1266 ACGGACAGACCCGATCCATCAG-CCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 1323  
QY 1283 ACCAACTCTCTCTGTATAATCTCTCTGTATAACCCCACTTGCACAGCTTTCTTCT 1342  
DB 1324 ACCAGTTCTCTCTGTATAATCTC-----CAGCCACATCTCCCAACTTTCTTCT 1374  
QY 1343 ACAACAGAGGCCCCCACA-----TGATGATTAACACCTGACATCT 1387  
DB 1375 ACAACAGAGGCTCCCAAAAAGTATGATGAACACCTGACATCT 1423

RESULT 13  
US-08-755-235-1  
; Sequence 1, Application US/08755235  
; Publication No. US20030059423A1  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Wu, Jun  
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES  
; FILE REFERENCE: 0575/50159  
; CURRENT APPLICATION NUMBER: US/08/755,235  
; CURRENT FILING DATE: 1996-11-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1438  
; TYPE: DNA  
; ORGANISM: Bovine  
US-08-755-235-1

Query Match 64.8%; Score 901.4; DB 8; Length 1438;

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 22:23:19 ; Search time 6173 Seconds  
(without alignments)  
10918.711 Million cell updates/sec

Title: US-10-091-019-1  
Perfect score: 1391  
Sequence: 1 ggggcagcgggaacagcgt.....aacacctgacacatttgcga 1391

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_ste.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1355	97.4	1436	9 BC020669	BC020669 Homo sapi
2	1289	92.7	1391	6 AR321600	AR321600 Sequence
3	1289	92.7	1391	9 HUMRAGE	M91211 Human recep
4	1242	89.3	1268	9 AB036432	AB036432 Homo sapi
5	1193	85.8	1451	9 AB061689	AB061689 Homo sapi
6	990	71.2	1223	6 BD176670	BD176670 Soluble R
7	990	71.2	1223	9 AB061668	AB061668 Homo sapi
8	821	59.0	1218	6 CQ730900	CQ730900 Sequence
9	623	44.8	1250	9 HSA133822	AX133822 Homo sapi
10	466	33.5	698	6 AX795283	AX795283 Sequence
11	466	33.5	698	9 AF537303	AF537303 Homo sapi
12	290	20.8	511	6 AX795282	AX795282 Sequence
13	290	20.8	511	9 AF536237	AF536237 Homo sapi
14	274	19.7	5062	9 HSM808526	BM48378 Homo sapi
15	274	19.7	10108	9 HUMH0X8AGE	D28769 Human H0X12
16	274	19.7	56747	9 AL845464	AL845464 Human DNA
17	274	19.7	62944	6 AX334775	AX334775 Sequence
18	274	19.7	62944	6 AX336090	AX336090 Sequence
19	274	19.7	62944	9 HSMHC3W5A	U89336 Homo sapien

C	20	274	19.7	80063	9	BX284686	Human DNA
C	21	274	19.7	87610	2	CR812478	CR812478 Homo sapi
C	22	274	19.7	102588	9	BX927239	Human DNA
C	23	274	19.7	103327	9	AL662830	Human DNA
C	24	274	19.7	137935	9	AL662884	Human DNA
C	25	274	19.7	200885	2	AP001455	Homo sapi
C	26	273	19.6	653	6	AX795281	Sequence
C	27	273	19.6	653	9	AF536236	Homo sapi
C	28	223	16.0	197811	2	AC009833	Homo sapi
C	29	181	13.0	610	6	AX333424	Sequence
C	30	181	13.0	610	6	AX410951	Sequence
C	31	176	12.7	176	11	G06703	human STS W
C	32	167	12.0	747	9	HSR238896	Homo sapi
C	33	136	9.8	159822	9	AC148714	Macaca mu
C	34	123	8.8	123	6	BD190119	Polypepti
C	35	97	7.0	189424	9	AC148664	Macaca mu
C	36	60	4.3	60	6	CQ544915	Sequence
C	37	58	4.2	255	9	HSR012753	Homo sapi
C	38	51	3.7	51	6	AX161745	Sequence
C	39	51	3.7	483	4	AY370908	Sus scrofa
C	40	45	3.2	1704	9	AF001095	Homo sapi
C	41	42	3.0	1426	4	BOVRAGE	Cow recepto
C	42	42	3.0	1426	6	AR321599	Sequence
C	43	37	2.7	127266	4	AL773562	Pig DNA
C	44	33	2.4	51	9	AF065212	Homo sapi
C	45	33	2.4	1832	9	AF208289	Homo sapi

ALIGNMENTS

RESULT 1	BC020669	Homo sapiens advanced glycosylation and product-specific receptor, transcript variant 1, mRNA (CDNA clone MGC:22357 IMAGE:4718076), complete cds.	1436 bp	mRNA	linear	PRI 29-JUN-2004
LOCUS	BC020669					
DEFINITION	BC020669					
ACCESSION	BC020669					
VERSION	BC020669.1	GI:18088362				
KEYWORDS	MGC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 1436)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Lequellano, N.A., Peters, G.J., Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouford, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.B., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.					
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26)	16899-16903	(2002)	
PUBMED	12477932					
REFERENCE	2	(bases 1 to 1436)				
AUTHORS	Strausberg, R.					
TITLE	Direct Submissions					
JOURNAL	Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,					

USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapba-re@mail.nih.gov](mailto:cgapba-re@mail.nih.gov)  
 Tissue Procurement: CLONTECH  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [med@paxil.stanford.edu](mailto:med@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 37 Row: e Column: 17  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 26787960.  
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 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 142 CCCAAGAAAACACCCAGCGGTGGAATGGAACTGAACACAGGCCCGGACAGAGCTTG 201  
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 DB 202 GAAGTCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGTCTGCTTCCCAA 261

REMARK  
 COMMENT

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 QY 1323 ACCTTGCCAAAGCTTCTTCTTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1357









**AUTHORS** Yonekura,H., Yamamoto,Y., Sakurai,S., Petrova,R.G., Abedin,Md.J., Li,H., Yasui,K., Takeuchi,M., Makita,Z., Takasawa,S., Okamoto,H., Watanabe,T. and Yamamoto H.

**TITLE** Novel splice variants of the receptor for advanced glycation end-products expressed in human vascular endothelial cells and pericytes, and their putative roles in diabetes-induced vascular injury

**JOURNAL** Biochem. J. 370 (Pt 3), 1097-1109 (2003)

**MEDLINE** 22510265

**PUBMED** 12495433

**REFERENCE** 2 (bases 1 to 1451)

**AUTHORS** Yonekura,H., Yamamoto,Y., Sakurai,S. and Yamamoto,H.

**TITLE** Direct Submission

**JOURNAL** Submitted (11-MAY-2001) Hideto Yonekura, Kanazawa University, Graduate School of Medical Science; 13-1 Takara-machi, Kanazawa, Ishikawa 920-8640, Japan (E-mail:hyone@med.kanazawa-u.ac.jp, Tel:81-76-285-2182, Fax:81-76-234-4226)

**FEATURES** Location/Qualifiers

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**gene** /organism="Homo sapiens"

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1. 1451

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511..1422

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/note="transmembrane domain"

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Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 319 TGTAAAGGGGCCCCAAGAAACACCCAGCGCTGGAATGGAACCTGAACACAGCCCGG 378

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DB 379 ACAGAGCTTGGAGAGTCTGTCTCCCGAGGAGAGGCCCTGGGACAGTGTGGTCTGT 438

QY 232 GTCTTTCCCAACCGCTCCCTTCTTCCCTCCCGCTGTCGGGATCCAGGATGAGGGGATTTTC 291

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QY 352 TACCAGATTCCTGGGAGCCAGAAATTGTAGATTCTCCCTCTGAACCTCAGCGCTGTGTT 411

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QY 412 CCCAATAAGTGGGGACATGTGTTCAGAGGGAAGCTACCTCGAGGGACTCTTAGCTGG 471

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**RESULT 6**

BD176670 1223 bp DNA linear PAT 18-MAR-2003

LOCUS Soluble RAGE protein.

DEFINITION BD176670

ACCESSION BD176670.1 GI:29122380

VERSION WO 02074805-A/1.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1223)

AUTHORS Yamamoto,H., Yonekura,H., Yamamoto,Y., Sakurai,S. and Watanabe,T.

TITLE Soluble RAGE protein

JOURNAL Patent: WO 02074805-A 1 26-SEP-2002;

1	1213	87.2	1215	9	AY421473	Homo sapi
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LOCUS			
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ACCESSION	AY421474		
VERSION	AY421474.1	GI:39748336	
KEYWORDS		GSS.	
SOURCE		Pan troglodytes (chimpanzee)	
ORGANISM		Pan troglodytes	
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REFERENCE		1 (bases 1 to 1163)	
AUTHORS		Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,	
		Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,	
		Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,	
		Adams,M.D. and Cargill,M.	
TITLE		Inferring nonneutral evolution from human-chimp-mouse orthologous	
		gene trios	
JOURNAL		Science 302 (5652), 1960-1963 (2003)	
PUBMED		14671302	
REFERENCE		2 (bases 1 to 1163)	
AUTHORS		Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,	
		Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,	
		Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,	
		Adams,M.D. and Cargill,M.	
TITLE		Direct Submision	
JOURNAL		Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,	
		Rockville, MD 20850, USA	
COMMENT		This sequence was made by sequencing genomic exons and ordering	
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Db	61	GTA AGG GGG G C C C C A A G A A A C C A C C C C A G C G G T G G A A C T G G A A C A C A C A G G C C G G A	120
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Db	181	T C C T T C C A A C G G C T C C C T C T T C T C G G C T C T G G G A T C C A G G A T G A G G G A T T T T C C	240
Qy	293	G G T G C C C A G G C A A T G A A C A G G A A T G G A A C C A A G T C C A A C T A C C G A G T C C G T G T C T	352

Db 241 GGTGCCAGGCAATGAACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCT 300  
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 QY 413 CCAATAGGTGGGACATGTGTCTCAGAGGAAAGTACCTCTCAGGAGCTCTTAGTGTGC 472  
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 Db 421 ACTTGATGGGAAGCCCTGCTGCTTAATGAGAAGGAGTATCTGTGAAGGACAGACCA 480  
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 QY 1133 ACCAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1192  
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 QY 1193 AGAGTAGTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1215  
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RESULT 3  
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 LOCUS  
 DEFINITION Mus musculus AGER gene, 1209 bp DNA linear GSS 17-DEC-2003  
 genomic survey sequence, VIRTUAL TRANSCRIPT, partial sequence,  
 AY421475  
 ACCESSION  
 VERSION AY421475.1 GI:39748337  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 1209)  
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 14671302  
 2 (bases 1 to 1209)  
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
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Query Match 57.5%; Score 800.4; DB 9; Length 1209;  
 Best Local Similarity 79.1%; Pred. No. 3.4e-195;  
 Matches 959; Conservative 0; Mismatches 248; Indels 6; Gaps 2;  
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 Db 3 GGCAGCGGGAACAGAGTTGGAGCCCTGGGCTGGTCTCTCAGTCTCTGGGGGACGTAGC 62  
 QY 63 AGTGTCTCAAAACATCACAGCCCGGATTCGCGAGCCACTGGTCTCAAGTGTAAAGGGGC 122  
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 QY 183 GAAGTCTCTCTCTCCAGGAGGAGGCGCCCTGGGACAGTGGCTCTGCTCTCTCCCAA 242  
 Db 183 GAAGTCTCTCTCTCCAGGAGGAGGCGCCCTGGGACAGTGGCTCTGCTCTCTCCCAA 239  
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 QY 363 TGGGAGCCAGAAATGTAGATTCTGCCTCTGAACTCACGGCTGGTGTTCCTCAATAGGT 422  
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 Db 420 GGGACATGTGTCTCAGAGGAGGAGTACCTCTGAGGAGCCCTTAGTGGCACTTAGATGG 479  
 QY 483 GAAGCCCTCTGCTCTCTAATGAGAAGGAGTATCTGTGAAGGAAACAGACAGGAGACCC 542  
 Db 480 GAACTTCTGATTCCCGATGGCAAGAAACACTCTGTGAAGGAGGAGACAGGAGACCC 539  
 QY 543 TGAGACAGGCTCTTCACTGAGTGGAGTAAATGGTGAATGGTGAATGGTGAATGGTGAAT 602



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 21:51:55 ; Search time 813 Seconds  
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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1391	100.0	1391	6 ABQ79955	Abq79955 Human RAG
2	1389	99.9	1415	6 ABQ99597	Abq99597 Human cod
3	1355	97.4	1436	12 ADX00130	Adx00130 Human RAG
4	1304	93.7	1582	4 AAH57444	Aah57444 Human lun
5	1289	92.7	1391	6 ABK10856	Abk10856 DNA encod
6	1289	92.7	1391	6 ABK84114	Abk84114 Human CDN
7	1289	92.7	1391	6 AAD36952	Aad36952 Human rec
8	1289	92.7	1391	10 AAD59952	Aad59952 Human RAG
9	1289	92.7	1391	10 ADG32021	Adg32021 Human DNA
10	1242	89.3	1268	10 ADG33024	Adg33024 Human DNA
11	1189	85.5	1678	9 ACC59907	Acc59907 Human REM
12	1142	83.5	1217	10 ADR95563	Adr95563 Human NOV
13	1117	80.3	1329	12 ADP19665	Adp19665 Human LP2
14	1088	78.2	1294	12 ADP19669	Adp19669 Human LP2
15	1044	75.1	1226	10 ADR95565	Adr95565 Human NOV
16	1018	73.2	1023	2 AAV12394	Aav12394 Human sol
17	1018	73.2	1023	2 AAV06517	Aav06517 Human RAG
18	1015	73.0	1173	10 ADR95567	Adr95567 Human NOV
19	1013	72.8	1020	6 ABQ79956	Abq79956 Human sol
20	990	71.2	1223	6 ABV73151	Abv73151 Human sol

21	990	71.2	1223	10 ADG37043	Adg37043 Receptor
22	990	71.2	1291	12 ADP19655	Adp19655 Human LP2
23	977	70.2	1146	13 ADS10302	Ads10302 Human the
24	973	69.9	1463	6 ABQ99598	Abq99598 Human cod
25	954	68.6	957	2 AAV06518	Aav06518 Human RAG
26	933	67.1	1323	12 ADP19667	Adp19667 Human LP2
27	877	63.0	1761	12 ADK00128	Adk00128 Human RAG
28	870	62.5	1384	12 ADP19659	Adp19659 Human LP2
29	852	61.3	957	2 AAV12395	Aav12395 Human mat
30	822	59.1	1239	12 ADP19663	Adp19663 Human LP2
31	820	59.0	1090	12 ADM80824	Adm80824 Human CAD
32	820	59.0	1194	12 ADP19657	Adp19657 Human LP2
33	697	50.1	1539	9 ACC59920	Acc59920 Human REM
34	697	50.1	1627	9 ACC59921	Acc59921 Human REM
35	574	41.3	1339	12 ADP19661	Adp19661 Human LP2
36	466	33.5	698	10 ADD40792	Add40792 Human RAG
37	336	24.2	336	6 ABQ79957	Abq79957 Human RAG
38	290	20.8	511	10 ADD40791	Add40791 Human RAG
39	274	19.7	62944	6 ABL68262	Ab168262 Kidney ca
40	274	19.7	62944	6 ABL66947	Ab166947 Lung canc
41	273	19.6	653	10 ADD40790	Add40790 Human RAG
42	255	18.3	255	4 AAH57236	Aah57236 Human lun
43	197	14.2	203	12 ACH83167	Ach83167 Human gen
44	197	14.2	218	10 ACD96717	Acd96717 Human col
45	197	14.2	553	12 ACH69467	Ach69467 Human gen

ALIGNMENTS

RESULT 1

ABQ79955

ID ABQ79955 standard; DNA; 1391 BP.

XX

AC ABQ79955;

XX

DT 23-DEC-2002 (first entry)

XX

DE Human RAGE nucleotide sequence.

XX

KW Receptor for Advanced Glycated end product; RAGE; recombinant; nontropic;

KW antiarteriosclerotic; antidiabetic; cytotstatic; nephrotropic; vasotropic;

KW neuroprotective; antiinflammatory; gene therapy; human; ds.

XX

OS Homo sapiens.

XX

PN WO200270667-A2.

XX

PD 12-SEP-2002.

XX

PF 05-MAR-2002; 2002WO-US006881.

XX

PR 05-MAR-2001; 2001US-0273418P.

XX

PA (TRAN-) TRANSTECH PHARMA INC.

XX

PI Harris R, Shen J, Shahbaz M;

XX

DR WPI; 2002-713443/77.

XX

PT High level expression of recombinant Receptors for Advanced Glycated end products (RAGE) proteins for treating increased levels of advanced glycosylation end products, comprises infecting cells with a high titer recombinant virus.

XX

PS Claim 12; Fig 2A; 5lpp; English.

XX

CC The invention relates to a method for high level expression of recombinant forms of the Receptor for Advanced Glycated end products (RAGE) or its fragments. The method involves (i) subcloning a nucleotide sequence encoding RAGE or its fragment into a virus; (ii) preparing a high titer stock of recombinant virus; and (iii) infecting host cells with the high titer recombinant virus under conditions such that



CC predetermined levels of RAGE or its fragment is produced, where the  
 CC predetermined levels of RAGE comprises at least 25 mg recombinant protein  
 CC per liter of culture. The method is useful for high level expression of  
 CC recombinant RAGE polypeptide or its fragment which may be useful in  
 CC preventing, treating or ameliorating diseases associated with increased  
 CC levels of advanced glycosylation end products, such as atherosclerosis,  
 CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's  
 CC disease, inflammation, systemic lupus nephritis, inflammatory lupus  
 CC nephritis, cancer or erectile dysfunction. The present sequence  
 CC represents the nucleotide sequence of human RAGE as reported in GenBank  
 CC /EMBL Accession no. XM004205  
 XX  
 SQ Sequence 1391 BP; 305 A; 408 C; 417 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 1391; DB 6; Length 1391;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 GGGGACGCGGAAACAGCAGTGGAGCTGGGTCTGCTCCTCAGTCTGTGGGGGCGAGTA 60

QY 61 GTAGGTGCTCAAAACATCAGACCCCGGATTGGCAGCCACTGTGTGAAGTGAAGGG 120  
 DB 61 GTAGGTGCTCAAAACATCAGACCCCGGATTGGCAGCCACTGTGTGAAGTGAAGGG 120

QY 121 GCCCCCAAGAAACACCCAGCGCTGGGAATGAACTGAACACAGCCGCGACAGAAGCT 180  
 DB 121 GCCCCCAAGAAACACCCAGCGCTGGGAATGAACTGAACACAGCCGCGACAGAAGCT 180

QY 181 TGAAGGTCTCTGCTCCGCCAGGAGGAGCCCTCGGACAGTGTGCTGTGCTTCCC 240  
 DB 181 TGAAGGTCTCTGCTCCGCCAGGAGGAGCCCTCGGACAGTGTGCTGTGCTTCCC 240

QY 241 AACGGTCTCTCTCTCCGCTGTGCGGATCCAGATCAGGGGATTTCCGGTCCAG 300  
 DB 241 AACGGTCTCTCTCTCCGCTGTGCGGATCCAGATCAGGGGATTTCCGGTCCAG 300

QY 301 GCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGT 360  
 DB 301 GCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGT 360

QY 361 CTTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTACGGCTGGTGTCCCAATAAG 420  
 DB 361 CTTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTACGGCTGGTGTCCCAATAAG 420

QY 421 GTGGGACATGTGTTCAGAGGAGAGCTACCTGCAGGAGCTTACCTGGCACTTGGAT 480  
 DB 421 GTGGGACATGTGTTCAGAGGAGAGCTACCTGCAGGAGCTTACCTGGCACTTGGAT 480

QY 481 GGGAAAGCCCTGTGCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540  
 DB 481 GGGAAAGCCCTGTGCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540

QY 541 CTTGAGACAGGGCTCTTACACTGCAGTCGAGCTAATGTGACCCCGAGCCGGGAGGA 600  
 DB 541 CTTGAGACAGGGCTCTTACACTGCAGTCGAGCTAATGTGACCCCGAGCCGGGAGGA 600

QY 601 GATCCCGCTCCACCTTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGCTTG 660  
 DB 601 GATCCCGCTCCACCTTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGCTTG 660

QY 661 CGCACAGCCCTCCAGCCCGCTGTCTGGAGCTGTGCTCTGGAGGAGGTCCCAATTG 720  
 DB 661 CGCACAGCCCTCCAGCCCGCTGTCTGGAGCTGTGCTCTGGAGGAGGTCCCAATTG 720

QY 721 GTGTGGAGCCAGAGGTGGAGCAGTAGCTCCTGGTGGAAACCGTAACCTGACCTGTGAA 780  
 DB 721 GTGTGGAGCCAGAGGTGGAGCAGTAGCTCCTGGTGGAAACCGTAACCTGACCTGTGAA 780

QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTGGCCCTT 840  
 DB 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTGGCCCTT 840

## RESULT 2

ABQ99597

ID ABQ99597 standard; cDNA; 1415 BP.

XX ABQ99597;

XX AC ABQ99597;

XX DT 25-FEB-2003 (first entry)

XX Human coding sequence SEQ ID 330.

XX DE

XX DE

XX KW Human; expressed sequence tag; EST; chromosome 6p21.3;

XX KW haematopoietic disorder; central nervous system disease; viral infection;

XX KW peripheral nervous system disease; non-healing wound; infectious disease;

XX KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;

XX KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;

XX KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;

XX KW cytosstatic; haemostatic; virucide; antibacterial; fungicide;

XX KW immunostimulant; cerebroprotective; gene therapy; gene; ss.

XX OS Homo sapiens.

XX PN WO200259260-A2.

XX PD 01-AUG-2002.

XX XX 16-NOV-2001; 2001WO-US042950.

XX XX 17-NOV-2000; 2000US-00714936.

XX XX (HYSE-) HYSEQ INC.

XX XX

PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;  
PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
XX WPI; 2002-590824/63.  
DR N-PSDB; ABP65011.  
XX  
XX New isolated polynucleotide, useful in research, diagnostic or  
PT therapeutic methods, e.g. preventing or treating disorders involving  
PT aberrant protein expression or biological activity.  
XX  
XX Claim 1; SEQ ID NO 330; 394pp; English.  
XX  
CC The present invention relates to novel human coding sequences (ABQ99268-  
CC ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in  
CC therapeutic, diagnostic and research methods. The polynucleotides may be  
CC used in the field of molecular biology as hybridisation probes, primers  
CC for PCR, for chromosome and gene mapping, for the recombinant production  
CC of protein, or in generation of anti-sense DNA or RNA. The  
CC polynucleotides are useful in diagnostics as expressed sequence tags  
CC (ESTs) for identifying expressed genes or for physical mapping of the  
CC human genome. The proteins may be used as molecular weight markers, or as  
CC nutritional sources or supplements. The proteins may be used to maintain  
CC and expand cell population in a totipotent or pluripotent state  
CC useful for re-engineering damaged or diseased tissues, transplantation.  
CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The  
CC polynucleotides and proteins are useful for preventing, treating or  
CC ameliorating disorders involving aberrant protein expression or  
CC biological activity, e.g. haematopoietic disorders, central/peripheral  
CC nervous system diseases, mechanical and traumatic disorders, non-healing  
CC wounds, immune deficiencies and disorders, infectious diseases caused by  
CC viral, bacterial or fungal infection, autoimmune disorders, allergic  
CC reactions and conditions, coagulation disorders, or cancer. The  
CC polynucleotide sequences of the invention were assembled from ESTs  
CC isolated mainly by sequencing by hybridisation, and in some cases,  
CC sequences obtained from one or more public databases. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1415 BP; 313 A; 414 C; 425 G; 263 T; 0 U; 0 Other;

Query Match 99.9%; Score 1389; DB 6; Length 1415;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 27 GGCAGCCGGAACAGCAGCTTGGAGCTGGGTGCTGCTCCTCAGTCTGTGGGGGCGAGTAGT 86  
DB |||||  
QY 63 AGGTGCTCAAAACATCAAGCCCGGATTTGGCGAGCCACTGGTCTGAAAGTGAAGGGGGC 122  
DB |||||  
QY 87 AGGTGCTCAAAACATCAAGCCCGGATTTGGCGAGCCACTGGTCTGAAAGTGAAGGGGGC 146  
DB |||||  
QY 123 CCCAAGAAACACCCAGCGGCTGGATGGAATGAACTGAACACAGGCGGGAAGAGCTTG 182  
DB |||||  
QY 147 CCCCAAGAAACACCCAGCGGCTGGATGGAATGAACTGAACACAGGCGGGAAGAGCTTG 206  
DB |||||  
QY 183 GAAGTCTCTGCTCCCGAGGAGGAGCCCTGGAGAGTGGCTGCTGCTGCTCCCA 242  
DB |||||  
QY 207 GAAGTCTCTGCTCCCGAGGAGGAGCCCTGGAGAGTGGCTGCTGCTGCTCCCA 266  
DB |||||  
QY 243 CGGCTCCCTCTCTCTCCCGAGTGTGGGATCCAGGATGAGGGGATTTTCGGTGCAGGC 302  
DB |||||  
QY 267 CGGCTCCCTCTCTCTCCCGAGTGTGGGATCCAGGATGAGGGGATTTTCGGTGCAGGC 356  
DB |||||  
QY 303 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 362  
DB |||||  
QY 327 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 386  
DB |||||  
QY 363 TGGGAGCCAGGAATTTGTAGATTCTGCTCTGAACTCACCGCTGGTGTCCCAATAGGT 422  
DB |||||  
QY 387 TGGGAGCCAGGAATTTGTAGATTCTGCTCTGAACTCACCGCTGGTGTCCCAATAGGT 446  
DB |||||

RESULT 3

ADK00130

ID ADK00130 standard; cDNA; 1436 BP.

XX

QY 423 GGGACATGTGTCTCAGAGGGAAGCTACCTCGAGGAGCTTCTAGCTGSCACTTGGATGG 482  
DB |||||  
QY 447 GGGACATGTGTCTCAGAGGGAAGCTACCTCGAGGGAAGCTTCTAGCTGSCACTTGGATGG 506  
DB |||||  
QY 483 GAAAGCCCTGGTGCCTTAATGAGAAGGAGTATCTGTGAAGGAACACAGACAGAGACACCC 542  
DB |||||  
QY 507 GAAAGCCCTGGTGCCTTAATGAGAAGGAGTATCTGTGAAGGAACACAGACAGAGACACCC 566  
DB |||||  
QY 543 TGAGACAGGGCTCTTTACACTGAGTGGAGCTAATGTGACCCAGCCCGGGGAGGAGA 602  
DB |||||  
QY 567 TGAGACAGGGCTCTTTACACTGAGTGGAGCTAATGTGACCCAGCCCGGGGAGGAGA 626  
DB |||||  
QY 603 TCCCGCTCCACCTTCTCTCTAGCTTTCAGCCAGCCAGCCCTTCCCGACACCCGGCCCTTGG 662  
DB |||||  
QY 627 TCCCGCTCCACCTTCTCTCTAGCTTTCAGCCAGCCAGCCCTTCCCGACACCCGGCCCTTGG 686  
DB |||||  
QY 663 CACAGCCCCCATTCAGCCCGCTGTCTGGAGGCTGTGCCCTCTGGAGGAGGTCCAATTGGT 722  
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QY 687 CACAGCCCCCATTCAGCCCGCTGTCTGGAGGCTGTGCCCTCTGGAGGAGGTCCAATTGGT 746  
DB |||||  
QY 723 GGTGAGCCAGAAAGGTGGAGCAGTAGTCTCTGGTGGAAACCGTAACCCCTGACCTGTGAAGT 782  
DB |||||  
QY 747 GGTGAGCCAGAAAGGTGGAGCAGTAGTCTCTGGTGGAAACCGTAACCCCTGACCTGTGAAGT 806  
DB |||||  
QY 783 CCTGCCAGCCCTCTCTCAATCCACTGGATGAGGTGTGTGCCCTTCCCTTCCCTTCC 842  
DB |||||  
QY 807 CCTGCCAGCCCTCTCTCAATCCACTGGATGAGGTGTGTGCCCTTCCCTTCCCTTCC 866  
DB |||||  
QY 843 CCCAGCCCTGTGTGATCTCTCCCTAGATAGGCTCAGGACCAAGGGAACCTACAGCTG 902  
DB |||||  
QY 867 CCCAGCCCTGTGTGATCTCTCCCTAGATAGGCTCAGGACCAAGGGAACCTACAGCTG 926  
DB |||||  
QY 903 TGTGGCCACCCATTCCAGCCAGCGGCCCGAGAAAGCCGTGTGTGTGTGTGTGTGTGTGTGT 962  
DB |||||  
QY 927 TGTGGCCACCCATTCCAGCCAGCGGCCCGAGAAAGCCGTGTGTGTGTGTGTGTGTGTGTGT 986  
DB |||||  
QY 963 CGAACAGCGGAGGAGGGGCGAACTGTCAGGCTCTGTGGAGGATCAGGCTGGGACTCT 1022  
DB |||||  
QY 987 CGAACAGCGGAGGAGGGGCGAACTGTCAGGCTCTGTGGAGGATCAGGCTGGGAACTCT 1046  
DB |||||  
QY 1023 AGCCCTGGCCCTGGGGATCTCTGGAGGCTCTGGGACAGCGCCCTCTCATTTGGGGTCTAT 1082  
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QY 1047 AGCCCTGGCCCTGGGGATCTCTGGAGGCTCTGGGACAGCGCCCTCTCATTTGGGGTCTAT 1106  
DB |||||  
QY 1083 CTTGTGGCAAAAGCGGCAACCGCGAGGAGAGAGAGGCGCCCAAGAAAACAGAGGA 1142  
DB |||||  
QY 1107 CTTGTGGCAAAAGCGGCAACCGCGAGGAGAGAGAGGCGCCCAAGAAAACAGAGGA 1166  
DB |||||  
QY 1143 AGAGGAGGAGCTGCAGAACTGAATCAGTTCGAGGAGACCTGAGGCGAGGAGTAGTATAC 1202  
DB |||||  
QY 1167 AGAGGAGGAGCTGCAGAACTGAATCAGTTCGAGGAGACCTGAGGCGAGGAGTAGTATAC 1226  
DB |||||  
QY 1203 TGGAGGCGCTTCAGGGGCGCCACAGACAGATCCCATCAGCTCCCTTTCTTTTTCCTCC 1262  
DB |||||  
QY 1227 TGGAGGCGCTTCAGGGGCGCCACAGACAGATCCCATCAGCTCCCTTTCTTTTTCCTCC 1286  
DB |||||  
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DB |||||  
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DB |||||  
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DB |||||  
QY 1383 CATCTTGCA 1391  
DB |||||  
QY 1407 CATCTTGCA 1415  
DB |||||

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AC ADK00130;
XX 20-MAY-2004 (first entry)
XX Human RAGE encoding sequence.
XX
XX Advanced Glycation End Product Ligand Binding Element; RAGE-LBE;
XX Cytostatic; Antidiabetic; Nootropic; Antiarthritic; Osteopathic;
XX Neuroprotective; Antiinflammatory; Dermatological; Immunosuppressive;
XX Vasotropic; Antipsoriatic; Antibacterial; Antiarteriosclerotic;
XX amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;
XX chronic inflammatory disease; osteoarthritis; irritable bowel disease;
XX multiple sclerosis; psoriasis; ss.
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 1..1436
XX /*tag= a
XX /product= "RAGE"
XX
XX WO2004016229-A2.
XX
XX 26-FEB-2004.
XX
XX 18-AUG-2003; 2003WO-US025996.
XX
XX 16-AUG-2002; 2002US-0404205P.
XX
XX (AMHP ) WYETH.
XX
XX Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FM;
XX Feldmann M, Foxwell BJM, Feldman JL;
XX
XX WPI; 2004-192067/19.
XX P-PSDB; ADK00129.
XX
XX New fusion protein comprising a Receptor for Advanced Glycation End
XX Product Ligand Binding Element (RAGE-LBE) and an immunoglobulin element,
XX useful for preparing a composition for treating e.g., Alzheimer's
XX disease.
XX
XX Disclosure; SEQ ID NO 44; 100pp; English.
XX
XX The present invention relates to a new fusion protein comprises a
XX Receptor for Advanced Glycation End Product Ligand Binding Element (RAGE-
XX LBE) and an immunoglobulin element. The fusion protein is useful for
XX preparing a composition for treating RAGE-associated disorder such as
XX amyloidosis, cancer, Crohn's disease, diabetes, complications of
XX diabetes, prion-related disorders, vasculitis, nephropathies,
XX retinopathies and/or neuropathies; Alzheimer's disease, chronic
XX inflammatory disease e.g., rheumatoid arthritis, osteoarthritis,
XX irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute
XX inflammatory disease e.g., sepsis, or cardiovascular disease, e.g.,
XX atherosclerosis or retinosis. The present sequence represents human RAGE
XX protein encoding sequence.
XX
XX Sequence 1436 BP; 340 A; 411 C; 422 G; 263 T; 0 U; 0 Other;
XX
XX Query Match 97.4%; Score 1355; DB 12; Length 1436;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 GGAGCCGGACAGAGTGGAGCCTGGGCTGGTCTGGTCTGGTCTGGTCTGGGCGGAGTACT 62
XX 22 GGAGCCGGACAGAGTGGAGCCTGGGCTGGTCTGGTCTGGTCTGGGCGGAGTACT 81
XX 63 AGGTGCTCAAAACATCACAGCCCGGATGGCGAGCCACTGGTCTGCTGAAAGTGTAAAGGGGC 122
XX 82 AGGTGCTCAAAACATCACAGCCCGGATGGCGAGCCACTGGTCTGCTGAAAGTGTAAAGGGGC 141
XX 123 CCCAAGAAACCAACCCAGCGGCTGGATGGAACTGGAACACAGGCCCGGACAGAGCTTG 182
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Db	1222	TGAGGGCCCTTGAGGGGCCACAGACAGATCCCATCATCAGCTCCCTTTCTTTTCCC	1281
Qy	1263	TTGAACCTGTTCTGGCCTCAGACCAACTCTCTCTGTATATAATCTCTCTCTGTATAACCCC	1322
Db	1282	TTGAACCTGTTCTGGCCTCAGACCAACTCTCTCTGTATATAATCTCTCTCTGTATAACCCC	1341
Qy	1323	ACCTTGGCAAGCTTTCTTCTACACAGAGCCCCC	1357
Db	1342	ACCTTGGCAAGCTTTCTTCTACACAGAGCCCCC	1376
RESULT 4			
AAH57444			
ID	AAH57444 standard; cDNA; 1582 BP.		
XX	AAH57444;		
XX			
DT	10-SEP-2001 (first entry)		
XX			
DE	Human lung cell specific cDNA sequence SEQ ID NO:284.		
XX			
KW	Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;		
KW	liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;		
KW	metabolic disease; developmental disease; cytostatic; immunomodulatory;		
KW	neuroprotective; gene therapy; cancer; immunopathology; neuropathology.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200132927-A2.		
XX			
PD	10-MAY-2001.		
XX			
PF	02-NOV-2000; 2000WO-US030396.		
XX			
PR	04-NOV-1999; 99US-0163508P.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
XX			
PI	Sornasse T, Seilhamer JJ, Watson GA;		
XX			
DR	WPI; 2001-291057/30.		
XX			
PT	New cell and tissue specific polynucleotides useful for diagnosis,		
PT	prognosis or monitoring of treatments for disorders where the gene is		
PT	associated with a cancer, immunopathology or neuropathology.		
XX			
PS	Claim 1; Page 210; 327pp; English.		
XX			
CC	AAH57161 to AAH57576 represent cell and tissue specific polynucleotide		
CC	sequences (I). (I) can have cytostatic, immunomodulatory and		
CC	neuroprotective activities, and can be used in gene therapy. (I) and		
CC	proteins (II) encoded by then are used in high throughput screening		
CC	assays to select DNA molecules, RNA molecules, peptide nucleic acids,		
CC	mimetics, peptides, proteins, agonists, antagonists, antibodies or their		
CC	fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical		
CC	agents. Expression of (I) in a sample indicates the differentiation of		
CC	embryonic stem cells into a tissue selected from brain, heart, kidney,		
CC	liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used		
CC	to produce an expression profile that defines a metabolic or		
CC	developmental process, treatment, condition, disease or disorder. The		
CC	gene profile can be used for diagnosis, prognosis or monitoring of		
CC	treatments and for investigating a predisposition to a disorder where the		
CC	gene is associated with a cancer, immunopathology or neuropathology		
XX			
SQ	Sequence 1582 BP; 355 A; 448 C; 486 G; 293 T; 0 U; 0 Other;		
Query Match 93.7%; Score 1304; DB 4; Length 1582;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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Db	203	GGCAGCCGGAACAGAGTTGGAGCCTGGGTGCTGCTCCTCAGTCTGTGGGGGCGAGTAGT	262

Qy	63	AGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTCTGAAGTGAAGGGGC	122
Db	263	AGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTCTGAAGTGAAGGGGC	322
Qy	123	CCCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAACTTG	182
Db	323	CCCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAACTTG	382
Qy	183	GAAGTCTCTGTCTCCCGAGGAGGCCCCCTGGGACAGTGTGGCTCTGTCTCTCCAA	242
Db	383	GAAGTCTCTGTCTCCCGAGGAGGCCCCCTGGGACAGTGTGGCTCTGTCTCTCCAA	442
Qy	243	CGGCTCCCTCTTCTCCCGGCTGTGGGATCAGAGATGAGGGGATTTCCGFTGCCAGGC	302
Db	443	CGGCTCCCTCTTCTCCCGGCTGTGGGATCAGAGATGAGGGGATTTCCGFTGCCAGGC	502
Qy	303	AATGAACAGAAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTCTACCAATTC	362
Db	503	AATGAACAGAAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTCTACCAATTC	562
Qy	363	TGGGAAGCCAGAAATTTGTAGATTCTGCCTCTGAACTCAGCGCTGGTGTTCCTAATAGGT	422
Db	563	TGGGAAGCCAGAAATTTGTAGATTCTGCCTCTGAACTCAGCGCTGGTGTTCCTAATAGGT	622
Qy	423	GGGACATCTGTCTCAGAGGGAAGTACCCTGCAGGACTCTTTAGCTGGCACTTGGATGG	482
Db	623	GGGACATCTGTCTCAGAGGGAAGTACCCTGCAGGACTCTTTAGCTGGCACTTGGATGG	682
Qy	483	GAAGCCCTGGTGCCTAATGAGAAAGGAGTATCTGTGAAGGACAGACAGGAGACCC	542
Db	683	GAAGCCCTGGTGCCTAATGAGAAAGGAGTATCTGTGAAGGACAGACAGGAGACCC	742
Qy	543	TGAGACAGGGCTCTTCACTGTCAGTCGGAGCTAATGGTGACCCAGCCGGGGAGAGA	602
Db	743	TGAGACAGGGCTCTTCACTGTCAGTCGGAGCTAATGGTGACCCAGCCGGGGAGAGA	802
Qy	603	TCCCGTCCACCTTCTCTGTAGTTTACGCCAGGCTTCCCGGACACCGGGCTTGGG	662
Db	803	TCCCGTCCACCTTCTCTGTAGTTTACGCCAGGCTTCCCGGACACCGGGCTTGGG	862
Qy	663	CACAGCCCATCCAGCCCGCTGTCTGGAGGCTGTGCTCTGGAGGAGGTCCAATGGT	722
Db	863	CACAGCCCATCCAGCCCGCTGTCTGGAGGCTGTGCTCTGGAGGAGGTCCAATGGT	922
Qy	723	GGTGAGCCAGAGGTGGAGCAGTAGTCTCTGTGTGAACCGTAACTGACCTGTGAAGT	782
Db	923	GGTGAGCCAGAGGTGGAGCAGTAGTCTCTGTGTGAACCGTAACTGACCTGTGAAGT	982
Qy	783	CCCTGCCAGCCCTCTCTCAAAATCCACTGGATGAGGATGGTGTGCCCTTGGCCCTTCC	842
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Qy	843	CCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCTCAGGACAGGGAACCTACAGCTG	902
Db	1043	CCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCTCAGGACAGGGAACCTACAGCTG	1102
Qy	903	TGTGGCCATTCAGCCAGCGGCCCCAGGAAAGCCGTGTCTCAGCATCAGCATCAT	962
Db	1103	TGTGGCCATTCAGCCAGCGGCCCCAGGAAAGCCGTGTCTCAGCATCAGCATCAT	1162
Qy	963	CGAAACAGGCGAGGAGGGGCCAACTCTGAGGCTCTGTGGGAGGATCAGGGCTGGAACTCT	1022
Db	1163	CGAAACAGGCGAGGAGGGGCCAACTCTGAGGCTCTGTGGGAGGATCAGGGCTGGAACTCT	1222
Qy	1023	AGCCCTGGCCCTGGGGATCTCTGGAGGCTCTGGGACAGCGCCCTCTCTATTTGGGGTCT	1082
Db	1223	AGCCCTGGCCCTGGGGATCTCTGGAGGCTCTGGGACAGCGCCCTCTCTATTTGGGGTCT	1282
Qy	1083	CTTTGGCAAAAGCGCGCAACGCCGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1142
Db	1283	CTTTGGCAAAAGCGCGCAACGCCGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1342





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361 CCTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACCTCAGCGTGTGTGTTCCCAATAAG 420  
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421 GTGGGACATGTGTGTGTCAGAGGGAAGCTACCTCTGACGGGACTCTTAGCTGGCACTTTGGAT 480  
Db |  
421 GTGGGACATGTGTGTGTCAGAGGGAAGCTACCTCTGACGGGACTCTTAGCTGGCACTTTGGAT 480  
Qy |  
481 GGGAGCCCTGTGTCCTAATGAGAGGGAGTATCTGTGAAGAACAGACACAGACAGACAC 540  
Db |  
481 GGGAGCCCTGTGTCCTAATGAGAGGGAGTATCTGTGAAGAACAGACACAGACAGACAC 540  
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661 CGCACAGCCCATCCAGCCCGCTGTCTGAGAGCTGTGCTCTGAGAGGTCCTCAATTG 720  
Qy |  
721 GTGTGGAGCCAGAGGTGGAGCAGTAGCTCTGTTGGAACCGTAAACCTGACCTGTGAA 780  
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721 GTGTGGAGCCAGAGGTGGAGCAGTAGCTCTGTTGGAACCGTAAACCTGACCTGTGAA 780  
Qy |  
781 GTCTCTGCCAGCCCTCTCTCTAAATCCATCTGATGAAGAGTGTGTGCCCTTGCCCTTT 840  
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781 GTCTCTGCCAGCCCTCTCTCTAAATCCATCTGATGAAGAGTGTGTGCCCTTGCCCTTT 840  
Qy |  
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Db |  
841 CCCCCAGCCCTGTGTGATCTCTCCCTGATAGAGGCTCAGACAGGGAACCTACAGC 900  
Qy |  
901 TGTGTGCCCAACCCATTCAGCCACGGGCCCCAGGAAAGCCGTCTGTCTGACATCAGCATC 960  
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901 TGTGTGCCCAACCCATTCAGCCACGGGCCCCAGGAAAGCCGTCTGTCTGACATCAGCATC 960  
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Db |  
961 ATCGAACAGGCGAGAGGGGCCCAACTGACAGGCTCTGTGGAGGATCAGGGCTGGAACT 1020  
Qy |  
1021 CTAGCCCTGGCCCTGGGATCTCTGGAGGCTGGGACAGCCCTGCTCATTTGGGCTC 1080  
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Qy |  
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Db |  
1081 ATCTTGTGCAAGGGCGCAACCCGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
Qy |  
1141 GAAGAGAGAGGCGTGCAGAACTGTAATCTAGTCGGAGGAACTCTGAGGAGGAGGAGGAGT 1200  
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1141 GAAGAGAGAGGCGTGCAGAACTGTAATCTAGTCGGAGGAACTCTGAGGAGGAGGAGT 1200  
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1201 ACTGGAGGCTGTGGGGCCACAGACAGATCCCATCCATCAGCTCCCTTTCTTTTTC 1260  
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Db |  
1261 CCTTGAATCTTCTGCGCTCAGACCAACTCTCTCTGTATTAATCTCTCTCTGTATAACC 1320  
Qy |  
1321 CGACCTTGCAGCTTTCTTCAACAGCAGAGGCCCCCAATGATGATTAACACCTGA 1380  
Db |  
1321 CGACCTTGCAGCTTTCTTCAACAGCAGAGGCCCCCAATGATGATTAACACCTGA 1380  
Qy |  
1381 CACATCTTGA 1391  
Db |  
1381 CACATCTTGA 1391

RESULT 7  
AAD36952  
ID AAD36952 standard; cDNA; 1391 BP.  
XX  
AC AAD36952;  
XX  
DT 27-AUG-2002 (first entry)  
XX  
DE Human receptor for advanced glycosylation end product (RAGE) cDNA.  
XX  
KW Human; Receptor for advanced glycosylation end product; RAGE; cardiac;  
tissue growth; neointimal formation; blood vessel; restenosis; diabetes;  
myocardial infarction; angioplasty; peripheral vascular surgery; angina;  
transgenic animal; acute thrombotic stroke; venous thrombosis; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT CDS  
FT 1. 1215  
FT /tag= a  
FT /product= "Human RAGE protein"  
FT /note= "CDS does not include start codon"  
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FT polyA\_signal 1368..1373  
FT /tag= b  
FT polyA\_site 1391  
FT /tag= c  
XX  
PN WO200230889-A2.  
XX  
PD 18-APR-2002.  
XX  
PF 12-OCT-2001; 2001WO-US032036.  
XX  
PR 13-OCT-2000; 2000US-00687528.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Stern DM, Schmidt A, Marso S, Topol E, Lincoff AM;  
XX  
DR WPI; 2002-426260/45.  
XX  
DR P-P8DB; AAE23219.  
XX  
PT Inhibiting new tissue growth or neointimal formation in blood vessels of  
subject suffering from diabetes, stroke and preventing restenosis,  
PT comprises administering inhibitor of receptor for advance glycation end  
PT product.  
XX  
PS Disclosure; Page 16-17; 43pp; English.  
XX  
CC The invention relates to a method for inhibiting new tissue growth or  
neointimal formation in blood vessels in a subject that has experienced  
CC blood vessel injury and preventing exaggerated restenosis in a diabetic  
CC subject. The method comprises administering an inhibitor of receptor for  
CC advanced glycation/glycosylation end product (RAGE), so as to inhibit new  
CC tissue growth or neointimal formation in subject's blood vessels and  
CC preventing restenosis in the subject. The method is useful for inhibiting  
CC new tissue growth or neointimal formation in blood vessels in a subject  
CC like non-human animal, a transgenic non-human animal or a human suffering  
CC from diabetes, acute thrombotic stroke, venous thrombosis, unstable  
CC angina, myocardial infarction, abrupt closure following angioplasty or  
CC stent placement, or thrombosis as a result of peripheral vascular surgery  
CC The method is also useful for preventing restenosis and for determining  
CC whether a compound inhibits new tissue growth in a blood vessel in a  
CC subject. The present sequence is human receptor for advanced  
CC glycosylation end product (RAGE) cDNA  
XX  
SQ Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;

Query Match 92.7%; Score 1289; DB 6; Length 1391;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1389; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



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Db 1 GGGGAGCCCGGAAACAGCAGTTGAGCCTGGGTCTCTCAGTCTGTGGGGGAGTA 60
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Db 61 GTAGTGTCTCAAAACATCAGCCCGGATTTGGGAGCCACTGGTCTGAAGTGTAGGGG 120
QY 121 GCCCCCAAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCCCGGACAGAAGCT 180
Db 121 GCCCCCAAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCCCGGACAGAAGCT 180
QY 181 TGAAGTGTCTGTCTCTCCCAAGGAGGAGGCCCTCTGGGACAGTGTGGCTCTGTCTCTTCCC 240
Db 181 TGAAGTGTCTGTCTCTCCCAAGGAGGAGGCCCTCTGGGACAGTGTGGCTCTGTCTCTTCCC 240
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Db 301 GCAATGAACAGGAATGAAGAGGAGACCAAGTCCAACTACCAGTCCGTGTCTACCAAGATT 360
QY 361 CCTGGGAGCCAGAAATTTAGATTCTGCCTCTGAACCTCACGGCTGGTGTTCCTCAATAAG 420
Db 361 CCTGGGAGCCAGAAATTTAGATTCTGCCTCTGAACCTCACGGCTGGTGTTCCTCAATAAG 420
QY 421 GTGGGACATGTGTCTCAGAGGAGGAGTACCTCTGCAGGAGCTCTTAGCTGGCACTTGGAT 480
Db 421 GTGGGACATGTGTCTCAGAGGAGGAGTACCTCTGCAGGAGCTCTTAGCTGGCACTTGGAT 480
QY 481 GGAAGCCCTGTGTCTAATGAAGAGGAGTATCTGTGAAGAAACAGACAGAGACAC 540
Db 481 GGAAGCCCTGTGTCTAATGAAGAGGAGTATCTGTGAAGAAACAGACAGAGACAC 540
QY 541 CCTGAGACAGGCTCTTTCACATGTCAGTTCGAGCTAATGTGTACCCCGCGGGAGGA 600
Db 541 CCTGAGACAGGCTCTTTCACATGTCAGTTCGAGCTAATGTGTACCCCGCGGGAGGA 600
QY 601 GATCCCGTCCAGCTCTCTCTGTAGTTTACGCCAGGCTTCCCGACACCGGGCCTTG 660
Db 601 GATCCCGTCCAGCTCTCTCTGTAGTTTACGCCAGGCTTCCCGACACCGGGCCTTG 660
QY 661 CGCACAGCCCTCCAGCCCGTGTCTGGAGCCTGTGCTCTGGAGGAGTCCCAATTG 720
Db 661 CGCACAGCCCTCCAGCCCGTGTCTGGAGCCTGTGCTCTGGAGGAGTCCCAATTG 720
QY 721 GTGTGGAGCCAGAAAGTGGAGCAGTAGCTCCTGGTGGAAACCGTAACCTGACCTGTGAA 780
Db 721 GTGTGGAGCCAGAAAGTGGAGCAGTAGCTCCTGGTGGAAACCGTAACCTGACCTGTGAA 780
QY 781 GTCCCTGCCAGCCCTCTCTCTAAATCCATGTGAATGAAGTGTGTGCCCTTGCCCTTT 840
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## RESULT 8

AAD5952

ID AAD5952 standard; DNA; 1391 BP.

XX AAD5952;

AC AAD5952;

XX DT

XX DT

XX DT

XX DT

XX DT

XX DT

XX DT

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XX DT

18-DEC-2003 (first entry)

Human RAGE (receptor for advanced glycation end product) DNA.

Transgenic mouse; transgenic; nerve tissue specific promoter; nootropic;  
receptor for advanced glycation end product; RAGE; neurological disorder;  
Alzheimer's disease; amnesia; amyotrophic lateral sclerosis; neuroleptic;  
brain injury; cerebral senility; degenerative disorder; Down's syndrome;  
chronic peripheral neuropathy; cognitive disability; memory dysfunction;  
electric shock; Guillain-Barre syndrome; head trauma; mental retardation;  
Huntington's disease; learning disability; dyslexia; Tourette's syndrome;  
neuromuscular disorder; Parkinson's disease; myasthenia gravis; dementia;  
Pick's disease; human; gene; ds.

Homo sapiens.

Key Location/Qualifiers

CDS 1..1215

FT /\*tag= a

FT /product= "Human RAGE protein"

FT /note= "No start codon"

FT /partial

FT polyA\_signal

FT 1368..1373

FT /\*tag= b

XX US6563015-B1.

XX 13-MAY-2003.

XX 14-AUG-2000; 2000US-00638649.

XX 14-AUG-2000; 2000US-00638649.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Stern DM, Schmidt AM, Yan SD;

XX WPI; 2003-687217/65.

XX P-PSDB; AAE39510.

XX Transgenic mouse whose genome contain recombinant deoxyribonucleic acid

XX sequence, comprises nerve tissue specific promoter encoding human

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PT receptor for advanced glycation end products, and mutant human amyloid  
PT precursor protein.  
XX  
XX  
XX Disclosure; Col 6-7; 40pp; English.

CC The invention relates to a transgenic mouse whose genome contain a  
CC recombinant DNA sequence, comprising a nerve tissue specific promoter  
CC operatively linked to a DNA sequence, which encodes human receptor for  
CC advanced glycation end products (RAGE), and a mutant human amyloid  
CC precursor protein hAP695, hAPP751, and hAPP770 bearing mutations linked  
CC to familial Alzheimer's disease in humans. The transgenic animal is used  
CC for evaluation of the potential therapeutic effect of an agent for  
CC treating Alzheimer's disease in a human. It is useful for screening of  
CC compounds, which would be useful in the treatment of neurological  
CC disorders in humans, e.g. amnesia, amvotrophic lateral sclerosis, a brain  
CC injury, cerebral senility, chronic peripheral neuropathy, a cognitive  
CC disability, a degenerative disorder associated with learning, Down's  
CC syndrome, dyslexia, electric shock induced amnesia or amnesia, Guillain-  
CC Barre syndrome, head trauma, Huntington's disease, a learning disability,  
CC a memory deficiency, memory loss, a mental illness, mental retardation,  
CC memory or cognitive dysfunction, multi-infarct dementia and senile  
CC dementia, myasthenia gravis, a neuromuscular disorder, Parkinson's  
CC disease, Pick's disease, a reduction in spatial memory retention,  
CC senility, or Tourette's syndrome. The present sequence is human RAGE DNA  
XX

SQ Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;

Query Match 92.7%; Score 1289; DB 10; Length 1391;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1389; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GGGGACGCGGAAACAGCAGTTGAGCTGGGTCTGCTCAGTCTGTGGGGGGCAGTA 60  
DB 1 GGGGACGCGGAAACAGCAGTTGAGCTGGGTCTGCTCAGTCTGTGGGGGGCAGTA 60  
QY 61 GTAGTGTCTCAAAACATCAGCCCGGATTTGGCGAGCCACTGTGTGAAGTGTAAAGGG 120  
DB 61 GTAGTGTCTCAAAACATCAGCCCGGATTTGGCGAGCCACTGTGTGAAGTGTAAAGGG 120  
QY 121 GCGCCCAAGAAACAGCCAGCGGTGGATGGAATGGAATGGAATGGAATGGAATGGAAT 180  
DB 121 GCGCCCAAGAAACAGCCAGCGGTGGATGGAATGGAATGGAATGGAATGGAATGGAAT 180  
QY 181 TGAAGGTCTCTGCTCCCGAGGAGGAGCGCCCTGGGACAGTGTGCTGTCTTCC 240  
DB 181 TGAAGGTCTCTGCTCCCGAGGAGGAGCGCCCTGGGACAGTGTGCTGTCTTCC 240  
QY 241 ACGGCTCCCTCTTCTTCCCGTGTCCGGATCCAGGATGAGGGGATTTCCGGTCCAG 300  
DB 241 ACGGCTCCCTCTTCTTCCCGTGTCCGGATCCAGGATGAGGGGATTTCCGGTCCAG 300  
QY 301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTACCAAGATT 360  
DB 301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTACCAAGATT 360  
QY 361 CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTAATAAG 420  
DB 361 CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTAATAAG 420  
QY 421 GTGGGACATGTGTTCAGGGGAAGTACCTTGCAGGGACTCTTAGCTGGCACTTTGGAT 480  
DB 421 GTGGGACATGTGTTCAGGGGAAGTACCTTGCAGGGACTCTTAGCTGGCACTTTGGAT 480  
QY 481 GGAAGCCCTCTGCTCTAATGAGAGGAGTATCTGTGAAGGAACAGACCCAGGACAC 540  
DB 481 GGAAGCCCTCTGCTCTAATGAGAGGAGTATCTGTGAAGGAACAGACCCAGGACAC 540  
QY 541 CTTGAGACAGGGCTCTTCACTGTGAGTCCGAGCTAATGTGACCCAGCCGGGAGGA 600  
DB 541 CTTGAGACAGGGCTCTTCACTGTGAGTCCGAGCTAATGTGACCCAGCCGGGAGGA 600  
QY 601 GATCCCGTCCACCTCTCTCTAGCTTACGCCAGGGCTTCCCGACACCGGGCTTG 660  
DB 601 GATCCCGTCCACCTCTCTCTAGCTTACGCCAGGGCTTCCCGACACCGGGCTTG 660

DB 601 GATCCCGTCCACCTCTCTCTAGCTTACGCCAGGGCTTCCCGACACCGGGCTTG 660  
QY 661 CGCAGAGCCCGCATCCAGCCCGGTCTCTGGGAGCCTGTGCTGAGGAGGTCCAATTG 720  
DB 661 CGCAGAGCCCGCATCCAGCCCGGTCTCTGGGAGCCTGTGCTGAGGAGGTCCAATTG 720  
QY 721 GTGGTGGAGCCAGAGGTGGAGCAGTAGTCTCTCTGGTGGAAACCGTAACTGACCTGTGAA 780  
DB 721 GTGGTGGAGCCAGAGGTGGAGCAGTAGTCTCTCTGGTGGAAACCGTAACTGACCTGTGAA 780  
QY 781 GTCCCTGGCCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTCCCTT 840  
DB 781 GTCCCTGGCCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTCCCTT 840  
QY 841 CCCCCAGCCCTGTGCTGATCTCTCTGAGATAGGSCCTCAGACACAGGAACTTACAGC 900  
DB 841 CCCCCAGCCCTGTGCTGATCTCTCTGAGATAGGSCCTCAGACACAGGAACTTACAGC 900  
QY 901 TGTGTGGCCACCATTTCCAGCCACCGGGCCCGAGGAAAGCGTGTCTGACGATCAGCATC 960  
DB 901 TGTGTGGCCACCATTTCCAGCCACCGGGCCCGAGGAAAGCGTGTCTGACGATCAGCATC 960  
QY 961 ATCGAACAGGCGAGAGGGGCAACTGTCAGGCTCTGTGGAGGATCAGGGCTGGAACT 1020  
DB 961 ATCGAACAGGCGAGAGGGGCAACTGTCAGGCTCTGTGGAGGATCAGGGCTGGAACT 1020  
QY 1021 CTAGCCCTGGCCCTGGGGATCTCTGGAGGCTTGGGAGACGCGCCCTGCTCATTTGGGTC 1080  
DB 1021 CTAGCCCTGGCCCTGGGGATCTCTGGAGGCTTGGGAGACGCGCCCTGCTCATTTGGGTC 1080  
QY 1081 ATCTTGTGCAAGGCGGCAACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
DB 1081 ATCTTGTGCAAGGCGGCAACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
QY 1141 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1200  
DB 1141 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1200  
QY 1201 ACTGGAGGCTTGGGGGCGGACAGAGATCCCATCCATCAGCTCCCTTTCTTTTTC 1260  
DB 1201 ACTGGAGGCTTGGGGGCGGACAGAGATCCCATCCATCAGCTCCCTTTCTTTTTC 1260  
QY 1261 CTTGAATCTGTTCTGGCCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACC 1320  
DB 1261 CTTGAATCTGTTCTGGCCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACC 1320  
QY 1321 CCACCTTGGCAGCTTTCTTCTACACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1380  
DB 1321 CCACCTTGGCAGCTTTCTTCTACACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1380  
QY 1381 CACATCTTGCA 1391  
DB 1381 CACATCTTGCA 1391

## RESULT 9

ADG32021

ID ADG32021 standard; DNA; 1391 BP.

XX AC ADG32021;

XX AC ADG32021;

DT 26-FEB-2004 (first entry)

XX Human DNA homologue of the lung-specific RAGE protein SeqID49.

DE human; tissue specific; targeted delivery; therapeutic complex; epilepsy;

XX schizophrenia; bipolar disorder; Parkinson's disease; bacterial;

KW fungal infection; asthma; cystic fibrosis; pulmonary oedema; diabetes;

KW pancreatitis; endocrine tumour; pancreatic cancer; infarction;

KW coronary heart disease; arrhythmia; nootropic; neuroprotective;

KW antiparkinsonian; cerebroprotective; cytostatic; antibacterial;

KW fungicidal; antiaesthetic; immunosuppressive; gene; ds.

XX



RESULT 10  
ADG33024  
ID ADG33024 standard; DNA; 1268 BP.  
XX  
XX  
AC ADG33024;  
XX  
XX  
DT 26-FEB-2004 (first entry)  
XX  
XX  
DE Human DNA differentially expressed in patients with SLE SeqID348.  
XX  
XX  
KW human; ds; autoimmune; chronic inflammatory disease; SLE;  
KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;  
KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;  
KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;  
KW diverticulitis; primary biliary sclerosis.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO2003090694-A2.  
XX  
XX  
PD 06-NOV-2003.  
XX  
XX  
PF 24-APR-2003; 2003WO-US013015.  
XX  
XX  
PR 24-APR-2002; 2002US-00131827.  
XX  
XX  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
XX  
XX  
PI Wohlgemuth J, Fry K, Woodward R, Ly N;  
XX  
XX  
DR WPI; 2003-877243/81.  
XX  
XX  
PT Diagnosing or monitoring autoimmune and chronic inflammatory diseases,  
PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative  
PT colitis, psoriasis and asthma by detecting the expression level of one or  
PT more genes.  
XX  
XX  
PS Claim 18; SEQ ID NO 348; 877pp; English.  
XX  
XX  
CC This invention relates to novel methods for diagnosing and monitoring  
CC autoimmune and chronic inflammatory diseases. Specifically, it refers to  
CC the identification of genes that have a clinical utility as diagnostic  
CC tools for the management of, in particular, patients with systemic lupus  
CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the  
CC present invention describes a method for determining the levels of  
CC multiple differentially expressed genes of a patient, in a concerted  
CC manner, in order to achieve an improved diagnostic assay with sensitivity  
CC and specificity for the disease in question. As such, these genes are  
CC useful for the diagnosis of various other inflammatory disorders  
CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,  
CC ankylosing spondylitis, ulcerative colitis, primary sclerosing  
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.  
CC This polynucleotide is a DNA sequence representing human mRNA that is  
CC differentially expressed in patients with SLE, used in an exemplification  
CC of the invention.  
XX  
XX  
SQ Sequence 1268 BP; 280 A; 361 C; 410 G; 217 T; 0 U; 0 Other;  
  
Query Match 89.3%; Score 1242; DB 10; Length 1268;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 GGCGAGCCGGAACAGAGTTGGAGCCCTGGGTGCTGGTCCCTCAGTCTCTGGGGGCACTAGT 62  
DB 27 GGCGAGCCGGAACAGAGTTGGAGCCCTGGGTGCTGGTCCCTCAGTCTCTGGGGGCACTAGT 86  
  
QY 63 AGGTGCTCAAAACATCACAGCCCGGATGGCGAGCCCACTGGTCTGAAAGTGAAGGGGGC 122  
DB 87 AGGTGCTCAAAACATCACAGCCCGGATGGCGAGCCCACTGGTCTGAAAGTGAAGGGGGC 146  
  
QY 123 CCCAAGAAGAACCCCCAGGGGTGAATGGAAACTGAACACAGGCCGGGACAGAACCTTG 182  
|||||

Db 147 CCCAAGAAGAACCCCCAGGGGTGAATGGAAACTGAACACAGGCCGGACAGAACTTG 206  
QY 183 GAAGTCTCTGTCTCCCGAGGAGAGGCCCTCGGACAGTGTGGCTCGTGTCTCTCCCAA 242  
Db 207 GAAGTCTCTGTCTCCCGAGGAGAGGCCCTCGGACAGTGTGGCTCGTGTCTCTCCCAA 266  
QY 243 CGGCTCCCTCTTCTCCGCTGTGGGATCCAGGATGAGGGGATTTCCGFTCCAGGC 302  
Db 267 CGGCTCCCTCTTCTCCGCTGTGGGATCCAGGATGAGGGGATTTCCGFTCCAGGC 326  
QY 303 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTCCTACAGATTCC 362  
Db 327 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTCCTACAGATTCC 386  
QY 363 TGGGAAGCCAGAAATTTAGATTCTGCCTCTGAACTCACGGCTGGTGTTCCTAAATAGGT 422  
Db 387 TGGGAAGCCAGAAATTTAGATTCTGCCTCTGAACTCACGGCTGGTGTTCCTAAATAGGT 446  
QY 423 GGGGACATGTGTCTCAGAGGGAAGCTTACCTCGAGGACTCTTTAGCTGGCACTTGGATGG 482  
Db 447 GGGGACATGTGTCTCAGAGGGAAGCTTACCTCGAGGACTCTTTAGCTGGCACTTGGATGG 506  
QY 483 GAAGCCCTGGTGCCTTAATGAGAGGGAGTATCTGTGAAGGAACACAGCAGAGACACC 542  
Db 507 GAAGCCCTGGTGCCTTAATGAGAGGGAGTATCTGTGAAGGAACACAGCAGAGACACC 566  
QY 543 TGAGACAGGGCTCTTCCACACTGCGAGTCAATGAGTACCCAGCCCGGGGAGGAGA 602  
Db 567 TGAGACAGGGCTCTTCCACACTGCGAGTCAATGAGTACCCAGCCCGGGGAGGAGA 626  
QY 603 TCCCGTCCCACTTCTCTGTAGTTTACGCCAGCCCTTCCCGACACCGGGCTTGGC 662  
Db 627 TCCCGTCCCACTTCTCTGTAGTTTACGCCAGCCCTTCCCGACACCGGGCTTGGC 686  
QY 663 CACAGCCCTTCCAGCCCGCTGTGCGAGCTGTGCTCTGGAGAGGTCCAAATGGT 722  
Db 687 CACAGCCCTTCCAGCCCGCTGTGCGAGCTGTGCTCTGGAGAGGTCCAAATGGT 746  
QY 723 GGTGGAGCCAGAGGTGGAGCAGTAGTCTCTGTGGAACCGTAACCTGACCTGTGAAGT 782  
Db 747 GGTGGAGCCAGAGGTGGAGCAGTAGTCTCTGTGGAACCGTAACCTGACCTGTGAAGT 806  
QY 783 CCTGCGCCAGCCCTCTCTCAAATCCATGGATGAAGATGGTGTGCTTGCCTTCC 842  
Db 807 CCTGCGCCAGCCCTCTCTCAAATCCATGGATGAAGATGGTGTGCTTGCCTTCC 866  
QY 843 CCCCAGCCCTGTGTGATCTCTCTGAGATAGGCTCAGGACCCAGGAACTTACAGCTG 902  
Db 867 CCCCAGCCCTGTGTGATCTCTCTGAGATAGGCTCAGGACCCAGGAACTTACAGCTG 926  
QY 903 TGTGGCCACCCATTCCAGCCAGGGGCCCGGAAAGCCGTGTGTGTCAGCATCAGCATCAT 962  
Db 927 TGTGGCCACCCATTCCAGCCAGGGGCCCGGAAAGCCGTGTGTGTCAGCATCAGCATCAT 986  
QY 963 CGAACCCAGCGAGGAGGGGCCAACTCAGGCTCTGTGGAGGATCAGGCTGGGAACTCT 1022  
Db 987 CGAACCCAGCGAGGAGGGGCCAACTCAGGCTCTGTGGAGGATCAGGCTGGGAACTCT 1046  
QY 1023 AGCCCTGGCCCTGGGGATCTCTGGAGGCTCTGGGACAGCCGCTCTCATTTGGGCTCAT 1082  
Db 1047 AGCCCTGGCCCTGGGGATCTCTGGAGGCTCTGGGACAGCCGCTCTCATTTGGGCTCAT 1106  
QY 1083 CTTTGTGGCAAAAGCGCGCAACGCGAGGAGAGAGAAAGGCCCAAGAAAACAGAGGGA 1142  
Db 1107 CTTTGTGGCAAAAGCGCGCAACGCGAGGAGAGAGAAAGGCCCAAGAAAACAGAGGGA 1166  
QY 1143 AGAGGAGAGCGTGCAGAACTGAATCAGTCCGAGGAACCTGAGGCGAGGCGAGTAGTAC 1202  
Db 1167 AGAGGAGAGCGTGCAGAACTGAATCAGTCCGAGGAACCTGAGGCGAGGCGAGTAGTAC 1226  
QY 1203 TGGAGGGCTTGGAGGGGCCCAAGACAGATCCATCCATCAG 1244  
Db 1227 TGGAGGGCTTGGAGGGGCCCAAGACAGATCCATCCATCAG 1268

RESULT 11	
ACC59907	
ID	ACC59907 standard; cDNA; 1678 BP.
XX	
AC	ACC59907;
XX	
DT	07-JUL-2003 . (first entry)
XX	
DE	Human REMAP-20 encoding cDNA SEQ ID NO:56.
XX	
KW	Human; receptor and membrane-associated protein; REMAP; cytotstatic;
KW	antiartherosclerotic; anticonvulsant; nootropic; neuroprotective;
KW	thermoprotective; anti-HIV; antiallergic; antiinflammatory; cancer;
KW	thymoprotetic; gene therapy; cell proliferative disorder; atherosclerosis;
KW	neurological disorder; epilepsy; Huntington's disease; stroke; AIDS;
KW	immune disorder; inflammatory disorder; allergy; developmental disorder;
KW	hypothyroidism; Cushing's syndrome; infection; gene; ss.
XX	
OS	Homo sapiens.
XX	
EH	Key
FT	Location/Qualifiers
FT	108..1373
FT	/*tag= a
FT	/product= "REMAP-20"
XX	
PN	WO2003025130-A2.
XX	
PD	27-MAR-2003.
XX	
PF	12-SEP-2002; 2002WO-US029220.
XX	
PR	14-SEP-2001; 2001US-0322157P.
PR	28-SEP-2001; 2001US-0326029P.
PR	05-OCT-2001; 2001US-0327380P.
PR	12-OCT-2001; 2001US-0329198P.
PR	19-OCT-2001; 2001US-0343742P.
PR	02-NOV-2001; 2001US-0343906P.
PR	02-NOV-2001; 2001US-0343980P.
PR	16-NOV-2001; 2001US-0332426P.
PR	13-MAR-2002; 2002US-0364338P.
PR	15-MAR-2002; 2002US-0364494P.
PR	29-MAR-2002; 2002US-0369248P.
XX	
PA	(INCY-) INCYTE GENOMICS INC.
XX	
PI	Warren BA, Gietzen KD, Lal PG, Xu Y, Tran UK, Lee S;
PI	Borowsky ML, Becha SJ, Sanjanwala WM, Thangavelu K, Tang YT;
PI	Honchell CD, Yue H, Elliott VS, Richardson TW, Azimzai Y, Chawla NK;
PI	Ramgun MR, Lu DAM, Nguyen DB, Kalafus DP, Sapperstein SK;
PI	Ramkumar J, Lehr-Mason PM, Griffin JA, Duggan BM, Lee SY;
PI	Zebairjadian Y, Khalifa AJA, Gururajan R, Swarnakar A, Lee EA;
PI	Marquis JP, Khare R, Emerling BM, Jiang X, Jackson RA;
XX	
DR	WPI: 2003-354596/33.
DR	P-PSDB; ABR43188.
XX	
PT	New human receptors and membrane-associated proteins (REMAP), useful for
PT	diagnosing, treating and preventing diseases or conditions associated
PT	with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or
PT	infections.
XX	
PS	Claim 5; Page 230-231; 241pp; English.
XX	
CC	ACC59888 to ACC59923 encode the human receptor and membrane-associated
CC	proteins given in ABR43169 to ABR43204 and designated REMAP-1 to REMAP-36
CC	(i). (I) have cytotstatic, antiatherosclerotic, anticonvulsant,
CC	nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
CC	antiinflammatory and thymoprotetic activities, and can be used in gene
CC	therapy. The REMAP polypeptides and polynucleotides are useful in
CC	diagnosing, treating and preventing diseases or conditions associated
CC	with the decreased expression or overexpression of REMAP, such as cell



```
Db 365 TGGGAAGCCAGAAATTGTAGATTCTCCCTCTGAACCTCAGCGCTGGTGTTCCTCCAAATAGGT 424
QY 423 GGGGACATGTGTCTCAGAGGGAAGCTACCTCGCAGGAGCTCTTAGCTGGCACTTGTGATGG 482
Db 425 GGGGACATGTGTCTCAGAGGGAAGCTACCTCGCAGGAGCTCTTAGCTGGCACTTGTGATGG 484
QY 483 GAAGCCCTTGGTCCCTTAATAGAGGAGATCTGTGAAGGAAACAGACAGGAGACACCC 542
Db 485 GAAGCCCTTGGTCCCTTAATAGAGGAGATCTGTGAAGGAAACAGACAGGAGACACCC 544
QY 543 TGAGACAGGCTCTTCCACATGTCAGTCGAGCTAATGGTGACCCAGCCGCGGGAGGAGA 602
Db 545 TGAGACAGGCTCTTCCACATGTCAGTCGAGCTAATGGTGACCCAGCCGCGGGAGGAGA 604
QY 603 TCCCCCTCCACCTTCTCTGTAGCTTACGCCAGCCAGCCCTTCCCGGACACCGGGCCCTTGG 662
Db 605 TCCCCCTCCACCTTCTCTGTAGCTTACGCCAGCCAGCCCTTCCCGGACACCGGGCCCTTGG 664
QY 663 CACAGCCCCCCTTCCAGCCCGCTCTGAGGAGCTGTGCCCTCTGGAGAGGTCCAAATGGT 722
Db 665 CACAGCCCCCCTTCCAGCCCGCTCTGAGGAGCTGTGCCCTCTGGAGAGGTCCAAATGGT 724
QY 723 GGTGGAGCCAGAGGTGGAGCAGTACTCTCTGTGGACCGGTAAACCGTAACTGTCAAGT 782
Db 725 GGTGGAGCCAGAGGTGGAGCAGTACTCTCTGTGGACCGGTAAACCGTAACTGTCAAGT 784
QY 783 CCTCTGCCAGCCCTCTCTCAAACTCACTGGATGAAGGATGGTGTGCCCTTGGCCCTTCC 842
Db 785 CCTCTGCCAGCCCTCTCTCAAACTCACTGGATGAAGGATGGTGTGCCCTTGGCCCTTCC 844
QY 843 CCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGCTCTCAGGACCGGGAACCTACAGCTG 902
Db 845 CCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGCTCTCAGGACCGGGAACCTACAGCTG 904
QY 903 TGTGGCCACCCATTCCAGCACCGGCCCCCAGGAAAGCCGTCTGTGAGCATCAGCATCAT 962
Db 905 TGTGGCCACCCATTCCAGCACCGGCCCCCAGGAAAGCCGTCTGTGAGCATCAGCATCAT 964
QY 963 CGAAACAGGCGAGGAGGGCCAACTCAGGCTCTGTGGAGGATCAGGCTGGGAACTCT 1022
Db 965 CGAAACAGGCGAGGAGGGCCAACTCAGGCTCTGTGGAGGATCAGGCTGGGAACTCT 1024
QY 1023 AGCCCTGGCCCTGGGATCTGGAGGCTCTGGGACAGCGCCCTCTCATTTGGGTCTAT 1082
Db 1025 AGCCCTGGCCCTGGGATCTGGGAGGCTCTGGGACAGCGCCCTCTCATTTGGGTCTAT 1084
QY 1083 CTTGTGGCAAGGCGCAACCGCGAGGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1142
Db 1085 CTTGTGGCAAGGCGCAACCGCGAGGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1144
QY 1143 AGAGGAGGAGCGTGCAGAACTGAATCAGTCGAGGAACTTGAGGAGGAGGAGGAGGAGGAGGAG 1202
Db 1145 AGAGGAGGAGCGTGCAGAACTGAATCAGTCGAGGAACTTGAGGAGGAGGAGGAGGAGGAGGAG 1204
QY 1203 TGGAGGCGCTTGA 1215
Db 1205 TGGAGGCGCTTGA 1217
```

## RESULT 13

ADP19665

ID ADP19665 standard; cDNA; 1329 BP.

XX AC ADP19665;

XX AC ADP19665;

XX DT 12-AUG-2004 (first entry)

XX DE Human LP2005 encoding cDNA SEQ ID NO:11.

XX KW human; LP2005; antidiabetic; neuroprotective; nootropic;

XX KW antinflammatory; antirheumatic; antiarthritic; vulnerable; cytostatic;

XX KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
systemic lupus erythematosus; gene; ss.

Homo sapiens.

Key Location/Qualifiers  
CDS 46..1206

/product= "LP2005"

/notes= "the present sequence only seems to encode amino  
acids 1 to 386 of the LP2005 protein"

46..114

/tag= a

115..1203

/tag= c

sig\_peptide

mat\_peptide

WO2004044126-A2.

27-MAY-2004.

05-NOV-2003; 2003WO-US032734.

14-NOV-2002; 2002US-0426253P.

(ELIL ) LILLY & CO ELI.

Na S, Perkins DR;

WPI; 2004-411705/38.

P-PSDB; ADP19666.

New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or LP2003) for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome identification.

Claim 1; SEQ ID NO 11; 111pp; English.

The present sequence encodes human LP2005, which is used in the exemplification of the present invention. The present invention describes: (1) an isolated nucleic acid (1) comprising DNA having at least 9% sequence identity to a polynucleotide selected from the group consisting of: (a) a polynucleotide having a nucleotide sequence as shown in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a polypeptide or mature form of a polypeptide having the amino acid sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide having a nucleotide sequence which is complementary to the nucleotide sequence of a polynucleotide as in (a), (b) or (c); (2) a vector comprising (1); (3) a host cell comprising the vector; (4) producing an LP polypeptide; (5) an isolated polypeptide produced by the above method and comprising an amino acid sequence comprising about 95% sequence identity to a sequence of amino acid residues comprising LP2001, LP2003, LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric molecule comprising an LP polypeptide fused to a heterologous amino acid sequence; (7) an antibody which specifically binds to an LP polypeptide described above; (8) a composition (C) comprising a therapeutic amount of an active agent selected from an LP polypeptide, an agonist to an LP polypeptide, an antagonist to an LP polypeptide, an LP polypeptide antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a polynucleotide in combination with a pharmaceutical carrier; and (9) diagnosing or treating a mammal suffering from a disease, condition or disorder associated with aberrant levels of an LP-polypeptide. (C) has antidiabetic, neuroprotective, nootropic, antiinflammatory, antirheumatic, antiarthritic, vulnerable, cytostatic, immunosuppressive, nephrotropic and dermatological activities, and can be used in gene therapy. The compositions (C) and methods are useful for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, such as diabetes and its complications, Alzheimer's disease, inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They may also be used for chromosome identification. The LP polypeptide can



CC also be used in manufacturing a medicament for the treatment of the above  
CC -mentioned diseases, conditions or disorders associated with aberrant  
CC levels of the LP polypeptide.

XX Sequence 1329 BP; 289 A; 379 C; 424 G; 235 T; 0 U; 2 Other;

Query Match 80.3%; Score 1117; DB 12; Length 1329;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGCGGGAACAGCAGTGGAGCCTGGGTCCTCAGTCTGTGGGGGCAAGT 62  
Db 48 GGAGCGGGAACAGCAGTGGAGCCTGGGTCCTCAGTCTGTGGGGGCAAGT 107  
QY 63 AGTGTCTCAAAACATCACAGCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGC 122  
Db 108 AGTGTCTCAAAACATCACAGCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGC 167  
QY 123 CCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAAGCTTG 182  
Db 168 CCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAAGCTTG 227  
QY 183 GAAGTCTCTCTCCAGGAGGAGGAGCCCTGGGACAGTGTGGTCTGTCTCCCAA 242  
Db 228 GAAGTCTCTCTCCAGGAGGAGGAGCCCTGGGACAGTGTGGTCTGTCTCCCAA 287  
QY 243 CGGCTCCCTCTCTCCGCTCTCGGATCCAGGATGAGGGATTTCCGGTGCCAGGC 302  
Db 288 CGGCTCCCTCTCTCCGCTCTCGGATCCAGGATGAGGGATTTCCGGTGCCAGGC 347  
QY 303 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 362  
Db 348 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 407  
QY 363 TGGGAAGCCGAATTTGTAGATTCTGCTCTGAACTCAAGCTGGTGTCTCCAAATAGGT 422  
Db 408 TGGGAAGCCGAATTTGTAGATTCTGCTCTGAACTCAAGCTGGTGTCTCCAAATAGGT 467  
QY 423 GGGGACATGTCTCAGAGGAAGTACCTCGAGGAGCTCTTGTAGCTGGCATTGTGATG 482  
Db 468 GGGGACATGTCTCAGAGGAAGTACCTCGAGGAGCTCTTGTAGCTGGCATTGTGATG 527  
QY 483 GAAGCCCTCTGTCTTAAGAGAGGAGTATCTGTGAAGAACACAGCAGGAGACACC 542  
Db 528 GAAGCCCTCTGTCTTAAGAGAGGAGTATCTGTGAAGAACACAGCAGGAGACACC 587  
QY 543 TGAGACAGGGCTTTACACTGAGTCTGAGGCTAATGGTGAACCCAGCCGGGGAGAGA 602  
Db 588 TGAGACAGGGCTTTACACTGAGTCTGAGGCTAATGGTGAACCCAGCCGGGGAGAGA 647  
QY 603 TCCCGTCCACCTCTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGCTTGG 662  
Db 648 TCCCGTCCACCTCTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGCTTGG 707  
QY 663 CACAGCCCCATCCAGCCCCGTGTCTGGAGCCTGTGCCCTCTGGAGAGGTCCAATTGT 722  
Db 708 CACAGCCCCATCCAGCCCCGTGTCTGGAGCCTGTGCCCTCTGGAGAGGTCCAATTGT 767  
QY 723 GGTGAGCCAGAGGTGGAGCAGTACTCTGTGTGAACCGTAACTGACCTGTGAAGT 782  
Db 768 GGTGAGCCAGAGGTGGAGCAGTACTCTGTGTGAACCGTAACTGACCTGTGAAGT 827  
QY 783 CCTGCGCCAGCCCTCTCTCAAACTCACTGGATGAAGGATGGTGTCCCTTGGCCCTCC 842  
Db 828 CCTGCGCCAGCCCTCTCTCAAACTCACTGGATGAAGGATGGTGTCCCTTGGCCCTCC 887  
QY 843 CCCAGCCCTGTGTCTGATCTTCCCTCAGATAGGGCTCTAGGACCAAGGAACTTACAGT 902  
Db 888 CCCAGCCCTGTGTCTGATCTTCCCTCAGATAGGGCTCTAGGACCAAGGAACTTACAGT 947  
QY 903 TGTGGCCACCCATTCAGCCAGCGGCCCCAGGAAGCGCTGTCTCAGCATCAGCAT 962  
Db 948 TGTGGCCACCCATTCAGCCAGCGGCCCCAGGAAGCGCTGTCTCAGCATCAGCAT 1007

QY 963 CGAACACAGCGGAGGAGGCGCAACTGCAGGCTCTGTGGAGGATCAGGCTGGGAACTCT 1022  
Db 1008 CGAACACAGCGGAGGAGGCGCAACTGCAGGCTCTGTGGAGGATCAGGCTGGGAACTCT 1067  
QY 1023 AGCCCTGGCCCTGGGGATCTCTGGAGGCTCTGGGACAGCCGCCCTCTCATTTGGGTCAT 1082  
Db 1068 AGCCCTGGCCCTGGGGATCTCTGGAGGCTCTGGGACAGCCGCCCTCTCATTTGGGTCAT 1127  
QY 1083 CTTGTGGCAAAAGCGCGCAACGCCGAGGAGGAGG 1119  
Db 1128 CTTGTGGCAAAAGCGCGCAACGCCGAGGAGGAGG 1164

RESULT 14  
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XX AC ADP19669;  
XX AC ADP19669;  
DT 12-AUG-2004 (first entry)  
XX Human LP2007 encoding cDNA SEQ ID NO:15.  
DE human; LP2007; antidiabetic; neuroprotective; nootropic;  
KW antinflammatory; antirheumatic; antiarthritic; vulnerary; cytostatic;  
KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;  
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
KW systemic lupus erythematosus; gene; ss.  
XX Homo sapiens.  
OS  
XX  
PH Key Location/Qualifiers  
FT CDS 46..1218  
FT /tag= b  
FT /product= "LP2007"  
FT sig\_peptide 46..114  
FT /tag= a  
FT mat\_peptide 115..1215  
FT /tag= c  
XX WO2004044126-A2.  
PN  
XX  
XX  
PD 27-MAY-2004.  
XX  
PF 05-NOV-2003; 2003WO-US032734.  
XX  
PR 14-NOV-2002; 2002US-0426253P.  
XX  
PA (ELIL ) LILLY & CO ELI.  
XX  
XX Na S, Perkins DR;  
XX  
XX WPI; 2004-411705/38.  
DR P-PSDB; ADP19670.  
XX  
PT New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or LP2003) for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome identification.  
XX  
XX Example 2; SEQ ID NO 15; 111pp; English.  
XX  
XX The present sequence encodes human LP2007, which is used in the exemplification of the present invention. The present invention describes: (1) an isolated nucleic acid (1) comprising DNA having at least 95% sequence identity to a polynucleotide selected from the group consisting of: (a) a polynucleotide having a nucleotide sequence as shown in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a polypeptide or mature form of a polypeptide having the amino acid sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide

CC having a nucleotide sequence which is complementary to the nucleotide  
 CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector  
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an  
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method  
 CC and comprising an amino acid sequence comprising about 95% sequence  
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,  
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric  
 CC molecule comprising an LP polypeptide fused to a heterologous amino acid  
 CC sequence; (7) an antibody which specifically binds to an LP polypeptide  
 CC described above; (8) a composition (C) comprising a therapeutic amount of  
 CC polypeptide, an agonist to an LP polypeptide, an agonist to an LP  
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide  
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a  
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)  
 CC diagnosing or treating a mammal suffering from a disease, condition or  
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has  
 CC antidiabetic, neuroprotective, nootropic, antiinflammatory,  
 CC antirheumatic, antiarthritic, vulnary, cytostatic, immunosuppressive,  
 CC nephrotropic and dermatological activities, and can be used in gene  
 CC therapy. The compositions (C) and methods are useful for diagnosing or  
 CC treating disorders associated with aberrant levels of an LP polypeptide,  
 CC such as diabetes and its complications, Alzheimer's disease,  
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple  
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
 CC may also be used for chromosome identification. The LP polypeptide can  
 CC also be used in manufacturing a medicament for the treatment of the above  
 CC -mentioned diseases, conditions or disorders associated with aberrant  
 CC levels of the LP polypeptide.

SQ Sequence 1294 BP; 282 A; 367 C; 414 G; 229 T; 0 U; 2 Other;

Query Match 78.2%; Score 1088; DB 12; Length 1294;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 321 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCCTGGGAAGCCAGAAATTGT 380  
 DB 324 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCCTGGGAAGCCAGAAATTGT 383  
 QY 381 AGATTCGCTCTGAATCAGGCTGGTGTTCCTCAATAGGTGGGACATGTGTGCAGA 440  
 DB 384 AGATTCGCTCTGAATCAGGCTGGTGTTCCTCAATAGGTGGGACATGTGTGCAGA 443  
 QY 441 GCGAAGCTACCCCTGCAGGACTCTTAGCTGGCACTTGGATGGGAAGCCCTGGTGCTAA 500  
 DB 444 GCGAAGCTACCCCTGCAGGACTCTTAGCTGGCACTTGGATGGGAAGCCCTGGTGCTAA 503  
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 DB 504 TGAGAAGGGAGTATCTGTGAAGAAACAGACAGGAGACACCCCTGAGACAGGGCTCTTTCAC 563  
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 DB 564 ACTGCAGTCGGAGCTAATGTGACCCAGCCCGGGAGGAGATCCCGTCCCACTTCTTC 623  
 QY 621 CTGTAGCTTCAGCCAGGCTCTCCCGACACCGGGCTTGGCGACAGCCCGCCATCCAGCC 680  
 DB 624 CTGTAGCTTCAGCCAGGCTCTCCCGACACCGGGCTTGGCGACAGCCCGCCATCCAGCC 683  
 QY 681 CCGTGTCTGGAGCTGTGCTCTGAGAGAGGTCCAATTGGTGTGGAGCCAGAGGTGG 740  
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 QY 741 AGCAGTAGCTCTCTGGTGGAAACCGTAACCTTGACTGTGAAGTCCCTGGCCAGCCCTCTCC 800

DB 744 AGCAGTAGCTCTCTGGTGGAAACCGTAACCTTGACTGTGAAGTCCCTGCCCAGCCCTCTCC 803  
 QY 801 TCAATCCCACTGATGAAGATGCTGTGCCCTTGTGCCCTTCCCCCAAGCCCTGTGTGTGAT 860  
 DB 804 TCAATCCCACTGATGAAGATGCTGTGCCCTTGTGCCCTTCCCCCAAGCCCTGTGTGTGAT 863  
 QY 861 CTCTCCCTGATAGAGGCTCTCAGACACAGGAACTTACAGCTGTGTGGCCACCCATTCAG 920  
 DB 864 CTCTCCCTGATAGAGGCTCTCAGACACAGGAACTTACAGCTGTGTGGCCACCCATTCAG 923  
 QY 921 CCACGGGCCCCAGGAAAGCCGTCTGTACGATCAGCATCATCGAACAGGCGGAGGAGG 980  
 DB 924 CCACGGGCCCCAGGAAAGCCGTCTGTACGATCAGCATCATCGAACAGGCGGAGGAGG 983  
 QY 981 GCCAACTGCAAGGCTCTGTGGAGGATCAGGGCTGGGAACCTCTAGCCCTGGCCCTGGGGAT 1040  
 DB 984 GCCAACTGCAAGGCTCTGTGGAGGATCAGGGCTGGGAACCTCTAGCCCTGGCCCTGGGGAT 1043  
 QY 1041 CTGGGAGGCTTGGGACAGCCGCCCTGTCTCATTTGGGTCATCTTGTGGCAAAAGGCGCA 1100  
 DB 1044 CTGGGAGGCTTGGGACAGCCGCCCTGTCTCATTTGGGTCATCTTGTGGCAAAAGGCGCA 1103  
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 DB 1104 ACSCCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1163  
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 DB 1164 ACTGAATAGTCTGGAGGAACTCTGAGGACGAGAGTAGTACTTGGAGGGCTTGGAGGGC 1223  
 QY 1221 CCACAGACAGATCCCATCCATCAGCTCCCTTTCTTTTCCCTTGAACCTGTCTGGCCTC 1280  
 DB 1224 CCACAGACAGATCCCATCCATCAGCTCCCTTTCTTTTCCCTTGAACCTGTCTGGCCTC 1283  
 QY 1281 AGACCAAC 1288  
 DB 1284 AGACCAAC 1291

RESULT 15  
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 AC ADE95565;  
 XX AC  
 XX XX  
 DT 12-FEB-2004 (first entry)  
 XX DT  
 DE Human NOVX16d protein cDNA sequence.  
 XX DE  
 KW NOVX protein; biochemical stimulation; physiological stimulation;  
 KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
 KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;  
 KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;  
 KW nootropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;  
 KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;  
 KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;  
 KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;  
 KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;  
 KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;  
 KW depression; allergy; fertility disorder; gene; ss; NOVX16d.  
 XX KW  
 OS Homo sapiens.  
 XX OS  
 XX WO2003050245-A2.  
 XX PN  
 XX 19-JUN-2003.  
 XX PD  
 XX 03-DEC-2002; 2002WO-US038594.  
 XX PF  
 XX 05-DEC-2001; 2001US-0336600P.  
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 XX 07-DEC-2001; 2001US-0338285P.  
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 XX 12-DEC-2001; 2001US-0341346P.  
 XX PR  
 XX 17-DEC-2001; 2001US-0341477P.

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PR 20-DEC-2001; 2001US-0342592P.  
PR 27-DEC-2001; 2001US-0344297P.  
PR 31-DEC-2001; 2001US-0344903P.  
PR 17-APR-2002; 2002US-0373288P.  
PR 15-MAY-2002; 2002US-0380981P.  
PR 17-MAY-2002; 2002US-0381495P.  
PR 28-MAY-2002; 2002US-0383534P.  
PR 28-MAY-2002; 2002US-0383744P.  
PR 29-MAY-2002; 2002US-0383829P.  
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PR 07-AUG-2002; 2002US-0401788P.  
PR 26-AUG-2002; 2002US-0406353P.  
PR 31-OCT-2002; 2002US-00401788.  
PR 02-DEC-2002; 2002US-00406353.  
XX (CURA-) CURAGEN CORP.  
XX  
XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;  
PI Edinger SR, Garlach VL, Gorman L, Gould-Rothberg BE, Guo X;  
PI Jeffers ME, Ji W, Li L, Malvankar UM, Miller CE, Murphy R;  
PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;  
PI Smithson G, Scarling R, Voss EZ, Zhong H, Zhong M;  
XX  
DR WPI; 2003-513974/48.  
DR P-PSDB; ADE95566.  
XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
XX Claim 20; SEQ ID NO 97; 211pp; English.  
XX  
XX This invention relates to novel NOVX proteins, and the DNA sequence which  
CC encode them, having properties related to stimulation of biochemical or  
CC physiological responses in a cell, a tissue, an organ or an organism.  
CC Compounds which modulate the proteins of the invention may have cardiac,  
CC antiarrhythmic, hypotensive, cytostatic, anorectic, antirheumatic,  
CC antiarthritic, antidiabetic, nephrotropic, dermatological,  
CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,  
CC nootropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,  
CC antidepressant, antiallergic or gynaecological activities. The DNA  
CC sequences of the invention may be useful for gene therapy whilst the  
CC protein sequences may allow the development of a vaccine. The protein is  
CC useful in the manufacture of a medicament for treating a syndrome  
CC associated with a human disease. The invention may be useful in  
CC diagnosing, treating or preventing NOVX-associated disorders, for example  
CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,  
CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin  
CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,  
CC Parkinson's disease, asthma, schizophrenia, depression, allergies or  
CC fertility disorders. The nucleic acids may further be used as  
CC hybridisation probes, in chromosome mapping, tissue typing, preventive  
CC medicine, and pharmacogenomics. The present sequence is the cDNA sequence  
CC which encodes the human NOVX16d protein of the invention.  
XX  
XX Sequence 1226 BP; 270 A; 348 C; 397 G; 211 T; 0 U; 0 Other;  
XX  
XX Query Match 75.1%; Score 1044; DB 10; Length 1226;  
Best Local Similarity 100.0%; Pred. No. 0;  
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DB 423 GGGAGCTACCTCTGAGGAGTCTTGTAGCTGGGACTTTGTAGTGGGAAAGCCCTCTGTGCTTAA 482  
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QY 561 ACTGAGTGGGAGTAAATGAGTACCCAGCCCGGAGGAGATCCCGTCCACCTTCTC 620  
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QY 621 CTGTAGCTTTCAGCCAGGCTTTCCCGACACCGGGCTTTGCGACACAGCCCCCATCCAGCC 680  
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QY 681 CCGTGTCTGGGAGCTCTGCTCTGAGAGAGTCCAAATTTGGTGGTGGAGCCAGAGGTGG 740  
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QY 741 AGCAGTAGCTCTCTGTTGGAACCTGACCTGTGAACTCCCTGCGCCAGCCCTCTCC 800  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1289	92.7	1391	4	US-09-638-649-4
2	1289	92.7	1391	4	US-09-638-648-4
3	1213	87.2	1215	4	US-09-949-016-5154
4	1018	73.2	1023	2	US-08-633-148-1
5	873	62.8	1405	4	US-08-755-235-3
6	852	61.3	957	2	US-08-633-148-3
7	274	19.7	5816	4	US-09-949-016-16900
8	274	19.7	7080	4	US-09-949-016-16896
9	108	7.8	601	4	US-09-949-016-178939
10	93	6.7	601	4	US-09-949-016-178940
11	72	5.2	601	4	US-09-949-016-178938
12	42	3.0	1426	4	US-09-638-649-2
13	42	3.0	1426	4	US-09-638-648-2
14	42	3.0	1438	4	US-08-755-235-1
15	40	2.9	601	4	US-09-949-016-178941
16	32	2.3	1347	4	US-09-638-648-6
17	32	2.3	1348	4	US-09-638-649-6
18	29	2.1	601	4	US-09-949-016-178942
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20	22	1.6	22	4	US-09-638-649-8
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27	20	1.4	1164	3	US-08-445-461-11

ALIGNMENTS

RESULT 1

US-09-638-649-4  
; Sequence 4, Application US/09638649  
; Patent No. 6563015  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND  
; FILE REFERENCE: 0575/62175  
; CURRENT APPLICATION NUMBER: US/09/638,649  
; CURRENT FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1391  
; TYPE: DNA  
; ORGANISM: Human  
US-09-638-649-4

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Sequence 12669, A  
Sequence 15501, A  
Sequence 15995, A  
Sequence 1, Appli  
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Sequence 22, Appl  
Sequence 993, App  
Sequence 16191, A  
Sequence 5121, Ap

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## RESULT 2

US-09-638-648-4  
; Sequence 4, Application US/09638648  
; Patent No. 6825164

GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie

APPLICANT: Yan, Shi Du  
; APPLICANT: Zlokovic, Berislav

TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID  
; FILE REFERENCE: 0575/62097  
; CURRENT APPLICATION NUMBER: US/09/638,648  
; NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 4

LENGTH: 1391  
; TYPE: DNA

ORGANISM: Human  
; US-09-638-648-4

Query Match 92.7%; Score 1289; DB 4; Length 1391;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1389; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1389	99.9	1415	18 US-10-115-635-351	Sequence 351, App
3	1162	83.5	1217	17 US-10-309-290-95	Sequence 95, Appl
4	1044	75.1	1226	17 US-10-309-290-97	Sequence 97, Appl
5	1015	73.0	1173	17 US-10-309-290-99	Sequence 99, Appl
6	1013	72.8	1020	16 US-10-091-019-2	Sequence 2, Appli
7	990	71.2	1223	19 US-10-472-507A-1	Sequence 1, Appli
8	973	69.9	1463	18 US-10-115-635-352	Sequence 352, App
9	873	62.8	1405	8 US-08-905-709-3	Sequence 3, Appli
10	873	62.8	1405	8 US-08-755-235-3	Sequence 3, Appli
11	873	62.8	1405	18 US-10-850-861-3	Sequence 3, Appli

12	336	24.2	336	16	US-10-091-019-4	Sequence 4, Appli
13	274	19.7	62944	9	US-09-954-456-2257	Sequence 2257, App
14	274	19.7	62944	11	US-09-968-007A-129	Sequence 129, App
15	197	14.2	203	16	US-10-029-386-16362	Sequence 16362, A
16	197	14.2	485	13	US-10-027-632-257559	Sequence 257559, A
17	197	14.2	485	17	US-10-027-632-257559	Sequence 257559, A
18	197	14.2	553	16	US-10-029-386-2662	Sequence 2662, App
19	181	13.0	610	9	US-09-954-456-906	Sequence 906, App
20	181	13.0	610	9	US-09-880-107-3595	Sequence 3595, App
21	142	10.2	582	16	US-10-029-386-9526	Sequence 9526, App
22	134	9.6	142	16	US-10-029-386-23226	Sequence 23226, A
23	123	8.8	123	18	US-10-484-364-64	Sequence 64, Appl
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28	60	4.3	60	10	US-09-908-975-14550	Sequence 14550, A
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31	42	3.0	1438	8	US-08-755-235-1	Sequence 1, Appli
32	42	3.0	1438	18	US-10-850-861-1	Sequence 1, Appli
33	29	2.1	823	17	US-10-433-965-8	Sequence 8, Appli
34	25	1.8	49	16	US-10-091-019-9	Sequence 9, Appli
35	23	1.7	23	19	US-10-472-507A-4	Sequence 4, Appli
36	22	1.6	23	17	US-10-309-290-219	Sequence 219, App
37	22	1.6	32	18	US-10-484-364-66	Sequence 66, Appl
38	22	1.6	275	18	US-10-425-115-23468	Sequence 23468, A
39	22	1.6	570	18	US-10-767-701-6728	Sequence 6728, App
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ALIGNMENTS

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US-10-091-019-1  
; Sequence 1, Application US/10091019  
; Publication No. US20030166063A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Robert B.  
; APPLICANT: Shen, Jane M.  
; APPLICANT: Shabbaz, Manouchehr M.  
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins  
; FILE REFERENCE: 41305-270555  
; CURRENT APPLICATION NUMBER: US/10/091,019  
; CURRENT FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/273,418  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1391  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-091-019-1

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			Gaps	0;
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RESULT 2

US-10-115-635-351  
; Sequence 351, Application US/10115635  
; Publication No. US20040137434A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Bing  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Xue, Aiding J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 797CON  
; CURRENT APPLICATION NUMBER: US/10/115,635  
; CURRENT FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: 09/714,936  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 362  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 351  
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; NAME/KEY: CDS  
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US-10-115-635-351

Query Match 99.9%; Score 1389; DB 18; Length 1415;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1263 TTGAATCTTGTGGCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATATCAACCC 1322  
Db 1287 TTGAATCTTGTGGCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATATCAACCC 1346  
QY 1323 ACCTTGGCAAGCTTTCTTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1382  
Db 1347 ACCTTGGCAAGCTTTCTTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1406

RESULT 3

US-10-309-290-95  
; Sequence 95, Application US/10309290  
; Publication No. US20040023241A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook II, John P.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Chillakuru, Rajeev A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Gould-Rothberg, Bonnie E.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Jeffers, Michael E.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Li, Li  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Murphy, Ryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Peyman, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Smithson, Glenn  
; APPLICANT: Starling, Gary  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Voss, Edward Z.  
; APPLICANT: Zhong, Hailong  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
; FILE REFERENCE: 21402-502A  
; CURRENT APPLICATION NUMBER: US/10/309,290  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/336,600  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,285  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/341,346  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/341,477  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/341,540  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/342,592  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/344,297  
; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/344,903  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/373,288  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 60/380,981  
; PRIOR FILING DATE: 2002-05-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 95  
; LENGTH: 1217  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)..(1214)  
US-10-309-290-95

Query Match		83.5%;	Score 1162;	DB 17;	Length 1217;		
Best Local Similarity		99.9%;	Pred. No. 0;				
Matches 1212;		Conservative	0;	Mismatches	1;	Indels	0; Gaps 0;
QY	3	GGCAGCCGGAACAGCAGTGTGAGCCTCGGTGCTGGTCTCCTCAGTCTGTGGGGGAGT	62				
Db	5	GGCAGCCGGAACAGCAGTGTGAGCCTCGGTGCTGGTCTCCTCAGTCTGTGGGGGAGT	64				
QY	63	AGTGTCTCAAAACATCACAGCCGATTGGCGACCACTGGTCTGAAAGTGAAGGGGC	122				
Db	65	AGTGTCTCAAAACATCACAGCTCGAATTGGCGACCACTGGTCTGAAAGTGAAGGGGC	124				
QY	123	CCCCAAGAAACCCACCCAGCGGCTGGAATGAAACACAGGCGGACAGAAAGCTTG	182				
Db	125	CCCCAAGAAACCCACCCAGCGGCTGGAATGAAACACAGGCGGACAGAAAGCTTG	184				
QY	183	GAAGTCTGTCTCCCGCAGGAGAGGCCCTCGGACAGTGTGGCTGTCTTCCCAA	242				
Db	185	GAAGTCTGTCTCCCGCAGGAGAGGCCCTCGGACAGTGTGGCTGTCTTCCCAA	244				
QY	243	CGGCTCCCTCTTCTCCGCTGTCCGATCCAGGATGAGGGATTTCCGGTGCCAGGC	302				
Db	245	CGGCTCCCTCTTCTCCGCTGTCCGATCCAGGATGAGGGATTTCCGGTGCCAGGC	304				
QY	303	AATGAACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC	362				
Db	305	AATGAACAGAAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC	364				
QY	363	TGGAGGCCAGAAATGTAGATTCTGCCTCTGAACTACGGCTGGTGTCCCAATAGGT	422				
Db	365	TGGAGGCCAGAAATGTAGATTCTGCCTCTGAACTACGGCTGGTGTCCCAATAGGT	424				
QY	423	GGGACATGTGTCTCAGAGGAAGTACCCCTGACGAGCTCTTAGCTGGCATTGTATG	482				
Db	425	GGGACATGTGTCTCAGAGGAAGTACCCCTGACGAGCTCTTAGCTGGCATTGTATG	484				
QY	483	GAAGCCCTGGTGCCTAATGAGAGGAGTATCTGTGAAGGAACAGACCAGGAGACCC	542				
Db	485	GAAGCCCTGGTGCCTAATGAGAGGAGTATCTGTGAAGGAACAGACCAGGAGACCC	544				
QY	543	TGAGACAGGCTCTTACACTGAGTCGGAGCTAATGTTGACCCAGCCGGGAGGAGA	602				
Db	545	TGAGACAGGCTCTTACACTGAGTCGGAGCTAATGTTGACCCAGCCGGGAGGAGA	604				
QY	603	TCCCGCTCCACCTTCTCTGTAGTTCAGCCAGGCTTCCCGACACCGGCTTGG	662				
Db	605	TCCCGCTCCACCTTCTCTGTAGTTCAGCCAGGCTTCCCGACACCGGCTTGG	664				
QY	663	CACAGCCCTCATCAGCCCTGTCTGGAGCTGTGCTCTGGAGAGGTCAAATTGT	722				
Db	665	CACAGCCCTCATCAGCCCTGTCTGGAGCTGTGCTCTGGAGAGGTCAAATTGT	724				
QY	723	GGTGGAGCAGAGGTGGAGCTAGCTCTCTGTGGAACCGTAACCTGACCTGTGAAGT	782				
Db	725	GGTGGAGCAGAGGTGGAGCTAGCTCTCTGTGGAACCGTAACCTGACCTGTGAAGT	784				
QY	783	CCCTGCCAGCCCTCTCTCAATCCACTGGATGAGTGTGTGCTTGCCTTGCCTTCC	842				
Db	785	CCCTGCCAGCCCTCTCTCAATCCACTGGATGAGTGTGTGCTTGCCTTGCCTTCC	844				
QY	843	CCCCAGCCTGTGCTGATCTCTCTGATAGTAGGCTCAGGACCGAGGAACCTACAGTG	902				
Db	845	CCCCAGCCTGTGCTGATCTCTCTGATAGTAGGCTCAGGACCGAGGAACCTACAGTG	904				
QY	903	TGTGGCCACCCATTCCAGCCAGCGGCCCCAGGAAGCCGTGTGTCTCAGCATCAGATCAT	962				
Db	905	TGTGGCCACCCATTCCAGCCAGCGGCCCCAGGAAGCCGTGTGTCTCAGCATCAGATCAT	964				
QY	963	CGAACAGGCGAGGAGGGCCAACTGTCAGGCTCTGTGGAGGATCAGGCTGGGAACCT	1022				
Db	965	CGAACAGGCGAGGAGGGCCAACTGTCAGGCTCTGTGGAGGATCAGGCTGGGAACCT	1024				

RESULT 4  
US-10-309-290-97  
; Sequence 97, Application US/10309290  
; Publication No. US20040023241A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook II, John P.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Chillakuru, Rajeev A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Gould-Rothberg, Bonnie E.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Jeffers, Michael E.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Li, Li  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Murphy, Ryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Peyman, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Starling, Gary  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Voss, Edward Z.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
; FILE REFERENCE: 21402-502A  
; CURRENT APPLICATION NUMBER: US/10/309,290  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/336,600  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,285  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/341,346  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/341,477  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/341,540  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/342,592  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/344,297  
; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/344,903  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/373,288  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 60/380,981  
; PRIOR FILING DATE: 2002-05-15

QY	1023	AGCCCTGGCCCTGGGATCCTGGAGGCTCTGGGACAGCCGCCCTCTCATTTGGGGTCAT	1082
Db	1025	AGCCCTGGCCCTGGGATCCTGGAGGCTCTGGGACAGCCGCCCTCTCATTTGGGGTCAT	1084
QY	1083	CTTGTGGCAAAAGCGCGCAACGCGAGGAGAGAGGAAAGGCCCAAGAAAAACAGGAGGA	1142
Db	1085	CTTGTGGCAAAAGCGCGCAACGCGAGGAGAGAGGAAAGGCCCAAGAAAAACAGGAGGA	1144
QY	1143	AGAGGAGGAGCCTGCAGAACTGAATCAGTCTGGAGGAACCTGAGGACGCGAGTAGTAC	1202
Db	1145	AGAGGAGGAGCCTGCAGAACTGAATCAGTCTGGAGGAACCTGAGGACGCGAGTAGTAC	1204
QY	1203	TGAGGCGCTTGA	1215
Db	1205	TGAGGCGCTTGA	1217

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 97
; LENGTH: 1226
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1194)
US-10-309-290-97

Query Match      75.1%; Score 1044; DB 17; Length 1226;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1044; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 201 GGGAGGAGGCCCTGGGACAGTGGCGTCTGGTGCTCTTCCCAACGGCTCCCTCTTCCTTCC 260
Db 183 GGGAGGAGGCCCTGGGACAGTGGCGTCTGGTGCTCTTCCCAACGGCTCCCTCTTCCTTCC 242
Qy 261 GGCTGTCCGGATCCAGGATGAGGGGATTTTCCGGTGCACGCAATGAACAGGAATGGA 320
Db 243 GGCTGTCCGGATCCAGGATGAGGGGATTTTCCGGTGCACGCAATGAACAGGAATGGA 302
Qy 321 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTGGGAAGCCAGAAATGT 380
Db 303 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTGGGAAGCCAGAAATGT 362
Qy 381 AGATTCTGCCTCTGAATCTACCGGTGGTGTTCCTCAATAAGGTGGGACATGTGTGTGAGA 440
Db 363 AGATTCTGCCTCTGAATCTACCGGTGGTGTTCCTCAATAAGGTGGGACATGTGTGTGAGA 422
Qy 441 GGGAAAGTCAACCTCAGGGACTCTTAGCTGGCACTTGGATGGGAAGCCCTGTGTGCCTAA 500
Db 423 GGGAAAGTCAACCTCAGGGACTCTTAGCTGGCACTTGGATGGGAAGCCCTGTGTGCCTAA 482
Qy 501 TGAGAAAGGAGTATCTGTGAAGAAACAGACAGAGAGACACCTTGAGACAGGGCTCTTTAC 560
Db 483 TGAGAAAGGAGTATCTGTGAAGAAACAGACAGAGAGACACCTTGAGACAGGGCTCTTTAC 542
Qy 561 ACTGCAGTCGGAGCTAATGTTGACCCAGCCCGGGAGGAGATCCCGTCCCACTTCTC 620
Db 543 ACTGCAGTCGGAGCTAATGTTGACCCAGCCCGGGAGGAGATCCCGTCCCACTTCTC 602
Qy 621 CTGTAGCTTCAGCCACAGCCCTTCCCACACACCGGGCTTGGCACAGCCCCCATCCAGCC 680
Db 603 CTGTAGCTTCAGCCACAGCCCTTCCCACACACCGGGCTTGGCACAGCCCCCATCCAGCC 662
Qy 681 CCGTGTCTGGAGCCTGTGCCTCTGGAGGAGGTCCAATTGGTGTGGAGCCAGAAAGTGG 740
Db 663 CCGTGTCTGGAGCCTGTGCCTCTGGAGGAGGTCCAATTGGTGTGGAGCCAGAAAGTGG 722
Qy 741 AGCAGTAGCTCTCGTGGAACCGTAAACCTGACCTGTGAAGTCCCTGCCAGGCCCTTCC 800
Db 723 AGCAGTAGCTCTCGTGGAACCGTAAACCTGACCTGTGAAGTCCCTGCCAGGCCCTTCC 782
Qy 801 TCAAACTCCACTGGATGAAGGATGTGTGCCCTTCCCTCCCTCCAGCCCTGTGCTGAT 860
Db 783 TCAAACTCCACTGGATGAAGGATGTGTGCCCTTCCCTCCCTCCAGCCCTGTGCTGAT 842
Qy 861 CCTCCCTGAGATAGGGCCTCAGGACACAGGAAACCTACAGCTGTGTGGCCACCCATCCAG 920
Db 843 CCTCCCTGAGATAGGGCCTCAGGACACAGGAAACCTACAGCTGTGTGGCCACCCATCCAG 902
Qy 921 CCACGGGCCCCAGGAAACCGGTGTGTTCAGCATCAGCATCATCGAAACAGCGCAGAGAGGG 980
Db 903 CCACGGGCCCCAGGAAACCGGTGTGTTCAGCATCAGCATCATCGAAACAGCGCAGAGAGGG 962
Qy 981 GCCAACTGCAGGCTCTGTGGAGAGATCAGGGCTGGGAACCTTAGCCCTGTGCCCTGGGGAT 1040
Db 963 GCCAACTGCAGGCTCTGTGGAGAGATCAGGGCTGGGAACCTTAGCCCTGTGCCCTGGGGAT 1022
Qy 1041 CCTGGGAGGCCCTGGGGAACAGCCGCCCTCTCATTTGGGGGTCTATCTTGTGGAAAGCGCGCA 1100

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[illegible]

; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: CuroSeqList version 0.1  
; SEQ ID NO 99  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1170)  
US-10-309-290-99

Query Match 73.0%; Score 1015; DB 17; Length 1173;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 201 GGGAGGAGGCGCCCTGGGACAGTGTGGCTGTCTTCCCAACGGCTCCCTCTTCTTCC 260  
Db 159 GGGAGGAGGCGCCCTGGGACAGTGTGGCTGTCTTCCCAACGGCTCCCTCTTCTTCC 218  
Qy 261 GGCTGTCCGGATCCAGATCAGGGGATTTCCGGTGCAGGCAATGAACAGGAATGAAA 320  
Db 219 GGCTGTCCGGATCCAGATCAGGGGATTTCCGGTGCAGGCAATGAACAGGAATGAAA 278  
Qy 321 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCCTGGGAAGCCAGAAATTGT 390  
Db 279 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCCTGGGAAGCCAGAAATTGT 338  
Qy 381 AGATTCTCGCTCTGAACCTACCGCTGGTGTGTCCCAATAAGTGGGACATGTGTGACGA 440  
Db 339 AGATTCTCGCTCTGAACCTACCGCTGGTGTGTCCCAATAAGTGGGACATGTGTGACGA 398  
Qy 441 GGGAAAGTACCTGCAGGACTCTTAGCTGGCACTTTGGATGGGAAGCCCTGTGTGCTAA 500  
Db 399 GGGAAAGTACCTGCAGGACTCTTAGCTGGCACTTTGGATGGGAAGCCCTGTGTGCTAA 458  
Qy 501 TGAGAGGGAGTATCTGTGAAGAAACAGACAGGACACACCTTGACAGAGGCTCTTAC 560  
Db 459 TGAGAGGGAGTATCTGTGAAGAAACAGACAGGACACACCTTGACAGAGGCTCTTAC 518  
Qy 561 ACTGCAATCGGAGCTAATGTGTACCCAGCCCGGGGAGGAGATCCCGCTCCCACTTCTC 620  
Db 519 ACTGCAATCGGAGCTAATGTGTACCCAGCCCGGGGAGGAGATCCCGCTCCCACTTCTC 578  
Qy 621 CTGTAGCTTCAAGCCAGGCTTCCCGACACCGGGCTTGGCGACAGCCGCCATCCAGCC 680  
Db 579 CTGTAGCTTCAAGCCAGGCTTCCCGACACCGGGCTTGGCGACAGCCGCCATCCAGCC 638  
Qy 681 CCGTGTCTGGAGCTGTGCTCTGGAGGAGTCCAAATTGGTGGAGCCAGAGGTGG 740  
Db 639 CCGTGTCTGGAGCTGTGCTCTGGAGGAGTCCAAATTGGTGGAGCCAGAGGTGG 698  
Qy 741 AGCAGTAGCTCTCTGGTGAACCGTAACCTGTGAAGTCCCTGCGCCAGCCCTCTCC 800  
Db 699 AGCAGTAGCTCTCTGGTGAACCGTAACCTGTGAAGTCCCTGCGCCAGCCCTCTCC 758  
Qy 801 TCAATTCAGTGAAGATGGTGTGCTTGGCCCTTCCCGCTTCCCGCCAGCCCTGTGTGAT 860  
Db 759 TCAATTCAGTGAAGATGGTGTGCTTGGCCCTTCCCGCTTCCCGCCAGCCCTGTGTGAT 818  
Qy 861 CTTCTCTGATAGGCGCTCAGGACAGGGAACCTACAGTGTGTGGCCACCCATTCAG 920  
Db 819 CTTCTCTGATAGGCGCTCAGGACAGGGAACCTACAGTGTGTGGCCACCCATTCAG 878  
Qy 921 CCAAGGCGCCAGGAAAGCGGTCTGTACAGCATCAGCATCAGCATCAGCATCAGCATCAG 980  
Db 879 CCAAGGCGCCAGGAAAGCGGTCTGTACAGCATCAGCATCAGCATCAGCATCAGCATCAG 938  
Qy 981 GCCAATGCAAGCTCTGTGGAGGATCAGGCTGGAACTTAGCCCTGGCCCTGGGGAT 1040  
Db 939 GCCAATGCAAGCTCTGTGGAGGATCAGGCTGGAACTTAGCCCTGGCCCTGGGGAT 998  
Qy 1041 CTTGGAGGCTGGGACAGCCCGCTGTCTATTGGGGTCACTTGTGGCAAGGCGCA 1100

## RESULT 6

US-10-091-019-2  
; Sequence 2, Application US/10091019  
; Publication No. US20030166063A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Robert B.  
; APPLICANT: Shen, Jane M.  
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins  
; FILE REFERENCE: 41305-270555  
; CURRENT APPLICATION NUMBER: US/10/091,019  
; CURRENT FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/273,418  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 1020  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1020)  
; OTHER INFORMATION:  
US-10-091-019-2

Query Match 72.8%; Score 1013; DB 16; Length 1020;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1013; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGCAGCGGAAACAGCAGTGTGGAGCCCTGGGTGTCTCCTCAGTCTGTGGGGGCAGTAGT 62  
Db 3 GGCAGCGGAAACAGCAGTGTGGAGCCCTGGGTGTCTCCTCAGTCTGTGGGGGCAGTAGT 62  
Qy 63 AGGTCTCAAAACATCACAGCCCGGATTTGGGAGCCACTGGTGTCTGAAGTGTAAAGGGGC 122  
Db 63 AGGTCTCAAAACATCACAGCCCGGATTTGGGAGCCACTGGTGTCTGAAGTGTAAAGGGGC 122  
Qy 123 CCCCAGAAACCCACCCAGCGCTGGATGGAATGGAACCTGAACACAGCCCGGACAGAAAGTTG 182  
Db 123 CCCCAGAAACCCACCCAGCGCTGGATGGAATGGAACCTGAACACAGCCCGGACAGAAAGTTG 182  
Qy 183 GAGGTCTGTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTGTCTTCCCA 242  
Db 183 GAGGTCTGTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTGTCTTCCCA 242  
Qy 243 CGGCTCCCTCTTCTCTTCCGGTGTCCGGATCAGGATCAGGGGATTTTCCGGTGCAGGC 302  
Db 243 CGGCTCCCTCTTCTCTTCCGGTGTCCGGATCAGGATCAGGGGATTTTCCGGTGCAGGC 302  
Qy 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGTTC 362  
Db 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGTTC 362  
Qy 363 TGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCAGGCTGTGTGTCCCAATAAGT 422  
Db 363 TGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCAGGCTGTGTGTCCCAATAAGT 422  
Qy 423 GGGACATGTGTGTGTCAGAGGGAAGCTACCCCTGCAAGGACTCTTAGCTGGCACTTGGATGG 482  
Db 423 GGGACATGTGTGTGTCAGAGGGAAGCTACCCCTGCAAGGACTCTTAGCTGGCACTTGGATGG 482

483 GAAGCCCTGGTCTTAATGAGAGGGAGTATCTGTGAAGGAAACAGACCAAGGAGACACCC 542  
483 GAAGCCCTGGTCTTAATGAGAGGGAGTATCTGTGAAGGAAACAGACCAAGGAGACACCC 542  
543 TGAGACAGGGCTCTTACACCTGAGCTGGAGCTAAATGGTGACCCACAGCCCGGGAGGAGA 602  
543 TGAGACAGGGCTCTTACACCTGAGCTGGAGCTAAATGGTGACCCACAGCCCGGGAGGAGA 602  
603 TCCCGCTCCACCTTCTCTCTGTAGCTTACAGCCAGGCTTCCCGGACACCCGGGCTTTGGC 662  
603 TCCCGCTCCACCTTCTCTCTGTAGCTTACAGCCAGGCTTCCCGGACACCCGGGCTTTGGC 662  
663 CACAGCCCCATCAGCCCGTGTCTGGAGACCTGTGCTCTCTGGAGAGGTCCAAATTTGGT 722  
663 CACAGCCCCATCAGCCCGTGTCTGGAGACCTGTGCTCTCTGGAGAGGTCCAAATTTGGT 722  
723 GGTGGAGCCAGAGGTGGAGCAGTACCTCTCTGTGGAAACCGTAACCTGACCTGTGAAGT 782  
723 GGTGGAGCCAGAGGTGGAGCAGTACCTCTCTGTGGAAACCGTAACCTGACCTGTGAAGT 782  
783 CCTGCCCAGCCCTCTCTCTCAATCCACTGGATGAAGGATGGTGTGCTTGCCTTTGCCCTTCC 842  
783 CCTGCCCAGCCCTCTCTCTCAATCCACTGGATGAAGGATGGTGTGCTTGCCTTTGCCCTTCC 842  
843 CCCAGCCCTGTGTGATCT 902  
843 CCCAGCCCTGTGTGATCT 902  
903 TGTGGCCACCCATTCACGACCCGCGCCAGGAAAGCCGCTGTGAGCATCAGCATCAT 962  
903 TGTGGCCACCCATTCACGACCCGCGCCAGGAAAGCCGCTGTGAGCATCAGCATCAT 962  
963 CGAACACAGGCGAGGGGCGCAACTGCAGGCTCTGTGGAGGATCAGGGCTGG 1015  
963 CGAACACAGGCGAGGGGCGCAACTGCAGGCTCTGTGGAGGATCAGGGCTGG 1015

RESULT 7

US-10-472-507A-1  
; Sequence 1, Application US/10472507A  
; Publication No. US20050033017A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamamoto, Hiroshi  
; APPLICANT: Yonekura, Hideto  
; APPLICANT: Yamamoto, Yasuhiko  
; APPLICANT: Sakurai, Shigeru  
; APPLICANT: Watanabe, Takuo  
; TITLE OF INVENTION: Soluble Rage Protein  
; FILE REFERENCE: 026350-089  
; CURRENT APPLICATION NUMBER: US/10/472, 507A  
; CURRENT FILING DATE: 2003-09-22  
; PRIOR APPLICATION NUMBER: PCT/JP02, 02623  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: JP 2001-78409  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: JP 2001-243114  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: JP 2002-48182  
; PRIOR FILING DATE: 2002-02-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1223  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)...(1068)  
US-10-472-507A-1

Query Match 71.2%; Score 990; DB 19; Length 1223;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 990; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 GGAGCCCGAAGCAGAGTTGGAGCCTGGGTGCTGGTCTCTCAGTCTGTGGGGGCGAGTAGT 62  
27 GGAGCCCGGAACAGCAGTTGGAGCCTGGGTGCTGGTCTCTCAGTCTGTGGGGGCGAGTAGT 86  
63 AGGTGCTCAAAACATCAGACCCCGGATTTGGCGAGCCACTGGTGTCTGAGTGTAAAGGGGC 122  
87 AGGTGCTCAAAACATCAGACCCCGGATTTGGCGAGCCACTGGTGTCTGAAAGTGTAAAGGGGC 146  
123 CCCAAGAAACACACCCCGGCTGGAATGGAACCTGAAACACAGGCGCGAGCAGAGCTTG 182  
147 CCCAAGAAACACACCCCGGCTGGAATGGAACCTGAAACACAGGCGCGAGCAGAGCTTG 206  
183 GAAAGTCTGTCTCTCTCCAGGAGAGGCGCTCTGGACAGTGTGGTGTCTCTCTCCAA 242  
207 GAAAGTCTGTCTCTCTCCAGGAGAGGCGCTCTGGACAGTGTGGTGTCTCTCTCCAA 266  
243 CGGCTCCCTCTCTCTCTCCGCTGTGGGATCCAGGATGAGGGATTTTCCGGTGGCAGGC 302  
267 CGGCTCCCTCTCTCTCTCCGCTGTGGGATCCAGGATGAGGGATTTTCCGGTGGCAGGC 326  
303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTTACCAAGATTCC 362  
327 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTTACCAAGATTCC 386  
363 TGGGAAGCCAGAAATTTGTAGTTCTGCTCTCTGAACTCAGCGCTGGTGTCTCCCAATAGGT 422  
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RESULT 8

US-10-115-635-352  
; Sequence 352, Application US/10115635



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; Publication No. US20040137434A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Weinman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 797CON
; CURRENT APPLICATION NUMBER: US/10/115,635
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/714,936
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 362
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 352
; LENGTH: 1463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1287)
; US-10-115-635--352

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Query Match 69.9%; Score 973; DB 18; Length 1463;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 973; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 599 GAGATCCCGTCCACCTTCTCTGTAGTTCAGCCAGGCTTCCCGGACACCGGGCT 658
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RESULT 9
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; Sequence 3, Application US/08905709
; Publication No. US2001003256A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Schmidt, Ann M.
; TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED
; TITLE OF INVENTION: ATHEROSCLEROSIS USING (sRAGE) SOLUBLE RECEPTOR FOR
; TITLE OF INVENTION: ADVANCED GLYCATION ENDPRODUCTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Cooper & Dunham LLP
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,709
; FILING DATE: 05-AUG-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/52876
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

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C 3	645	46.4	663	5	BU677612	UI-CF-ECO	BU677612
4	644	46.3	841	4	BI771266		BI771266
5	604	43.4	729	4	BG545652		BG545652
6	602	43.3	1163	9	AY421474	Pan trogl	AY421474
7	597	42.9	777	4	BG545464	602572696	BG545464
8	586	42.1	715	4	BG529831	602558918	BG529831
9	584	42.0	1194	4	BQ667161	AGENCOURT	BQ667161
10	562	40.4	724	4	BG536369	602564760	BG536369
11	549	39.5	553	4	BI772105	602505188	BI772105
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19	442	31.8	567	5	BI105560	BX105560	BI105560
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23	411	29.5	730	4	BG539104	602568478	BG539104
24	402	28.9	653	4	BG535354	602563012	BG535354



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 18:50:14 ; Search time 4741.31 Seconds  
(without alignments)  
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Perfect score: 1020  
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Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sta.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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5	992	97.3	BD176670 Soluble R
6	992	97.3	AB061668 Homo sapi
7	974.8	95.6	CQ730900 Sequence
8	964.6	94.6	AB061669 Homo sapi
9	746.4	73.2	BOVRAGE
10	746.4	73.2	AR321599 Sequence
11	729	71.5	HSAL13822
12	696.6	68.3	AR321601 Sequence
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14	691.8	67.8	BC061182 Mus muscu
15	680.6	66.7	L33413 Rat' recepto
16	477.2	46.8	AY530943 Canis fam
17	388.8	38.1	AX795282 Sequence
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19	384.2	37.7	AY370908 Sus scrof

20	326.2	32.0	698	6	AX795283	Sequence
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22	302.6	29.7	653	6	AX795281	Sequence
23	302.6	29.7	653	9	AF536236	Homo sapi
24	274.6	26.9	358	4	AY382178	Canis fam
25	197	19.3	5062	9	HSN808526	Homo sapi
26	197	19.3	10108	9	HUMHXRAGE	Human DNA
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34	197	19.3	137935	9	AL662884	Human DNA
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ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Homo sapiens RAGE mRNA for advanced glycation endproducts receptor, complete cds.  
ACCESSION AB036432  
VERSION AB036432.1 GI:6691625  
KEYWORDS advanced glycation endproducts receptor.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Abedin,M.J., Yonekura,H., Migita,H., Karasawa,J., Yamamoto,Y. and Yamamoto,H.  
TITLE Molecular heterogeneity of the receptor for advanced glycation endproducts  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1268)  
AUTHORS Abedin,M.J., Yonekura,H. and Yamamoto,H.  
TITLE Direct Submission  
JOURNAL Submitted (05-JAN-2000) Hideto Yonekura, Kanazawa University School of Medicine, Department of Biochemistry, 13-1 Takara-machi, Kanazawa, Ishikawa 920-8640, Japan  
(E-mail:hyone@med.kanazawa-u.ac.jp, Tel: +81-76-265-2181, Fax: +81-76-234-4226)

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## ORIGIN

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complete cds.  
ACCESSION BC020669  
VERSION BC020669.1 GI:18088362  
KEYWORDS MGC.  
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ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 1436)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausch, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheet, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
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Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahney, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,  
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
JOURNAL  
PUBMED  
2 (bases 1 to 1436)  
REFERENCE Strausberg, R.  
AUTHORS Direct Submission  
TITLE Submitted (03-JAN-2002) National Institutes of Health, Mammalian  
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue procurement: CLONTECH  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 37 Row: e Column: 17  
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source

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ORIGIN

Query Match 99.5%; Score 1015; DB 9; Length 1436;  
Best Local Similarity 100.0%; Pred. No. 3e-246;  
Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCGAGCGGAACAGCAGTTGAGCTGGGTCTCTAGTCTGTGGGGGGCAGTA 60  
DB 20 ATGCGAGCGGAACAGCAGTTGAGCTGGGTCTCTAGTCTGTGGGGGGCAGTA 79  
QY 61 GTAGGTCTCAAAACATCAAGCCCGGATTTGGGAGCCACTGTGTGAAGTGAAGGG 120  
DB 80 GTAGGTCTCAAAACATCAAGCCCGGATTTGGGAGCCACTGTGTGAAGTGAAGGG 139  
QY 121 GCCCCCAAGAAACACCCAGCGCTGGAATGGAACCTGAACACAGCCCGGACAGAAGCT 180  
DB 140 GCCCCCAAGAAACACCCAGCGCTGGAATGGAACCTGAACACAGCCCGGACAGAAGCT 199  
QY 181 TGAAGTCTCTGTCCTCCAGGAGGAGGCCCTTGGGACAGTGTGGTCTGTCTTCCC 240  
DB 200 TGAAGTCTCTGTCCTCCAGGAGGAGGCCCTTGGGACAGTGTGGTCTGTCTTCCC 259  
QY 241 AACGGCTCCCTCTCTTCCGCTGTGGGATCCAGATGAGGGATTTTCGGTCCAG 300  
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QY 301 GCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGAT 360  
DB 320 GCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGAT 379  
QY 361 CTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACCTACGGCTGTGTTCCTCAATAAG 420  
DB 380 CTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACCTACGGCTGTGTTCCTCAATAAG 439  
QY 421 GTGGGACATGTGTGTCAGAGGAGGACTACCTGCGAGGACTCTTAGCTGGCATTTGGAT 480  
DB 440 GTGGGACATGTGTGTCAGAGGAGGACTACCTGCGAGGACTCTTAGCTGGCATTTGGAT 499

QY 481 GGGAGCCCTCGTGTGCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540  
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QY 541 CTGTGAGACAGGCTCTTTCACACTGCGAGCTGAATGTTGACCCACCGCGGGAGGA 600  
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QY 601 GATCCCGCTCCACCTTCTCTGTAGTTCAGCCACCGGCTTCCCGGACACCGGGCTTTG 660  
DB 620 GATCCCGCTCCACCTTCTCTGTAGTTCAGCCACCGGCTTCCCGGACACCGGGCTTTG 679  
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DB 680 CGCAGAGCCCATCCAGCCCGCTGTCTGGAGCCCTGTGCTCTGGAGAGGTCCTCAATTG 739  
QY 721 GTGGTGGAGCCAGAGGTGGAGCAGTAGTCTCTGTGGAACCGTAACTGACCTGTGAA 780  
DB 740 GTGGTGGAGCCAGAGGTGGAGCAGTAGTCTCTGTGGAACCGTAACTGACCTGTGAA 799  
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGGAATGAAGATGGTGTGCTTGCCTTGCCTTT 840  
DB 800 GTCCCTGCCAGCCCTCTCTCAATCCACTGGAATGGTGTGCTTGCCTTGCCTTTGCCTTT 859  
QY 841 CCCCCAGCCCTGTGTGATCTCTCTGAGATAGGCTTCAGGACCGAGGAACTTACAGC 900  
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QY 901 TGTGTGGCCACCATTTCCAGCCACCGGGCCAGGAAAGCCGTGTCTGACGATCAGCATC 960  
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QY 961 ATCGAACAGGCGAGGAGGGGCAACTGCAAGCTCTGTGGAGGATCAGGGCTGG 1015  
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RESULT 3  
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LOCUS AR321600 1391 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 4 from patent US 6563015.  
ACCESSION AR321600  
VERSION AR321600.1 GI:33706929  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1391)  
AUTHORS Stern,D.M., Schmidt,A.M. and Yan,S.D.  
TITLE Transgenic mice over-expressing receptor for advanced glycation  
endproduct (RAGE) and mutant APP in brain and uses thereof  
JOURNAL Patent: US 6563015-A 4 13-MAY-2003;  
FEATURES  
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ORIGIN  
Query Match 99.0%; Score 1009.8; DB 6; Length 1391;  
Best Local Similarity 99.8%; Pred. No. 6.2e-245;  
Matches 1011; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GGCAGCCGGAAACAGCAGTTGGAGCCCTGGGTGTGCTTCTCAGTCTGTGGGGGCACTAGT 62  
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QY 63 AGGTGTCTAAACATCAAGCCCGGATTTGGGAGCCACTGTGGTCTGTAAGGGGCG 122  
DB 63 AGGTGTCTAAACATCAAGCCCGGATTTGGGAGCCACTGTGGTCTGTAAGGGGCG 122  
QY 123 CCCCAGAAACCAACCCAGCGGCTGGAATGGAACCTGACACAGGCGCGACAGAAGCTTG 182  
DB 123 CCCCAGAAACCAACCCAGCGGCTGGAATGGAACCTGACACAGGCGCGACAGAAGCTTG 182

TITLE		Cloning and expression of a cell surface receptor for advanced glycosylation end products of proteins	
JOURNAL		J. Biol. Chem.	267 (21), 14998-15004 (1992)
MEDLINE		92340547	
PUBMED		1378843	
REFERENCE	2 (bases 1 to 1391)		
AUTHORS		Shaw,A.	
JOURNAL		Direct Submission	
COMMENT		Submitted (15-APR-1992) A. Shaw, Department of Cellular and Molecular Biology, Merck Sharp and Dohme Research Laboratories, West Point, PA 19486 USA	
FEATURES		Original source text: Homo sapiens cDNA to mRNA.	
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		/tissue_type="lung"	
		<1..1215	
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		/protein_id="AAA03574.1"	
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		polyA_signal	
		1368..1373	
		polyA_site	
		1391	
ORIGIN			
		Query Match	
		Best Local Similarity	
		99.0%; Score 1009.8; DB 9; Length 1391;	
		99.8%; Pred. No. 6.2e-245;	
		Matches 1011; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	3	GGCAGCCGGAAACAGCAGTTGGAGCCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTAGT	62
Db	3	GGCAGCCGGAAACAGCAGTTGGAGCCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTAGT	62
QY	63	AGGTGCTCTCAAAACATCAGACCCCGGATTTGGCGAGCCACTGGTGCTGAAGTGTAAAGGGGC	122
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QY	123	CCCCAAGAAACACACCCCGAGCGGCTGGAATGGAATCTGAACACAGGCCCGGACAGAGCTTG	182
Db	123	CCCCAAGAAACACACCCCGAGCGGCTGGAATGGAATCTGAACACAGGCCCGGACAGAGCTTG	182
QY	183	GAAGTCTCTGCTCTCCCGAGGAGAGGCCCTCTGGACAGTGTGGCTGCTCTTCCCA	242
Db	183	GAAGTCTCTGCTCTCCCGAGGAGAGGCCCTCTGGACAGTGTGGCTGCTCTTCCCA	242
QY	243	CGGCTCCCTCTCTTCCCTTCGGCTGTCCGGATCAGGATGAGGGGATTTTCCGGTGGAGGC	302
Db	243	CGGCTCCCTCTCTTCCCTTCGGCTGTCCGGATCAGGATGAGGGGATTTTCCGGTGGAGGC	302
QY	303	AATGAACAGGAATGAAAGGAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGTTC	362
Db	303	AATGAACAGGAATGAAAGGAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGTTC	362
QY	363	TGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAACTCAGGCTGTGTGTCTCCCAATAAGT	422
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QY	423	GGGGACATGTGTGTCTCAGAGGGAAGTACCTTCAGGGGAGTCTTGTAGCTGTGATGG	482
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QY	183	GAAGGTCTCTGCTCTCCCGAGGAGAGGCCCTCTGGACAGTGTGGCTCGTGTCTCTCCCAA	242
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QY	243	CGGCTCCCTCTCTTCCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTGGAGGC	302
Db	243	CGGCTCCCTCTCTTCCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTGGAGGC	302
QY	303	AATGAACAGGAATGAAAGGAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGTTC	362
Db	303	AATGAACAGGAATGAAAGGAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGTTC	362
QY	363	TGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAACTCAGGCTGTGTCTCCCAATAAGT	422
Db	363	TGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAACTCAGGCTGTGTCTCCCAATAAGT	422
QY	423	GGGGACATGTGTCTCAGAGGGAAGTACCTTCGAGGGAAGTCTTGTAGCTGTGATGG	482
Db	423	GGGGACATGTGTCTCAGAGGGAAGTACCTTCGAGGGAAGTCTTGTAGCTGTGATGG	482
QY	483	GAAGCCCTCTGCTCTCACTCGAGTGGAGGAGTATCTGTGAAGGACAGACAGGAGACACC	542
Db	483	GAAGCCCTCTGCTCTCACTCGAGTGGAGGAGTATCTGTGAAGGACAGACAGGAGACACC	542
QY	543	TGAGACAGGGCTCTTCACTCGAGTGGAGGAGTATCTGTGAAGGACAGACAGGAGACACC	602
Db	543	TGAGACAGGGCTCTTCACTCGAGTGGAGGAGTATCTGTGAAGGACAGACAGGAGACACC	602
QY	603	TCCCCCTCCACCTCTCTCTGTAGTTCAGCCAGGAGTCTTGTAGCTGTGATGG	662
Db	603	TCCCCCTCCACCTCTCTCTGTAGTTCAGCCAGGAGTCTTGTAGCTGTGATGG	662
QY	663	CACAGCCCTCTCAGCCCGCTGTCTGGAGGAGTCTGCTCTGGAGGAGTCCAATTGT	722
Db	663	CACAGCCCTCTCAGCCCGCTGTCTGGAGGAGTCTGCTCTGGAGGAGTCCAATTGT	722
QY	723	GGTGGAGCCAGAGGTGGAGCAGTAGTCTCTGTGGAAACCGTAACCTGACCTGTGAAGT	782
Db	723	GGTGGAGCCAGAGGTGGAGCAGTAGTCTCTGTGGAAACCGTAACCTGACCTGTGAAGT	782
QY	783	CCCTGCCAGCCCTCTCTCAATCACTGATGAGGAGTGTGTGCTTGCCTTGCCTTCC	842
Db	783	CCCTGCCAGCCCTCTCTCAATCACTGATGAGGAGTGTGTGCTTGCCTTGCCTTCC	842
QY	843	CCCCAGCCCTGTCTCTCTCAGATAGGCTCTAGGACCGAGGAGGAGTGTGCTGCTG	902
Db	843	CCCCAGCCCTGTCTCTCTCAGATAGGCTCTAGGACCGAGGAGGAGTGTGCTGCTG	902
QY	903	TGTGGCCACCCATTCCAGCCAGGGCCCGAGGAAAGCCGTGTGTGCTGCTGATCAT	962
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QY	963	CGAACAGGGAGGAGGGGCGCACTCAGGCTCTGTGGAGGATCAGGCTGG	1015
Db	963	CGAACAGGGAGGAGGGGCGCACTCAGGCTCTGTGGAGGATCAGGCTGG	1015

RESULT 4			
HUMRAGE	1391 bp	mRNA	linear
LOCUS			
DEFINITION	Human receptor for advanced glycosylation end products (RAGE) mRNA, partial cds.		
ACCESSION	M91211	GI:190845	
VERSION			
KEYWORDS	RAGE; cell surface receptor.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1391)		
AUTHORS	Neer,M., Schmidt,A.M., Brett,J., Yan,S.D., Wang,F., Pan,Y.C., Elliston,K., Stern,D. and Shaw,A.		





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961 ATCGAACCGGCGGAGGAGGGCCAACTGCAGG 992
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985 ATCGAACCGGCGGAGGAGGGCCAACTGCAGG 1016

RESULT 6
AB061668 1223 bp mRNA linear PRI 15-MAR-2003
LOCUS Homo sapiens RAGE mRNA for soluble form of receptor for advanced
DEFINITION glycation endproducts, complete cds.
ACCESSION AB061668
VERSION AB061668.1 GI:28971759
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Yonekura,H., Yamamoto,Y., Sakurai,S., Petrova,R.G., Abedin,Md.J.,
Li,H., Yasui,K., Takeuchi,M., Makita,Z., Takasawa,S., Okamoto,H.,
Watanabe,T. and Yamamoto,H.
Novel splice variants of the receptor for advanced glycation
end-products expressed in human vascular endothelial cells and
pericytes, and their putative roles in diabetes-induced vascular
injury
Biochem. J. 370 (Pt 3), 1097-1109 (2003)
JOURNAL 22510265
MEDLINE 12495433
PUBMED
REFERENCE 2 (bases 1 to 1223)
Yonekura,H., Yamamoto,Y., Sakurai,S. and Yamamoto,H.
Direct Submission
TITLE Submitted (11-MAY-2001) Hideto Yonekura, Kanazawa University,
Graduate School of Medical Science; 13-1 Takara-machi, Kanazawa,
Ishikawa 920-8640, Japan (E-mail:hyone@med.kanazawa-u.ac.jp,
Tel:81-76-265-2182, Fax:81-76-234-4226)
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/evidence=experimental
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Query Match 97.3%; Score 992; DB 9; Length 1223;
Best Local Similarity 100.0%; Pred. No. 2e-240;
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DB 265 AACGGCTCCTCTCTCTCCCGGTGTGGGATCCAGGATGAGGGGATTTTCGGGTGCCAG 324
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QY 481 GGGAGCCCTCTGTCCTTAATGAAAGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540
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QY 721 GTGGTGGAGCCAGAGGTGGAGCAGTACTCTGTGGAAACCGTAACCTGACCTGTGAA 780
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QY 961 ATCGAACCGGCGGAGGAGGGCCAACTGCAGG 992
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985 ATCGAACCGGCGGAGGAGGGCCAACTGCAGG 1016

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RESULT 7
CQ730900      1218 bp      DNA      linear      PAT 03-FEB-2004
LOCUS         Sequence 16834 from Patent WO2068579.
DEFINITION
ACCESSION    CQ730900
VERSION      CQ730900.1 GI:42306010
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE        Kits, such as nucleic acid arrays, comprising a majority of
             humanexons or transcripts, for detecting expression and other uses
             thereof
JOURNAL      Patent: WO 02068579-A 16834 06-SEP-2002;
             PE Corporation (NY) (US)
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Best Local Similarity 98.0%; Pred. No. 4.7e-236;
Matches 998; Conservative 0; Mismatches 17; Indels 3; Gaps 1;
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QY 301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATT 360
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QY 361 CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAATCACTACGGCTGGTGTCTCCCAATAG 420
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901 AGCTGTGTGGCCCAACCCATTCCAGCCAGCGGGCCCCAGAAAGCGTCTGTGACATCAGC 960
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RESULT 8
AB061669      1451 bp      mRNA      linear      PRI 15-MAR-2003
LOCUS         Homo sapiens RAGE mRNA for N-terminal truncated form of receptor
DEFINITION    for advanced glycation endproducts, complete cds.
ACCESSION    AB061669
VERSION      AB061669.1 GI:28971761
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Yonekura, H., Yamamoto, Y., Sakurai, S., Petrova, R.G., Abedin, Md. J.,
             Li, H., Yasui, K., Takeuchi, M., Makita, Z., Takasawa, S., Okamoto, H.,
             Watanabe, T. and Yamamoto, H.
TITLE        Novel splice variants of the receptor for advanced glycation
             end-products expressed in human vascular endothelial cells and
             pericytes, and their putative roles in diabetes-induced vascular
             injury
JOURNAL      Biochem. J. 370 (Pt 3), 1097-1109 (2003)
MEDLINE      22510265
PUBMED       12495433
AUTHORS      Yonekura, H., Yamamoto, Y., Sakurai, S. and Yamamoto, H.
TITLE        Direct Submission
JOURNAL      Submitted (11-MAY-2001) Hideto Yonekura, Kanazawa University,
             Graduate School of Medical Science, 13-1 Takara-machi, Kanazawa,
             Ishikawa 920-8640, Japan (E-mail: hyone@med.kanazawa-u.ac.jp,
             Tel:81-76-265-2182, Fax:81-76-234-4226)
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QY	825	TGTGCCCTTTCCTCCCGACAGCCCTGTGTGATCTCTCTCTGATAGAGGCTTCAGAA	884
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LOCUS			
DEFINITION			
BOVRAGE 1426 bp mRNA linear MAM 09-DEC-1993			
Cow receptor for advanced glycosylation end products (RAGE) mRNA,			
complete cds.			
ACCESSION			
M91212.1 GI:163650			
VERSION			
RAGE; cell surface receptor.			
KEYWORDS			
SOURCE			
Bos taurus (cow)			
ORGANISM			
Bos taurus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
Bovinae; Bos.			
REFERENCE			
1 (bases 1 to 1426)			
Neeper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,			
Elliston K., Stern D. and Shaw A.			
Cloning and expression of a cell surface receptor for advanced			
glycosylation end products of proteins			
J. Biol. Chem. 267 (21), 14998-15004 (1992)			
JOURNAL			
MEDLINE			
PUBMED			
92340547			
REFERENCE			
2 (bases 1 to 1426)			
1378843			
AUTHORS			
Shaw A.			
TITLE			
Direct Submission			
Submitted (15-APR-1992) A. Shaw, Department of Cellular and			
Molecular Biology, Merck Sharp and Dohme Research Laboratories,			
West Point, PA 19486 USA			
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Best Local Similarity 84.1%; Pred. No. 3.5e-178;			
Matches 881; Conservative 0; Mismatches 131; Indels 36; Gaps 2;			
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DB	10	ATGGCAGCGGGAACAGAGTTGGAGCCCTGGTGGTCTCTCAGTCTGTGGGGGACAGTA	69
QY	61	GTAGTGTCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGGTGTCTGAAGTGAAGGG	120

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 17:18:58 ; Search time 643.487 Seconds

(without alignments)  
9383.456 Million cell updates/sec

Title: US-10-091-019-2

Perfect score: 1020

Sequence: 1 atggcagccggaacagcagt.....gaggatcagggctgtcttag 1020

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
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5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
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8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
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13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1015	99.5	1023	2	AAV06517 Human RAG
4	1015	99.5	1268	10	ADG33024 Human DNA
5	1015	99.5	1329	12	ADP19665 Human LP2
6	1015	99.5	1415	6	ABQ99597 Human cod
7	1015	99.5	1436	12	ADK00130 Human RAG
8	1013.4	99.4	1217	10	ADP95563 Human NOV
9	1013.4	99.4	1582	4	AAH57444 Human lun
10	1013	99.3	1391	6	ABQ79955 Human RAG
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12	1010.2	99.0	1761	12	ADK00128 Human RAG
13	1009.8	99.0	1391	6	ABK10856 DNA encod
14	1009.8	99.0	1391	6	ABK84114 Human cdn
15	1009.8	99.0	1391	6	ADP36952 Human rec
16	1009.8	99.0	1391	10	ADP59952 Human RAG
17	1009.8	99.0	1391	10	ADG32021 Human DNA
18	992	97.3	1223	6	ABV73151 Human sol
19	992	97.3	1223	10	ADG37043 Receptor
20	992	97.3	1291	12	ADP19655 Human LP2

21	979	96.0	1323	12	ADP19667	Adp19667 Human LP2
22	957	93.8	1384	12	ADP19659	Adp19659 Human LP2
23	957	93.8	1463	6	ABQ99598	Abq99598 Human cod
24	949	93.0	957	2	AAV06518	AAV06518 Human RAG
25	945.8	92.7	957	2	AAV12395	AAV12395 Human mat
26	934	91.6	1339	12	ADP19661	Adp19661 Human LP2
27	933	91.5	1539	9	ACC59920	Acc59920 Human REM
28	921	90.3	1173	10	ADP95567	Adp95567 Human NOV
29	921	90.3	1294	12	ADP19669	Adp19669 Human LP2
30	921	90.3	1678	9	ACC59907	Acc59907 Human REM
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40	696.6	68.3	1347	6	ABK10858	Abk10858 DNA encod
41	696.6	68.3	1348	6	ABK10857	Abk10857 DNA encod
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43	696.6	68.3	1348	10	ADP59953	Adp59953 Murine RA
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ALIGNMENTS

RESULT 1

ABQ79956  
ID ABQ79956 standard; DNA; 1020 BP.

XX ABQ79956;

DT 23-DEC-2002 (first entry)

DE Human soluble RAGE (sRAGE) encoding DNA.

XX Receptor for Advanced Glycated end product; RAGE; recombinant; nootropic;  
KW antiarteriosclerotic; antidiabetic; cytosolic; nephrotropic; vasotropic;  
KW neuroprotective; antiinflammatory; gene therapy; human; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1020

FT /\*tag= a

FT /product= "sRAGE"

FT /note= "soluble, extracellular portion of RAGE"

XX W0200270667-A2.

XX 12-SEP-2002.

XX 05-MAR-2002; 2002WO-US006881.

XX 05-MAR-2001; 2001US-0273418P.

XX (TRAN-) TRANSTECH PHARMA INC.

XX Harris R, Shen J, Shahbaz M;

XX WPI; 2002-713443/77.

XX P-PSDB; AB882164.

XX High level expression of recombinant Receptors for Advanced Glycated end  
PT products (sRAGE) proteins for treating increased levels of advanced  
PT glycosylation end products, comprises infecting cells with a high titer  
PT recombinant virus.

XX Claim 13; Fig 2B; 5lpp; English.



CC and purification of human RAGE polypeptide

XX	Sequence	1023 BP; 218 A; 299 C; 317 G; 189 T; 0 U; 0 Other;	
QY	Query Match	99.5%; Score 1015; DB 2; Length 1023;	
XX	Best Local Similarity	100.0%; Pred. No. 7.6e-261; Indels 0; Gaps 0;	
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DB	61	GTAGGTGCTCAAAACATACAGCCCGGATGGGACCACTGGTGTGAAGTGTAAAGGG	120
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DB	121	GGCCCCAAGAAACACCCAGCGGCTGGAACTGAACACAGCCCGGACAGAGCT	180
QY	181	TGGAAGTCTCTGTCTCCAGGAGGAGGCCCTGGGACAGTGTGGCTGTCTCTTCCC	240
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QY	301	GCAATGAACAGGAATGGAAGGAGCAAGTCCAACTACGAGTCCGTCTACCAATG	360
DB	301	GCAATGAACAGGAATGGAAGGAGCAAGTCCAACTACGAGTCCGTCTACCAATG	360
QY	361	CTTGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTACGGCTGGTGTCCCAATAAG	420
DB	361	CTTGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTACGGCTGGTGTCCCAATAAG	420
QY	421	GTGGGACATGTGTTCAGAGGAACTACCTGACGGAAGTCTTAGCTGGCACTTGGAT	480
DB	421	GTGGGACATGTGTTCAGAGGAACTACCTGACGGAAGTCTTAGCTGGCACTTGGAT	480
QY	481	GGGAAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACACAGGAGAC	540
DB	481	GGGAAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACACAGGAGAC	540
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DB	601	GATCCCGTCCACCTTCTCTGTAGCTTCAGCCAGGCTTCCCGACACCGGGCTTG	660
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DB	781	GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTGCCCTT	840
QY	841	CCCCCAGCCCTGTGTGATCTCTCTGATAGAGGCTTCAGACACAGGAACTACAC	900
DB	841	CCCCCAGCCCTGTGTGATCTCTCTGATAGAGGCTTCAGACACAGGAACTACAC	900
QY	901	TGTGTGGCCACCCATTCAGACACAGGCCCCAGGAAAGCGTCTGTACGATCAGCATC	960
DB	901	TGTGTGGCCACCCATTCAGACACAGGCCCCAGGAAAGCGTCTGTACGATCAGCATC	960
QY	961	ATCGAACAGGCGAGGAGGGGCCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGG	1015

DB	961	ATCGAACAGGCGAGGAGGGGCCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGG	1015
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AAV06517			
ID	AAV06517	standard; DNA; 1023 BP.	
AC	AAV06517;		
XX	08-MAY-1998	(first entry)	
DE	Human RAGE polypeptide (340 amino acid residues) encoding DNA.		
XX	Advanced glycosylation end-product receptor; RAGE; screening; AGE;		
KW	vascular permeability; diabetes mellitus; treatment; atherosclerosis;		
KW	Alzheimer's disease; ds.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
PH	1..1023		
FT	/tag= a		
FT	/product= "RAGE polypeptide"		
XX	W09739121-A1.		
PN	23-OCT-1997.		
PD	11-APR-1997; 97WO-EP001832.		
XX	16-APR-1996; 96US-00633147.		
PR	(SCHD ) SCHERING AG.		
XX	Morser MJ, Nagashima M;		
PI	WPI; 1997-526458/48.		
XX	P-PSDB; AAW33753.		
DR	New soluble advanced glycosylation end-product receptor polypeptide -		
PT	used for reducing vascular permeability, complications of diabetes etc.,		
PT	also for purification and to screen for modulators.		
XX	Claim 12; Fig 1A; 91pp; English.		
PS	This genomic DNA encodes a human advanced glycosylation end-product		
XX	receptor (RAGE) polypeptide (340 amino acid residues). The RAGE		
CC	polypeptides and its active fragments or their mimetics, inhibit		
CC	interaction between advanced glycosylation end-products (AGE) and a		
CC	receptor (specifically RAGE). They are used to treat diseases associated		
CC	with AGE/RAGE interaction, such as increased vascular permeability,		
CC	diabetes mellitus (particularly complications such as micro- or macro-		
CC	vasculopathy or occlusive vascular disorders such as neuropathy,		
CC	nephropathy, retinopathy or atherosclerosis) or haemodialysis-associated		
CC	amyloidosis, also activation of microglial cells by beta-amyloid peptides		
CC	in Alzheimer's disease or age-related disorders such as oxidative stress.		
CC	These RAGE polypeptides are also used, when immobilised, to purify AGE		
CC	from a protein mixture and to screen for compounds that are agonists and		
CC	antagonists of AGE/RAGE interaction. They can also be used diagnostically		
CC	to detect abnormal levels of AGE. Antibodies against RAGE polypeptides		
CC	are useful as immunoassay reagents for measurement of RAGE levels, and as		
CC	inhibitors of interaction between AGE and RAGE or other receptors and for		
CC	purification and quantification of RAGE polypeptides. The encoding		
CC	nucleic acids are used to express recombinant RAGE and as probes for		
CC	isolating related genes		
XX	Sequence 1023 BP; 218 A; 299 C; 317 G; 189 T; 0 U; 0 Other;		

Query Match 99.5%; Score 1015; DB 2; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 7.6e-261; Indels 0; Gaps 0;  
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QY	61	GTAGGTGCTCAAAAATCACAGCCCGGATTTGGCGAGCCACTGGTGCTGAAGTGTAAAGGGG	120
Db	61	GTAGGTGCTCAAAAATCACAGCCCGGATTTGGCGAGCCACTGGTGCTGAAGTGTAAAGGGG	120
QY	121	GCCTCCAGAGAAACACCCAGAGGGCTGGAAATGGAAACTTGAAACACAGGCCGGACAGAAAGCT	180
Db	121	GCCTCCAGAGAAACACCCAGAGGGCTGGAAATGGAAACTTGAAACACAGGCCGGACAGAAAGCT	180
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QY	241	AACGGTCTCCCTCTTCTTCTCCGCTGTGCGGATTCAGAGTAGAGGGGATTTTCCGGTGCAG	300
Db	241	AACGGTCTCCCTCTTCTTCTCCGCTGTGCGGATTCAGAGTAGAGGGGATTTTCCGGTGCAG	300
QY	301	GCAATGAACAGGAATCGAAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATT	360
Db	301	GCAATGNAACAGGAATCGAAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATT	360
QY	361	CTTGGGAGCCAGAAATTTAGATTCTGTCTCTGAACTCACGGCTGTGTGTCCCAATAAG	420
Db	361	CTTGGGAAGCCAGAAATTTAGATTCTGTCTCTGAACTCACGGCTGTGTGTCCCAATAAG	420
QY	421	GTGGGACATGTGTGTACAGAGGAAGTACCTCGCAGGGACTCTTACGTGGCACTTGGAT	480
Db	421	GTGGGACATGTGTGTACAGAGGAAGTACCTCGCAGGGACTCTTACGTGGCACTTGGAT	480
QY	481	GGGAAGCCCTGTGTCTTAATCAGAAAGGAGTATCTGTGAAGGAACACAGACAGGAGACAC	540
Db	481	GGGAAGCCCTGTGTGTCTTAATCAGAAAGGAGTATCTGTGAAGGAACACAGACAGGAGACAC	540
QY	541	CCTGAGACAGGGCTCTTACACTGCAGTCTGGAGCTTAATGTGTACCCACAGCCCGGGAGGA	600
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QY	661	CGCACAGCCCATCCAGCCCGTGTCTGGAGACTGTGCCTCTGTGAGGAGTCCCAATTG	720
Db	661	CGCACAGCCCATCCAGCCCGTGTCTGGAGACTGTGCCTCTGTGAGGAGTCCCAATTG	720
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Db	721	GTGGTGGAGCCAGAAAGGTGGAGCAGTAGCTCTCTGTGTGAACCGTAAACCTCTGAGAA	780
QY	781	GTCCCTGCCAGCCCTCTCCTCAAAATCCACTGGATGAGGATGTGTGCCCTTGCCCTT	840
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QY	841	CCCCCAGCCCTGTGTGATCTCTCCCTCAGATAGGGCTCAGGACACAGGAAACCTACAGC	900
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RESULT 4  
ADG33024  
ID ADG33024 standard; DNA; 1268 BP.  
XX

AC	ADG33024;
XX	
DT	26-FEB-2004 (first entry)
XX	
DE	Human DNA differentially expressed in patients with SLE SeqID348.
XX	
KW	human; ds; autoimmune; chronic inflammatory disease; SLE;
KW	systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW	Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
KW	ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW	diverticulitis; primary biliary sclerosis.
XX	
OS	Homo sapiens.
XX	
PN	WO2003090694-A2.
XX	
PD	06-NOV-2003.
XX	
PF	24-APR-2003; 2003WO-US013015.
XX	
PR	24-APR-2002; 2002US-00131827.
XX	
PA	(EXPR-) EXPRESSION DIAGNOSTICS INC.
XX	
PI	Wohlgemuth J, Fry K, Woodward R, Ly N;
XX	
DR	WPI; 2003-877243/81.
XX	
PT	Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
PT	such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
PT	colitis, psoriasis and asthma by detecting the expression level of one or
PT	more genes.
XX	
PS	Claim 18; SEQ ID NO 348; 877pp; English.
XX	
CC	This invention relates to novel methods for diagnosing and monitoring
CC	autoimmune and chronic inflammatory diseases. Specifically, it refers to
CC	the identification of genes that have a clinical utility as diagnostic
CC	tools for the management of, in particular, patients with systemic lupus
CC	erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
CC	present invention describes a method for determining the levels of
CC	multiple differentially expressed genes of a patient, in a concerted
CC	manner, in order to achieve an improved diagnostic assay with sensitivity
CC	and specificity for the disease in question. As such, these genes are
CC	useful for the diagnosis of various other inflammatory disorders
CC	including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
CC	ankylosing spondylitis, ulcerative colitis, primary sclerosing
CC	cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
CC	This polynucleotide is a DNA sequence representing human mRNA that is
CC	differentially expressed in patients with SLE, used in an exemplification
CC	of the invention.
XX	
SQ	Sequence 1268 BP; 280 A; 361 C; 410 G; 217 T; 0 U; 0 Other;

RESULT 4  
ADG33024  
ID ADG  
XX

```
QY 241 AACGGCTCCCTCTCTCTCCGCTGTCGGGATCCAGGATCAGGGGATTTTCGGTGCCAG 300
DB 265 AACGGCTCCCTCTCTCTCCGCTGTCGGGATCCAGGATCAGGGGATTTTCGGTGCCAG 324
QY 301 GCATGAACAGGAATGGAAGGAGCAAGTCAACTACCGAGTCGCTGTCTACAGATT 360
DB 325 GCATGAACAGGAATGGAAGGAGCAAGTCAACTACCGAGTCGCTGTCTACAGATT 384
QY 361 CTGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTCAGGCTCGTGTCTCCCAATAG 420
DB 385 CTGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTCAGGCTCGTGTCTCCCAATAG 444
QY 421 GTGGGACATGTGTGTGAGAGGAAGTACCTCTGAGGGAGCTCTTAGCTGGCACTTGGAT 480
DB 445 GTGGGACATGTGTGTGAGAGGAAGTACCTCTGAGGGAGCTCTTAGCTGGCACTTGGAT 504
QY 481 GGGAGCCCTGTGTGCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540
DB 505 GGGAGCCCTGTGTGCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC 564
QY 541 CCTGACAGAGGCTCTTCACTGACGTGAGCTAATGTGACCCAGCCAGCCGGGAGGA 600
DB 565 CCTGACAGAGGCTCTTCACTGACGTGAGCTAATGTGACCCAGCCAGCCGGGAGGA 624
QY 601 GATCCCGTCCCACTTCTCTGTAGCTTTCAGCCAGGCTTCCCGACACCGGGCCTTG 660
DB 625 GATCCCGTCCCACTTCTCTGTAGCTTTCAGCCAGGCTTCCCGACACCGGGCCTTG 684
QY 661 CGCAGAGCCCTTCACTGAGCCCGTGTCTGGAGCCTGTGCTGTGAGGAGTCCAAATG 720
DB 685 CGCAGAGCCCTTCACTGAGCCCGTGTCTGGAGCCTGTGCTGTGAGGAGTCCAAATG 744
QY 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGTGGAACCTGACCTGTGTGAA 780
DB 745 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGTGGAACCTGACCTGTGTGAA 804
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGGATGGTGTGCCCTTGGCCCTT 840
DB 805 GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGGATGGTGTGCCCTTGGCCCTT 864
QY 841 CCCCCAGCCCTGTGTGATCTCTCTGATAGATAGGCTCAGACAGGAGAACCTACAGC 900
DB 865 CCCCCAGCCCTGTGTGATCTCTCTGATAGATAGGCTCAGACAGGAGAACCTACAGC 924
QY 901 TGTGTGGCCACCATTCAGCCACGGCCGCCAGGAAGCCGTGCTCAGCATCAGCATC 960
DB 925 TGTGTGGCCACCATTCAGCCACGGCCGCCAGGAAGCCGTGCTCAGCATCAGCATC 984
QY 961 ATCGAACCCAGGAGGAGGGGCCAACTGAGGCTCTGTGGGAGGATCAGGGCTGG 1015
DB 985 ATCGAACCCAGGAGGAGGGGCCAACTGAGGCTCTGTGGGAGGATCAGGGCTGG 1039

RESULT 5
ADP19665
ID ADP19665 standard; cDNA; 1329 BP.
XX
AC ADP19665;
XX
XX 12-AUG-2004 (first entry)
XX
DE Human LP2005 encoding cDNA SEQ ID NO:11.
XX
XX human; LP2005; antidiabetic; neuroprotective; nontropic;
KW antinflammatory; antirheumatic; antiarthritic; vulnery; cytosstatic;
KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
XX systemic lupus erythematosus; gene; ss.
OS Homo sapiens.
XX
```

```

FH Key Location/Qualifiers
FT CDS 46..1206
FT /*tag= b
FT /product= "LP2005"
FT /note= "the present sequence only seems to encodes amino
FT acids 1 to 386 of the LP2005 protein"
FT sig_peptide 46..114
FT /*tag= a
FT mat_peptide 115..1203
FT /*tag= c
XX WO2004044126-A2.
XX
XX 27-MAY-2004.
XX
XX 05-NOV-2003; 2003WO-US032734.
XX
XX 14-NOV-2002; 2002US-0426253P.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Na S, Perkins DR;
XX
XX WPI; 2004-411705/38.
XX P-PSDB; ADP19666.
XX
XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
XX LP2003) for diagnosing or treating disorders associated with aberrant
XX levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
XX identification.
XX
XX Claim 1; SEQ ID NO 11; 111pp; English.
XX
XX The present sequence encodes human LP2005, which is used in the
XX exemplification of the present invention. The present invention
XX describes: (1) an isolated nucleic acid (I) comprising DNA having at
XX least 95% sequence identity to a polynucleotide selected from the group
XX consisting of: (a) a polynucleotide having a nucleotide sequence as shown
XX in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
XX polypeptide or mature form of a polypeptide having the amino acid
XX sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
XX fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
XX having a nucleotide sequence which is complementary to the nucleotide
XX sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
XX comprising (I); (3) a host cell comprising the vector; (4) producing an
XX LP polypeptide; (5) an isolated polypeptide produced by the above method
XX and comprising an amino acid sequence comprising about 95% sequence
XX identity to a sequence of amino acid residues comprising LP2001, LP2003,
XX LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
XX molecule comprising an LP polypeptide fused to a heterologous amino acid
XX sequence; (7) an antibody which specifically binds to an LP polypeptide
XX described above; (8) a composition (C) comprising a therapeutic amount of
XX an active agent selected from an LP polypeptide, an agonist to an LP
XX polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
XX antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
XX polynucleotide in combination with a pharmaceutical carrier; and (9)
XX diagnosing or treating a mammal suffering from a disease, condition or
XX disorder associated with aberrant levels of an LP-polypeptide. (C) has
XX antidiabetic, neuroprotective, nontropic, antiinflammatory,
XX antirheumatic, antiarthritic, vulnery, cytosstatic, immunosuppressive,
XX nephrotropic and dermatological activities, and can be used in gene
XX therapy. The compositions (C) and methods are useful for diagnosing or
XX treating disorders associated with aberrant levels of an LP polypeptide,
XX such as diabetes and its complications, Alzheimer's disease,
XX inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
XX sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
XX may also be used for chromosome identification. The LP polypeptide can
XX also be used in manufacturing a medicament for the treatment of the above
XX mentioned diseases, conditions or disorders associated with aberrant
XX levels of the LP polypeptide.
XX
XX Sequence 1329 BP; 289 A; 379 C; 424 G; 235 T; 0 U; 2 Other;
```

Query Match		99.5%;	Score 1015;	DB 12;	Length 1329;
Best Local Similarity		100.0%;	Pred. No. 8.3e-261;		
Matches 1015;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGCGACCGGAAACAGCAGTTGAGCCTCGGGTCTGCTCCTCAGTCTGTGGGGGGCAGTA	60		
Db	46	ATGCGACCGGAAACAGCAGTTGAGCCTCGGGTCTGCTCCTCAGTCTGTGGGGGGCAGTA	105		
Qy	61	GTAGGTGCTCAAAACATCAAGCCCGATTGGGAGCCACTGCTGAAGTGTAAAGGG	120		
Db	106	GTAGGTGCTCAAAACATCAAGCCCGATTGGGAGCCACTGCTGAAGTGTAAAGGG	165		
Qy	121	GCCTCCAAAGAAACACACCCAGCGCTGGAATGAAACTGAACACAGCCCGGACAGAAGCT	180		
Db	166	GCCTCCAAAGAAACACACCCAGCGCTGGAATGAAACTGAACACAGCCCGGACAGAAGCT	225		
Qy	181	TGAAGTCTCTGCTTCCCAAGGAGGAGGCCCTCGGACAGTGTGGCTGTCTCTTCCC	240		
Db	226	TGAAGTCTCTGCTTCCCAAGGAGGAGGCCCTCGGACAGTGTGGCTGTCTCTTCCC	285		
Qy	241	AACGGCTCCCTCTCTCTTCCGGCTGTCCGGATCCAGATCAGGGGATTTCCGGTCCAG	300		
Db	286	AACGGCTCCCTCTCTCTTCCGGCTGTCCGGATCCAGATCAGGGGATTTCCGGTCCAG	345		
Qy	301	GCAATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATT	360		
Db	346	GCAATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATT	405		
Qy	361	CTTGGGAGCCAGAAATTTAGATTCTGCTCTGAACTACCGCTGGTGTTCCTCAATAG	420		
Db	406	CTTGGGAGCCAGAAATTTAGATTCTGCTCTGAACTACCGCTGGTGTTCCTCAATAG	465		
Qy	421	GTGGGACATGTGTGTGACAGGGAAGCTACCTGCGAGGACTCTTAGCTGGCACTTGGAT	480		
Db	466	GTGGGACATGTGTGTGACAGGGAAGCTACCTGCGAGGACTCTTAGCTGGCACTTGGAT	525		
Qy	481	GGAAAGCCCTGTGCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC	540		
Db	526	GGAAAGCCCTGTGCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC	585		
Qy	541	CTTGAGACAGGCTCTTCACTGCGAGTGGAGCTAATGGTGACCCAGCCCGGGAGGA	600		
Db	586	CTTGAGACAGGCTCTTCACTGCGAGTGGAGCTAATGGTGACCCAGCCCGGGAGGA	645		
Qy	601	GATCCCGCTCCCACTTCTCTGTAGCTTCAGCCAGGCTTCCCGACACACCGGGCTTG	660		
Db	646	GATCCCGCTCCCACTTCTCTGTAGCTTCAGCCAGGCTTCCCGACACACCGGGCTTG	705		
Qy	661	CGCACAGCCCATCCAGCCCGCTGTGTGGAGCCTGTGCTGTGAGAGGTCCAAATG	720		
Db	706	CGCACAGCCCATCCAGCCCGCTGTGTGGAGCCTGTGCTGTGAGAGGTCCAAATG	765		
Qy	721	GTGGTGGAGCCAGAGGTGGAGCAGTCTCTGTGGTGGAACTGACCTGACCTGTGAA	780		
Db	766	GTGGTGGAGCCAGAGGTGGAGCAGTCTCTGTGGTGGAACTGACCTGACCTGTGAA	825		
Qy	781	GTCCCTGCCAGCCCTCTCTCAAAATCCACTGTGATGAAGGATGGTGTGCCCTT	840		
Db	826	GTCCCTGCCAGCCCTCTCTCAAAATCCACTGTGATGAAGGATGGTGTGCCCTT	885		
Qy	841	CCCCCAGCCCTGTGTGATCTCTCTGATAGAGGCTTCAGACAGGGAACCTACAGC	900		
Db	886	CCCCCAGCCCTGTGTGATCTCTCTGATAGAGGCTTCAGACAGGGAACCTACAGC	945		
Qy	901	TGTGTGGCCACCCATTCAGCCACGGGCCCCAGGAAGCCGTCTGTGAGCATCAGCATC	960		
Db	946	TGTGTGGCCACCCATTCAGCCACGGGCCCCAGGAAGCCGTCTGTGAGCATCAGCATC	1005		
Qy	961	ATCGAACCGAGGAGGAGGGCCCACTGCAAGGCTCTGTGGGAGGATCAGGGCTGG	1015		
Db	1006	ATCGAACCGAGGAGGAGGGCCCACTGCAAGGCTCTGTGGGAGGATCAGGGCTGG	1060		

RESULT 6	
ABQ99597	
ID	ABQ99597 standard; cDNA; 1415 BP.
XX	ABQ99597;
XX	AC
XX	AC
DT	25-FEB-2003 (first entry)
XX	Human coding sequence SEQ ID 330.
DE	
XX	
KW	Human; expressed sequence tag; EST; chromosome 6p21.3;
KW	haematopoietic disorder; central nervous system disease; viral infection;
KW	peripheral nervous system disease; non-healing wound; infectious disease;
KW	immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW	fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW	antiallergic; antinflammatory; immunosuppressive; neuroprotective;
KW	cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW	immunostimulant; cerebroprotective; gene therapy; gene; ss.
OS	Homo sapiens.
XX	
PN	WO200259260-A2.
XX	
PD	01-AUG-2002.
XX	
PP	16-NOV-2001; 2001WO-US042950.
XX	
PR	17-NOV-2000; 2000US-00714936.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
PI	Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX	
DR	WPI; 2002-590824/63.
DR	N-PSDB; ABP65011.
XX	
PT	New isolated polynucleotide, useful in research, diagnostic or
PT	therapeutic methods, e.g. preventing or treating disorders involving
PT	aberrant protein expression or biological activity.
PS	Claim 1; SEQ ID NO 330; 394pp; English.
XX	
CC	The present invention relates to novel human coding sequences (ABQ99268-
CC	ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in
CC	therapeutic, diagnostic and research methods. The polynucleotides may be
CC	used in the field of molecular biology as hybridisation probes, primers
CC	for PCR, for chromosome and gene mapping, for the recombinant production
CC	of protein, or in generation of anti-sense DNA or RNA. The
CC	polynucleotides are useful in diagnostics as expressed sequence tags
CC	(ESTs) for identifying expressed genes or for physical mapping of the
CC	human genome. The proteins may be used as molecular weight markers or as
CC	nutritional sources or supplements. The proteins may be used to maintain
CC	and expand cell population in a totipotent or pluripotent state
CC	useful for re-engineering damaged or diseased tissues, transplantation,
CC	manufacture of bio-pharmaceuticals or the development of bio-sensors. The
CC	polynucleotides and proteins are useful for preventing, treating or
CC	ameliorating disorders involving aberrant protein expression or
CC	biological activity, e.g. haematopoietic disorders, central/peripheral
CC	nervous system diseases, mechanical and traumatic disorders, non-healing
CC	wounds, immune deficiencies and disorders, infectious diseases caused by
CC	viral, bacterial or fungal infection, autoimmune disorders, allergic
CC	reactions and conditions, coagulation disorders, or cancer. The
CC	polynucleotide sequences of the invention were assembled from ESTs
CC	isolated mainly by sequencing by hybridisation, and in some cases,
CC	sequences obtained from one or more public databases. Note: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 1415 BP; 313 A; 414 C; 425 G; 263 T; 0 U; 0 Other;

Query Match 99.5%; Score 1015; DB 6; Length 1415;

Best Local Similarity 100.0%; Pred. No. 8.4e-261; Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGCAGCGGAAACAGCAGTTGGAGCTGGGTCTGCTCCTCAGTCTGTGGGGGGCAGTA	60
DB	25	ATGGCAGCGGAAACAGCAGTTGGAGCTGGGTCTGCTCCTCAGTCTGTGGGGGGCAGTA	84
QY	61	GTAGGTGCTCAAAACATCAAGCCCGGATTTGGGAGCCACTGGTGTGAAGTGAAGGGG	120
DB	85	GTAGGTGCTCAAAACATCAAGCCCGGATTTGGGAGCCACTGGTGTGAAGTGAAGGGG	144
QY	121	GCCCCCAAGAAACACCCAGCGCTGGAACTGAACACAGCCGAGCAGAAAGCT	180
DB	145	GCCCCCAAGAAACACCCAGCGCTGGAACTGAACACAGCCGAGCAGAAAGCT	204
QY	181	TGAAAGTCTCTGCTCCCTCCAGGAGAGGCGCTGGGACAGTGTGGCTGTGCTCTTCCC	240
DB	205	TGAAAGTCTCTGCTCCCTCCAGGAGAGGCGCTGGGACAGTGTGGCTGTGCTCTTCCC	264
QY	241	AACGGTCTCTCTCTTCCGCTGTGCGGATCCAGATGAGGGATTTTCGGTGGCAG	300
DB	265	AACGGTCTCTCTCTTCCGCTGTGCGGATCCAGATGAGGGATTTTCGGTGGCAG	324
QY	301	GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAATT	360
DB	325	GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAATT	384
QY	361	CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTACGGCTGGTGTTCCTCAATAAG	420
DB	385	CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTACGGCTGGTGTTCCTCAATAAG	444
QY	421	GTGGGACATGTGTGTCAGAGGAAAGTACCTGCGAGGACTCTTAGCTGGCACTTGGAT	480
DB	445	GTGGGACATGTGTGTCAGAGGAAAGTACCTGCGAGGACTCTTAGCTGGCACTTGGAT	504
QY	481	GGGAAGCCCTGTGCTTAATGAGAGGAGTATCTGTAGAGAAACAGACCAGGACAC	540
DB	505	GGGAAGCCCTGTGCTTAATGAGAGGAGTATCTGTAGAGAAACAGACCAGGACAC	564
QY	541	CTTGAGACAGGGCTCTTCACTGTCAGTCCGAGCTAATGTGACCCAGCCCGGGGAGGA	600
DB	565	CTTGAGACAGGGCTCTTCACTGTCAGTCCGAGCTAATGTGACCCAGCCCGGGGAGGA	624
QY	601	GATCCCGTCCCACTTCTCTAGCTTCCAGCCAGGCTTCCCGACACCGGGCCTTG	660
DB	625	GATCCCGTCCCACTTCTCTAGCTTCCAGCCAGGCTTCCCGACACCGGGCCTTG	684
QY	661	CGCAGACCCCATCCAGCCCGCTGTCTGGAGCCTGTGCTCTGGAGAGGTCCAAATTG	720
DB	685	CGCAGACCCCATCCAGCCCGCTGTCTGGAGCCTGTGCTCTGGAGAGGTCCAAATTG	744
QY	721	GTGGTGGAGCCAGAAGTGGAGCAGTAGCTCTCTGGTGGAACTTAACCTGACCTGTGAA	780
DB	745	GTGGTGGAGCCAGAAGTGGAGCAGTAGCTCTCTGGTGGAACTTAACCTGACCTGTGAA	804
QY	781	GTCCCTGCCAGCCCTCTCTCAAAATCCAATGATGAAGATGGTGGCCCTTGCCCTT	840
DB	805	GTCCCTGCCAGCCCTCTCTCAAAATCCAATGATGAAGATGGTGGCCCTTGCCCTT	864
QY	841	CCCCCAGCCCTGTGCTGATCTCTCTGATGATAGGCGCTCAGGACAGGGAACCTACGC	900
DB	865	CCCCCAGCCCTGTGCTGATCTCTCTGATGATAGGCGCTCAGGACAGGGAACCTACGC	924
QY	901	TGTGTGGCCACCATTCAGCCAGCGGCCCCAGGAAAGCGTCTGTACGATCAGCATC	960
DB	925	TGTGTGGCCACCATTCAGCCAGCGGCCCCAGGAAAGCGTCTGTACGATCAGCATC	984
QY	961	ATCGAACCAGCGGAGGAGGGCCCAACTGCAAGGCTCTGTGGGAGGATCAGGGCTGG	1015
DB	985	ATCGAACCAGCGGAGGAGGGCCCAACTGCAAGGCTCTGTGGGAGGATCAGGGCTGG	1039

ADK00130 ID ADK00130 standard; cDNA; 1436 BP.			
XX	AC	ADK00130;	
XX	DT	20-MAY-2004 (first entry)	
XX	DE	Human RAGE encoding sequence.	
XX	KW	Advanced Glycation End Product Ligand Binding Element; RAGE-LBE;	
XX	KW	Cytostatic; Antidiabetic; Nootropic; Antiarthritic; Osteopathic;	
KW	KW	Neuroprotective; Antiinflammatory; Dermatological; Immunosuppressive;	
KW	KW	Vasotropic; Antipsoriatic; Antibacterial; Antiartherosclerotic;	
KW	KW	amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;	
KW	KW	chronic inflammatory disease; osteoarthritis; irritable bowel disease;	
XX	OS	Homo sapiens.	
OS	XX	Synthetic.	
XX	XX	Location/Qualifiers	
XX	XX	1. .1436	
XX	XX	/*tag= a	
XX	XX	/product= "RAGE"	
XX	XX	WO2004016229-A2.	
XX	XX	26-FEB-2004.	
XX	XX	18-AUG-2003; 2003WO-US025996.	
XX	XX	16-AUG-2002; 2002US-0404205P.	
XX	XX	(AMHP ) WYETH.	
XX	XX	Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FM;	
XX	XX	Feldmann M, Foxwell BJM, Feldman JL;	
XX	XX	WPI; 2004-192067/18.	
XX	XX	P-PSDB; ADK00129.	
XX	XX	New fusion protein comprising a Receptor for Advanced Glycation End	
XX	XX	Product Ligand Binding Element (RAGE-LBE) and an immunoglobulin element,	
XX	XX	useful for preparing a composition for treating e.g., Alzheimer's	
XX	XX	disease.	
XX	XX	Disclosure; SEQ ID NO 44; 100pp; English.	
XX	XX	The present invention relates to a new fusion protein comprises a	
XX	XX	Receptor for Advanced Glycation End Product Ligand Binding Element (RAGE-	
XX	XX	LBE) and an immunoglobulin element. The fusion protein is useful for	
XX	XX	preparing a composition for treating RAGE-associated disorders such as	
XX	XX	amyloidosis, cancer, Crohn's disease, diabetes, complications of	
XX	XX	diabetes, prion-related disorders, vasculitis, nephropathies,	
XX	XX	retinopathies and/or neuropathies; Alzheimer's disease, chronic	
XX	XX	inflammatory disease e.g., rheumatoid arthritis, osteoarthritis,	
XX	XX	irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute	
XX	XX	inflammatory disease e.g., sepsis, or cardiovascular disease, e.g.,	
XX	XX	atherosclerosis or restenosis. The present sequence represents human RAGE	
XX	XX	protein encoding sequence.	
XX	XX	Sequence 1436 BP; 340 A; 411 C; 422 G; 263 T; 0 U; 0 Other;	
Query Match 99.5%; Score 1015; DB 12; Length 1436;			
Best Local Similarity 100.0%; Pred. No. 8.5e-261;			
Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGCAGCGGAAACAGCAGTTGGAGCTGGGTCTGCTCCTCAGTCTGTGGGGGGCAGTA	60
DB	20	ATGGCAGCGGAAACAGCAGTTGGAGCTGGGTCTGCTCCTCAGTCTGTGGGGGGCAGTA	79
QY	61	GTAGGTGCTCAAAACATCAAGCCCGGATTTGGGAGCCACTGGTGTGAAGTGAAGGGG	120

Db 80 GTAGTGCTCAAAACATCATCAGCCCGGATTGGGAGCCACTGGTGTCTGAAGTGTAAAGGG 139  
QY 121 GCCCCCAAGAAACACACCCAGCGCTGGAATGAACTGAACACAGCCGCGACAGAAGCT 180  
Db 140 GCCCCCAAGAAACACACCCAGCGCTGGAATGAACTGAACACAGCCGCGACAGAAGCT 199  
QY 181 TGAAGGTCTCTCTCCCAAGGAGGAGGCCCTCGGACAGTGTGGCTGTGTCCTTCCC 240  
Db 200 TGAAGGTCTCTCTCCCAAGGAGGAGGCCCTCGGACAGTGTGGCTGTGTCCTTCCC 259  
QY 241 AACGGCTCCCTCTCTCCCAAGGAGGAGGCCCTCGGACAGTGTGGCTGTGTCCTTCCC 300  
Db 260 AACGGCTCCCTCTCTCCCAAGGAGGAGGCCCTCGGACAGTGTGGCTGTGTCCTTCCC 319  
QY 301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGT 360  
Db 320 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGT 379  
QY 361 CTTGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCAACGCTGGTGTTCCTCAATAAG 420  
Db 380 CTTGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCAACGCTGGTGTTCCTCAATAAG 439  
QY 421 GTGGGACATCTGTCTCAGAGGAAAGTACCTCGAGGAGCTCTTAGCTGGCACTTTGGAT 480  
Db 440 GTGGGACATCTGTCTCAGAGGAAAGTACCTCGAGGAGCTCTTAGCTGGCACTTTGGAT 499  
QY 481 GGAAGCCCTGTGCTTAATGAAGGAGGATCTGTGAAGAAACAGACACAGGAGACAC 540  
Db 500 GGAAGCCCTGTGCTTAATGAAGGAGGATCTGTGAAGAAACAGACACAGGAGACAC 559  
QY 541 CTTGAGACAGGGCTCTTCACTGCACTCGAGTGGAGCTAATGGTACCCAGCCCGGGAGGA 600  
Db 560 CTTGAGACAGGGCTCTTCACTGCACTCGAGTGGAGCTAATGGTACCCAGCCCGGGAGGA 619  
QY 601 GATCCCGTCCCACTCTCTGTAGCTTCAAGCCAGGCTTCCCGACACACCGGCTTG 660  
Db 620 GATCCCGTCCCACTCTCTGTAGCTTCAAGCCAGGCTTCCCGACACACCGGCTTG 679  
QY 661 CGCACAGCCCACTCAGACCCCTGTCTGGAGCCTGTGCTCTGGAGGAGTGCCTCAATTG 720  
Db 680 CGCACAGCCCACTCAGACCCCTGTCTGGAGCCTGTGCTCTGGAGGAGTGCCTCAATTG 739  
QY 721 GTGGTGGAGCAGAGGTGAGCAGTAGTCTCTGTGGAAACCGTAACCTGTACCTGTGAA 780  
Db 740 GTGGTGGAGCAGAGGTGAGCAGTAGTCTCTGTGGAAACCGTAACCTGTACCTGTGAA 799  
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGATGGTGTGCTTGCCTTCCCTT 840  
Db 800 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGATGGTGTGCTTGCCTTCCCTT 859  
QY 841 CCCCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGCGCTCAGACCCAGGAACTACAGC 900  
Db 860 CCCCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGCGCTCAGACCCAGGAACTACAGC 919  
QY 901 TGTGTGGCCACCATTCAGACCCAGGCGCCCGAGGAAAGCGTGTCTCAGCATCAGCATC 960  
Db 920 TGTGTGGCCACCATTCAGACCCAGGCGCCCGAGGAAAGCGTGTCTCAGCATCAGCATC 979  
QY 961 ATCGAACCCAGGCGAGGAGGCGCACTGAGGCTCTGTGGAGGATCAGGGCTGG 1015  
Db 980 ATCGAACCCAGGCGAGGAGGCGCACTGAGGCTCTGTGGAGGATCAGGGCTGG 1034  
RESULT 8  
ID ADE95563 standard; cDNA; 1217 BP.  
AC ADE95563;  
XX  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human NOVX16c protein cDNA sequence.  
XX

KW NOVX protein; biochemical stimulation; physiological stimulation;  
KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;  
KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;  
KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;  
KW neurotropic; antipsoriatic; antiparkinsonian; antiaschmatic; neuroleptic;  
KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;  
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;  
KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;  
KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;  
KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;  
KW depression; allergy; fertility disorder; gene; ss; NOVX16c.  
XX  
OS Homo sapiens.  
XX WO2003050245-A2.  
PN 19-JUN-2003.  
XX  
XX 03-DEC-2002; 2002WO-US038594.  
PR 05-DEC-2001; 2001US-0336600P.  
PR 07-DEC-2001; 2001US-0338285P.  
PR 12-DEC-2001; 2001US-0341346P.  
PR 17-DEC-2001; 2001US-0341477P.  
PR 17-DEC-2001; 2001US-0341540P.  
PR 20-DEC-2001; 2001US-0342592P.  
PR 27-DEC-2001; 2001US-0344297P.  
PR 31-DEC-2001; 2001US-0344903P.  
PR 17-APR-2002; 2002US-0373288P.  
PR 15-MAY-2002; 2002US-0380981P.  
PR 17-MAY-2002; 2002US-0381495P.  
PR 28-MAY-2002; 2002US-0383534P.  
PR 28-MAY-2002; 2002US-0383744P.  
PR 29-MAY-2002; 2002US-0383829P.  
PR 29-MAY-2002; 2002US-0384024P.  
PR 07-AUG-2002; 2002US-0401788P.  
PR 26-AUG-2002; 2002US-0406353P.  
PR 31-OCT-2002; 2002US-00401788.  
PR 02-DEC-2002; 2002US-00406353.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA,  
PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;  
PI Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphy R;  
PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG,  
PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;  
XX WPI; 2003-513974/48.  
DR P-PSDB; ADE95564.  
XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
XX Claim 20; SEQ ID NO 95; 211pp; English.  
XX  
XX This invention relates to novel NOVX proteins, and the DNA sequence which  
CC encode them, having properties related to stimulation of biochemical or  
CC physiological responses in a cell, a tissue, an organ or an organism.  
CC Compounds which modulate the proteins of the invention may have cardiant,  
CC antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,  
CC antiarthritic, antidiabetic, nephrotropic, dermatological,  
CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,  
CC neurotropic, antipsoriatic, antiparkinsonian, antiaschmatic, neuroleptic,  
CC antidepressant, antiallergic or gynaecological activities. The DNA  
CC sequences of the invention may be useful for gene therapy whilst the  
CC protein sequences may allow the development of a vaccine. The protein is  
CC useful in the manufacture of a medicament for treating a syndrome  
CC associated with a human disease. The invention may be useful in  
CC diagnosing, treating or preventing NOVX-associated disorders, for example  
CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,

CC	rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
CC	disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
CC	Parkinson's disease, asthma, schizophrenia, depression, allergies or
CC	fertility disorders. The nucleic acids may further be used as
CC	hybridisation probes, in chromosome mapping, tissue typing, preventive
CC	medicine, and pharmacogenomics. The present sequence is the cDNA sequence
XX	which encodes the human NOV16c protein of the invention.
XX	
SQ	Sequence 1217 BP; 265 A; 343 C; 393 G; 216 T; 0 U; 0 Other;
Query Match 99.4%; Score 1013.4; DB 10; Length 1217;	
Best Local Similarity 99.9%; Pred. No. 2.1e-260;	
Matches 1014; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 ATGGCAGCGGAAACAGCAGTTGGAGCTGGGTCTGGTCTCTCAGTCTGTGGGGGCGAGTA 60
DB	3 ATGGCAGCGGAAACAGCAGTTGGAGCTGGGTCTGGTCTCTCAGTCTGTGGGGGCGAGTA 62
QY	61 GTAGTGTCTCAAAACATCAGCCCGATTTGGGAGCCACTGGTCTGAAGTGTAAAGGG 120
DB	63 GTAGTGTCTCAAAACATCAGCTCGGATTTGGGAGCCACTGGTCTGAAGTGTAAAGGG 122
QY	121 GCCCCCAAGAAACCCAGCGGCTGGATGAACTGAACACAGCCGCGACAGAGCT 180
DB	123 GCCCCCAAGAAACCCAGCGGCTGGATGAACTGAACACAGCCGCGACAGAGCT 182
QY	181 TGAAGGTCTCTCTCCCGAGGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCC 240
DB	183 TGAAGGTCTCTCTCCCGAGGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCC 242
QY	241 AACGGTCTCTCTCTCCCGTGTGGGATCCAGGATGAGGGGATTTCCGGTGCCAG 300
DB	243 AACGGTCTCTCTCTCCCGTGTGGGATCCAGGATGAGGGGATTTCCGGTGCCAG 302
QY	301 GCAATCAACAGGAATGGAAGGAGCAAGTCCAACTACGAGTCCGTCTTACCAAGATT 360
DB	303 GCAATCAACAGGAATGGAAGGAGCAAGTCCAACTACGAGTCCGTCTTACCAAGATT 362
QY	361 CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGCTCGTGTTCCTCAATAAG 420
DB	363 CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGCTCGTGTTCCTCAATAAG 422
QY	421 GTGGGACATGTGTGTGACAGGGAAGCTACCTGTGACGAGACTTTAGCTGGCACTTGGAT 480
DB	423 GTGGGACATGTGTGTGACAGGGAAGCTACCTGTGACGAGACTTTAGCTGGCACTTGGAT 482
QY	481 GGGAGCCCTGTGTGCTTAATGAGGAGGATATCTGTGAAGAACAGACAGGAGACAC 540
DB	483 GGGAGCCCTGTGTGCTTAATGAGGAGGATATCTGTGAAGAACAGACAGGAGACAC 542
QY	541 CCTGAGACAGGGCTCTTTCACACTGCACTGGAGCTAATGTGACCCAGCCCGGGAGGA 600
DB	543 CCTGAGACAGGGCTCTTTCACACTGCACTGGAGCTAATGTGACCCAGCCCGGGAGGA 602
QY	601 GATCCCGTCCCACTTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGGCTTGG 660
DB	603 GATCCCGTCCCACTTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGGCTTGG 662
QY	661 CGCAGAGCCCATTCAGCCCGCTGTCTGGAGCTGTGCTCTGAGAGGCTTCAATTG 720
DB	663 CGCAGAGCCCATTCAGCCCGCTGTCTGGAGCTGTGCTCTGAGAGGCTTCAATTG 722
QY	721 GTGGTGGAGCCAGAAGGTGAGCAGTAGCTCTGTGGTGAACCGTAACCTGACCTGTGAA 780
DB	723 GTGGTGGAGCCAGAAGGTGAGCAGTAGCTCTGTGGTGAACCGTAACCTGACCTGTGAA 782
QY	781 GTCCCTGCCAGCCCTCTCTCAAAATCCACTGGATGAAGGATGGTGTGCCCTTGGCCCTT 840
DB	783 GTCCCTGCCAGCCCTCTCTCAAAATCCACTGGATGAAGGATGGTGTGCCCTTGGCCCTT 842
QY	841 CCCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCGCTCAGACACAGGGAACCTACAGC 900
DB	843 CCCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCGCTCAGGACACAGGGAACCTACAGC 902
QY	901 TGTGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAAGCCGTGTGTCTCAGCATCAGCATC 960
DB	903 TGTGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAAGCCGTGTGTCTCAGCATCAGCATC 962
QY	961 ATCGAACCAAGGAGGAGGGGCACTGCAGGCTCTGTGGGAGGATCAGGGCTGG 1015
DB	963 ATCGAACCAAGGAGGAGGGGCACTGCAGGCTCTGTGGGAGGATCAGGGCTGG 1017
RESULT 9	
AAH57444	
ID	AAH57444 standard; cDNA; 1582 BP.
XX	AAH57444;
AC	
DT	10-SEP-2001 (first entry)
XX	Human lung cell specific cDNA sequence SEQ ID NO:284.
DE	
XX	Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
KW	liver; uterus; ovary; stomach; intestine; kidney; pancreas; es;
KW	metabolic disease; developmental disease; cytostatic; immunomodulatory;
KW	neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
OS	Homo sapiens.
XX	
PN	WO200132927-A2.
XX	
PD	10-MAY-2001.
XX	
PF	02-NOV-2000; 2000WO-US030396.
XX	
PR	04-NOV-1999; 99US-0163508P.
XX	
PA	(INCY-) INCYTE GENOMICS INC.
XX	
PI	Sornasse T, Seilhamer JJ, Watson GA;
XX	WPI; 2001-291057/30.
DR	
XX	
PT	New cell and tissue specific polynucleotides useful for diagnosis,
PT	prognosis or monitoring of treatments for disorders where the gene is
PT	associated with a cancer, immunopathology or neuropathology.
XX	
PS	Claim 1: Page 210; 327pp; English.
XX	
CC	AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
CC	sequences (I). (I) can have cytostatic, immunomodulatory and
CC	neuroprotective activities, and can be used in gene therapy. (I) and
CC	proteins (II) encoded by then are used in high throughput screening
CC	assays to select DNA molecules, RNA molecules, peptide nucleic acids,
CC	mimetics, peptides, proteins, agonists, antagonists, antibodies or their
CC	fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
CC	agents. Expression of (I) in a sample indicates the differentiation of
CC	embryonic stem cells into a tissue selected from brain, heart, kidney,
CC	liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
CC	to produce an expression profile that defines a metabolic or
CC	developmental process, treatment, condition, disease or disorder. The
CC	gene profile can be used for diagnosis, prognosis or monitoring of
CC	treatments and for investigating a predisposition to a disorder where the
CC	gene is associated with a cancer, immunopathology or neuropathology
XX	
SQ	Sequence 1582 BP; 355 A; 448 C; 486 G; 293 T; 0 U; 0 Other;
Query Match 99.4%; Score 1013.4; DB 4; Length 1582;	
Best Local Similarity 99.9%; Pred. No. 2.3e-260;	
Matches 1014; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 ATGGCAGCGGAAACAGCAGTTGGAGCTGGGTCTGGTCTCTCAGTCTGTGGGGGCGAGTA 60
DB	201 ATGGCAGCGGAAACAGCAGTTGGAGCTGGGTCTGGTCTCTCAGTCTGTGGGGGCGAGTA 260

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QY 61 GTAGTGCTCAAAACATCAAGCCCGGATTGGAGCCACTGTGCTGAAGTGTAAAGGG 120
Db 261 GTAGTGCTCAAAACATCAAGCCCGGATTGGAGCCACTGTGCTGAAGTGTAAAGGG 320
QY 121 GCCCCCAAGAAACACCCAGCGCTGGAATGAAACTGAACACAGCCCGGACAGAAGCT 180
Db 321 GCCCCCAAGAAACACCCAGCGCTGGAATGAAACTGAACACAGCCCGGACAGAAGCT 380
QY 181 TGAAGGTCTGTCTCTCCAGGAGAGAGCCCTCGGACAGTGTGCTGTCTTCC 240
Db 381 TGAAGGTCTGTCTCTCCAGGAGAGAGCCCTCGGACAGTGTGCTGTCTTCC 440
QY 241 AACGGTCCCTCTCTCTCCGCTGTGCGGATCCAGGATGAGGGGATTTTCGGTCCAG 300
Db 441 AACGGTCCCTCTCTCTCCGCTGTGCGGATCCAGGATGAGGGGATTTTCGGTCCAG 500
QY 301 GCAATGAACAGGAATGGAAGGAGACCAAGTCAACTACCGAGTCCGTGTCTACAGATT 360
Db 501 GCAATGAACAGGAATGGAAGGAGACCAAGTCAACTACCGAGTCCGTGTCTACAGATT 560
QY 361 CTTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTACGGCTGTGTCTCCATAAG 420
Db 561 CTTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTACGGCTGTGTCTCCATAAG 620
QY 421 GTGGGACATGTGTGTGACAGGGAAGCTACCTGACGGGACTCTTAGCTGGCACTTGGAT 480
Db 621 GTGGGACATGTGTGTGACAGGGAAGCTACCTGACGGGACTCTTAGCTGGCACTTGGAT 680
QY 481 GGGAAAGCCCTGTGCTCTAATGAGAGGAGATCTGTGAAGAAACAGACACAGGAGAC 540
Db 681 GGGAAAGCCCTGTGCTCTAATGAGAGGAGATCTGTGAAGAAACAGACACAGGAGAC 740
QY 541 CTTGACAGAGGCTCTTCACTACGTGAGTGGAGCTAATGTGACCCACGCCGGGAGGA 600
Db 741 CTTGACAGAGGCTCTTCACTACGTGAGTGGAGCTAATGTGACCCACGCCGGGAGGA 800
QY 601 GATCCCGTCCCACTCTCTGTAGCTTTCAGCCAGGCTTCCCGACACCGGCGCTTG 660
Db 801 GATCCCGTCCCACTCTCTGTAGCTTTCAGCCAGGCTTCCCGACACCGGCGCTTG 860
QY 661 CGCAGAGCCCATCCAGCCCGTGTCTGGAGCCTGTGCTGTGAGAGGATCCAAATG 720
Db 861 CGCAGAGCCCATCCAGCCCGTGTCTGGAGCCTGTGCTGTGAGAGGATCCAAATG 920
QY 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGGTGAACCGTAACTGACCTGTGAA 780
Db 921 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGGTGAACCGTAACTGACCTGTGAA 980
QY 781 GTCCCTGCCAGCCCTCTCTCAAAATCCACTGGATGAAGATGGTGTGCCCTTGCCCTT 840
Db 981 GTCCCTGCCAGCCCTCTCTCAAAATCCACTGGATGAAGATGGTGTGCCCTTGCCCTT 1040
QY 841 CCCCCAGCCCTGTGTGATCTCTCCCTGATAGTAGGCTCAGGACAGGGAACCTACAGC 900
Db 1041 CCCCCAGCCCTGTGTGATCTCTCCCTGATAGTAGGCTCAGGACAGGGAACCTACAGC 1100
QY 901 TGTGTGGCCACCATTTCCAGCCACAGGCCCCCAGGAAAGCCGTGTGTGACATCAGCATC 960
Db 1101 TGTGTGGCCACCATTTCCAGCCACAGGCCCCCAGGAAAGCCGTGTGTGACATCAGCATC 1160
QY 961 ATCGAAACAGGAGAGAGGGGCAACTGACGCTCTGTGGGAGATCAGGGCTGG 1015
Db 1161 ATCGAAACAGGAGAGAGGGGCAACTGACGCTCTGTGGGAGATCAGGGCTGG 1215
```

## RESULT 10

ABQ79955

ID ABQ79955 standard; DNA; 1391 BP.

XX

AC ABQ79955;

XX

DT 23-DEC-2002 (first entry)

XX

DE Human RAGE nucleotide sequence.

XX Receptor for Advanced Glycated end product; RAGE; recombinant; nootropic;  
KW antiarteriosclerotic; antidiabetic; cytostatic; nephrotropic; vasotropic;  
KW neuroprotective; antiinflammatory; gene therapy; human; db.  
XX Homo sapiens.  
OS

PN WO200270667-A2.

XX

PD 12-SEP-2002.

XX

PF 05-MAR-2002; 2002WO-US006881.

XX

PR 05-MAR-2001; 2001US-0273418P.

XX

PA (TRAN-) TRANSTECH PHARMA INC.

XX

PI Harris R, Shen J, Shahbaz M;

XX

XX WPI; 2002-713443/77.

DR

XX Claim 12; Fig 2A; 51pp; English.

XX

PT High level expression of recombinant Receptors for Advanced Glycated end  
PT products (RAGE) proteins for treating increased levels of advanced  
PT glycosylation end products, comprises infecting cells with a high titer  
PT recombinant virus.  
XX

PS

XX

CC The invention relates to a method for high level expression of  
CC recombinant forms of the Receptor for Advanced Glycated end products  
CC (RAGE) or its fragments. The method involves (i) subcloning a nucleotide  
CC sequence encoding RAGE or its fragment into a virus; (ii) preparing a  
CC high titer stock of recombinant virus; and (iii) infecting host cells  
CC with the high titer recombinant virus under conditions such that  
CC predetermined levels of RAGE or its fragment is produced, where the  
CC predetermined levels of RAGE comprises at least 25 mg recombinant protein  
CC per liter of culture. The method is useful for high level expression of  
CC recombinant RAGE polypeptide or its fragment which may be useful in  
CC preventing, treating or ameliorating diseases associated with increased  
CC levels of advanced glycosylation end products, such as Alzheimer's  
CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's  
CC disease, inflammation, systemic lupus nephritis, inflammatory lupus  
CC nephritis, cancer or erectile dysfunction. The present sequence  
CC represents the nucleotide sequence of human RAGE as reported in GenBank  
CC /EMBL Accession no. XM004205  
XX

SQ

Sequence 1391 BP; 305 A; 408 C; 417 G; 261 T; 0 U; 0 Other;

Query Match 99.3%; Score 1013; DB 6; Length 1391;

Best Local Similarity 100.0%; Pred. No. 2.9e-260;

Matches 1013; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGAGCCGGAACAGCAGTTGGAGCCTGGGTGCTGTCTCAGTCTGTGGGGGCGAGTAGT 62

Db 3 GCGAGCCGGAACAGCAGTTGGAGCCTGGGTGCTGTCTCAGTCTGTGGGGGCGAGTAGT 62

QY 63 AGGTGCTCAAAACATCAAGCCCGGATTGGGAGCCACTGGTGTGAAGTGTAAAGGGGCG 122

Db 63 AGGTGCTCAAAACATCAAGCCCGGATTGGGAGCCACTGGTGTGAAGTGTAAAGGGGCG 122

QY 123 CCCCAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGGCCCGGACAGAGCTTG 182

Db 123 CCCCAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGGCCCGGACAGAGCTTG 182

QY 183 GAAGTCTCTCTCCAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCCA 242

Db 183 GAAGTCTCTCTCCAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCCA 242

QY 243 CGGCTCCCTCTTCTCCGCTGTGCGGATCCAGATCAGGGGATTTTCCGCTGCCAGGC 302

Db 243 CGGCTCCCTCTTCTCCGCTGTGCGGATCCAGATCAGGGGATTTTCCGCTGCCAGGC 302



QY	303	AATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTC	362
Db	303	AATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTC	362
QY	363	TGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACCTACGGCTGGTGTCCCAATAGGT	422
Db	363	TGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACCTACGGCTGGTGTCCCAATAGGT	422
QY	423	GGGGACATGTGTCTCAGAGGAAGTACCTCGCAGGACTCTTGTAGCTGGCACTTGGATGG	482
Db	423	GGGGACATGTGTCTCAGAGGAAGTACCTCGCAGGACTCTTGTAGCTGGCACTTGGATGG	482
QY	483	GAAGCCCTGCTGCTTAATGAGAAGGGAGTATCTGTGAAGGAACACACGAGAGACACC	542
Db	483	GAAGCCCTGCTGCTTAATGAGAAGGGAGTATCTGTGAAGGAACACACGAGAGACACC	542
QY	543	TGAGACAGGGCTCTTACACTGTCAGTCCGAGTAAATGGTGACCCACCGCCGGGAGGAGA	602
Db	543	TGAGACAGGGCTCTTACACTGTCAGTCCGAGTAAATGGTGACCCACCGCCGGGAGGAGA	602
QY	603	TCCCGTCCACCTTCTCTGTAGCTTTCAGCCAGGCTTTCGCCGACACCGGGCTTGGG	662
Db	603	TCCCGTCCACCTTCTCTGTAGCTTTCAGCCAGGCTTTCGCCGACACCGGGCTTGGG	662
QY	663	CACAGCCCTCATCAGCCCGTGTCTGGAGCTGTGCTCTCTGGAGAGGTCCAATTGGT	722
Db	663	CACAGCCCTCATCAGCCCGTGTCTGGAGCTGTGCTCTCTGGAGAGGTCCAATTGGT	722
QY	723	GGTGGAGCCAGAGGTGGAGCTAGCTCTGTGGTGAACCGTAACTGACCTGTCAAGT	782
Db	723	GGTGGAGCCAGAGGTGGAGCTAGCTCTGTGGTGAACCGTAACTGACCTGTCAAGT	782
QY	783	CCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGGATGGTGTGCCCTTGCCTTCC	842
Db	783	CCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGGATGGTGTGCCCTTGCCTTCC	842
QY	843	CCCGAGCCCTGTCTGATCTCTCTGATATAGGCTCTCAGGACCGAGGAACCTACAGCTG	902
Db	843	CCCGAGCCCTGTCTGATCTCTCTGATATAGGCTCTCAGGACCGAGGAACCTACAGCTG	902
QY	903	TGTGGCCACCCATTCAGCCACCGGCCCCAGGAAGCCGTGTCTCAGCATCAGCATCAT	962
Db	903	TGTGGCCACCCATTCAGCCACCGGCCCCAGGAAGCCGTGTCTCAGCATCAGCATCAT	962
QY	963	CGAACAGGCGAGGAGGGCCAACTGCAGGCTCTGTGGAGGATCAGGGCTGG 1015	
Db	963	CGAACAGGCGAGGAGGGCCAACTGCAGGCTCTGTGGAGGATCAGGGCTGG 1015	
RESULT 11			
ID	ADS10302	standard; DNA; 1146 BP.	
XX	AC	ADS10302;	
XX	DT	16-DEC-2004 (first entry)	
XX	DE	Human therapeutic DNA - SEQ ID 539.	
XX	KW	antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;	
XX	KW	inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;	
XX	KW	aplaastic anaemia; cancer; wound healing; gene therapy; ds; gene.	
OS	XX	Homo sapiens.	
PN	XX	WO2004080148-A2.	
PD	XX	23-SEP-2004.	
PF	XX	30-SEP-2003; 2003WO-US030720.	
XX	XX	02-OCT-2002; 2002US-0416186P.	

PA	(NUVE-) NUVELO INC.	
PI	Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;	
PI	Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Wang G, Zhou P;	
XX	WPI; 2004-568857/65.	
DR	P-PSDB; ADS10986.	
XX	New polynucleotide, useful in preparing a composition for diagnosing or	
PT	treating inflammation, neurodegenerative or stem cell disorders, e.g.,	
PT	aplaastic anemia or cancer for promoting wound healing.	
XX	Claim 1; SEQ ID NO 539; 718pp; English.	
CC	The invention relates to a novel isolated polynucleotide and the encoded	
CC	polypeptide. The molecules of the invention demonstrate antiinflammatory,	
CC	neuroprotective, antianaemic, cytostatic and vulnerary activities and may	
CC	be useful in preparing a composition for diagnosing or treating	
CC	inflammatory, haematopoietic, immune, neurodegenerative or stem cell	
CC	disorders, such as aplastic anaemia or cancer, as well as for promoting	
CC	wound healing. The molecules may also be utilised during gene therapy	
CC	procedures. The current sequence is that of a human therapeutic DNA of	
CC	the invention. The current sequence is not shown explicitly within the	
CC	specification but can be accessed from the WIPO web-site.	
XX	Sequence 1146 BP; 248 A; 332 C; 362 G; 204 T; 0 U; 0 Other;	
SQ	Query Match 99.0%; Score 1010.2; DB 13; Length 1146;	
	Best Local Similarity 99.7%; Pred. No 1.5e-259;	
	Matches 1012; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	1	ATGGCAGCCGGAACAGCAGTTCGGAGCTCGGTGCTGCTCCTCAGTCTGGGGGGCAGTA 60
Db	1	ATGGCAGCCGGAACAGCAGTTCGGAGCTCGGTGCTGCTCCTCAGTCTGGGGGGCAGTA 60
QY	61	GTAGTGTCTCAAAACATCATCAGCCCGGATTCGGAGCCACTGGTCTGAAGTGTAGGGG 120
Db	61	GTAGTGTCTCAAAACATCATCAGCCCGGATTCGGAGCCACTGGTCTGAAGTGTAGGGG 120
QY	121	GCCTCCCAAGAAACACCCAGCGCTGGAAATGMAACTGAACACAGCCCGGACAGAAAGCT 180
Db	121	GCCTCCCAAGAAACACCCAGCGCTGGAAATGMAACTGAACACAGCCCGGACAGAAAGCT 180
QY	181	TGGAAGTCTCTGTCTCCAGGAGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCC 240
Db	181	TGGAAGTCTCTGTCTCCAGGAGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCC 240
QY	241	AACGGCTCCCTCTTCTTCCGCTGTCCGGATCCAGGATGAGGGATTTTCGGTCCAG 300
Db	241	AACGGCTCCCTCTTCTTCCGCTGTCCGGATCCAGGATGAGGGATTTTCGGTCCAG 300
QY	301	GCAATGAACAGCAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGAT 360
Db	301	GCAATGAACAGCAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGAT 360
QY	361	CCTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAG 420
Db	361	CCTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAG 420
QY	421	GTGGGACATGTGTCTCAGAGGAGTACCTTCAGGGAGCTCTTACCTGAGCTTGGAT 480
Db	421	GTGGGACATGTGTCTCAGAGGAGTACCTTCAGGGAGCTCTTACCTGAGCTTGGAT 480
QY	481	GGGAAGCCCTCTGTGCTTAATGAGAAGGAGTATCTGTGAAGGAACAGACAGGAGACAC 540
Db	481	GGGAAGCCCTCTGTGCTTAATGAGAAGGAGTATCTGTGAAGGAACAGACAGGAGACAC 540
QY	541	CCTGAGACAGGGCTCTTTCACACTGCACTCGAGTGGAGCTTAATGGTGTGAGGAGGAGGA 600
Db	541	CCTGAGACAGGGCTCTTTCACACTGCACTCGAGTGGAGCTTAATGGTGTGAGGAGGAGGA 600
QY	601	GATCCCGTCCCACTTCTCTGTAGCTTCAGCCAGGCTTCCCGGACACCGGGCTTGG 660
Db	601	GATCCCGTCCCACTTCTCTGTAGCTTCAGCCAGGCTTCCCGGACACCGGGCTTGG 660

Db 601 GATCCCGTCCACCTTCTCTGTAGCTTCAGCCCGAGCCCTCCCGACACACCGGCGCTTG 660  
QY 661 CGCACAGCCCCCATCCAGCCCGCTGTCTGGAGCCTGTGCTCTGGAGAGGTCCCAATG 720  
Db 661 CGCACAGCCCCCATCCAGCCCGCTGTCTGGAGCCTGTGCTCTGGAGAGGTCCCAATG 720  
QY 721 GTGGTGGAGCAGAGGTGGAGCAGTAGCTCTCTGGTGGAAACCCCTGACCTGTGAA 780  
Db 721 GTGGTGGAGCAGAGGTGGAGCAGTAGCTCTCTGGTGGAAACCCCTGACCTGTGAA 780  
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAGATGGTGTGCCCTTGCCCTT 840  
Db 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAGATGGTGTGCCCTTGCCCTT 840  
QY 841 CCCCCAGCCCTGTGTGATCTCTCTGATAGGCTCTCAGACAGGGAACCTACAG 900  
Db 841 CCCCCAGCCCTGTGTGATCTCTCTGATAGGCTCTCAGACAGGGAACCTACAG 900  
QY 901 TGTGTGGCCACCCATTCAGCCACGGGCCCCAGGAAAGCGTGTCTGTCAGCATCAGCATC 960  
Db 901 TGTGTGGCCACCCATTCAGCCACGGGCCCCAGGAAAGCGTGTCTGTCAGCATCAGCATC 960  
QY 961 ATCGAACCCAGGAGGAGGCGGCAACTGCAAGCTCTGTGGAGGATCAGGGCTGG 1015  
Db 961 ATCGAACCCAGGAGGAGGCGGCAACTGCAAGCTCTGTGGAGGATCAGGGCTGG 1015  
RESULT 12  
ADK00128  
ID ADK00128 standard; DNA; 1761 BP.  
XX AC ADK00128;  
XX DT 20-MAY-2004 (first entry)  
XX DE Human RAGE-LBE fused to Fc element DNA sequence.  
XX KW Advanced Glycation End Product Ligand Binding Element; RAGE-LBE;  
KW Cystostatic; Antidiabetic; Nootropic; Antiarthritic; Osteopathic;  
KW Neuroprotective; Antiinflammatory; Dermatological; Immunosuppressive;  
KW Vasotropic; Antiproliferative; Antibacterial; Antiarteriosclerotic;  
KW amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;  
KW chronic inflammatory disease; osteoarthritis; irritable bowel disease;  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PH Key Location/Qualifiers  
FT CDS 1..1761  
FT FT /\*tag= a  
FT FT /product= "RAGE-LBE"  
XX PN WO2004016229-A2.  
XX PD 26-FEB-2004.  
XX PF 18-AUG-2003; 2003WO-US025996.  
XX PR 16-AUG-2002; 2002US-0404205P.  
XX XX (AMHP ) WYETH.  
XX XX Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FW;  
PI Feldmann M, Foxwell BJM, Feldman JL;  
XX DR WPI: 2004-192067/18.  
DR F-PSDB; ADK00127.  
XX XX New fusion protein comprising a Receptor for Advanced Glycation End  
PT Product Ligand Binding Element (RAGE-LBE) and an immunoglobulin element,  
PT useful for preparing a composition for treating e.g., Alzheimer's  
PT disease.

XX Disclosure; SEQ ID NO 42; 100pp; English.  
XX The present invention relates to a new fusion protein comprises a  
CC Receptor for Advanced Glycation End Product Ligand Binding Element (RAGE-  
CC LBE) and an immunoglobulin element. The fusion protein is useful for  
CC preparing a composition for treating RAGE-associated disorders such as  
CC amyloidosis, cancer, Crohn's disease, diabetes, complications of  
CC diabetes, prion-related disorders, vasculitis, nephropathies,  
CC retinopathies and/or neuropathies; Alzheimer's disease, chronic  
CC inflammatory disease e.g., rheumatoid arthritis, osteoarthritis,  
CC irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute  
CC inflammatory disease e.g., sepsis, or cardiovascular disease, e.g.,  
CC atherosclerosis or restenosis. The present sequence represents human RAGE  
CC -LBE fused to Fc element encoding sequence.  
XX  
SQ Sequence 1761 BP; 398 A; 537 C; 522 G; 303 T; 0 U; 1 Other;  
Query Match 99.0%; Score 1010.2; DB 12; Length 1761;  
Best Local Similarity 99.7%; Pred. No. 1.7e-259;  
Matches 1012; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ATGGCAGCCGGAACAGCAGTTGGAGCCTGGGTGCTCTCAGTCTGTGGGGGCGAGTA 60  
Db 1 ATGGCAGCCGGAACAGCAGTTGGAGCCTGGGTGCTCTCAGTCTGTGGGGGCGAGTA 60  
QY 61 GTAGTGTCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGCTGCTGAAGTGAAGGG 120  
Db 61 GTAGTGTCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGCTGCTGAAGTGAAGGG 120  
QY 121 GCCCCCAAGAAACACCCAGCGCTGGAAATGGAATGAACTGAACACAGCGCGGACAGAAGCT 180  
Db 121 GCCCCCAAGAAACACCCAGCGCTGGAAATGGAATGGAATGAACTGAACACAGCGCGGACAGAAGCT 180  
QY 181 TGAAGTGTCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTCTCTTCCC 240  
Db 181 TGAAGTGTCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTCTCTTCCC 240  
QY 241 AACGGCTCCCTCTTCTCCCGCTCTCGGGATCCAGGATGAGGGATTTTCGGGTGCCAG 300  
Db 241 AACGGCTCCCTCTTCTCCCGCTCTCGGGATCCAGGATGAGGGATTTTCGGGTGCCAG 300  
QY 301 GCAATGAACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTACAGATT 360  
Db 301 GCAATGAACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTACAGATT 360  
QY 361 CCTGGAGAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTACCGGCTGGTTCCTCAATAG 420  
Db 361 CCTGGAGAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTACCGGCTGGTTCCTCAATAG 420  
QY 421 GTGGGACATGTGTCTCAGAGGGAAGTACCTCTGAGGAGTCTTTAGCTGGCATTGGAT 480  
Db 421 GTGGGACATGTGTCTCAGAGGGAAGTACCTCTGAGGAGTCTTTAGCTGGCATTGGAT 480  
QY 481 GGGAGAGCCCTGTGCTCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACACAGGAGACAC 540  
Db 481 GGGAGAGCCCTGTGCTCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACACAGGAGACAC 540  
QY 541 CCTGAGACAGGCTCTTCCACTGAGTCCGAGCTAATGTGACCCCGGAGGAGGA 600  
Db 541 CCTGAGACAGGCTCTTCCACTGAGTCCGAGCTAATGTGAGTCCCGGAGGAGGA 600  
QY 601 GATCCCGTCCACCTTCTCTCTAGCTTCAGCCAGGCTTCCCGACACACCGGCGCTTG 660  
Db 601 GATCCCGTCCACCTTCTCTCTAGCTTCAGCCAGGCTTCCCGACACACCGGCGCTTG 660  
QY 661 CGCAGAGCCCATCCAGCCCGTGTCTGGAGCCTGTGCTCTGGAGAGGTCCAATTG 720  
Db 661 CGCAGAGCCCATCCAGCCCGTGTCTGGAGCCTGTGCTCTGGAGAGGTCCAATTG 720  
QY 721 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGTGTGGAACCGTAACCTGACCTGTGAA 780  
Db 721 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGTGTGGAACCGTAACCTGACCTGTGAA 780

QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTGCCCTTT 840  
Dd |||||||  
781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTGCCCTTT 840  
QY 841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCGCTCAGACAGGGAACCTACAGC 900  
Dd |||||||  
841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCGCTCAGACAGGGAACCTACAGC 900  
QY 901 TGTGTGGCCACCCATTCAGCCACAGCGGCGCCCGCCAGGAAAGCGTGCTGTACGATCAGCATC 960  
Dd |||||||  
901 TGTGTGGCCACCCATTCAGCCACAGCGGCGCCCGCCAGGAAAGCGTGCTGTACGATCAGCATC 960  
QY 961 ATGAACACAGCGAGAGGCGCCCACTGACAGGCTCTGTGGAGGATCAGGGCTGG 1015  
Dd |||||||  
961 ATGAACACAGCGAGAGGCGCCCACTGACAGGCTCTGTGGAGGATCAGGGCTGG 1015

RESULT 13  
ABK10856  
ID ABK10856 standard; cDNA; 1391 BP.  
XX  
AC ABK10856;  
XX  
DT 05-JUN-2002 (first entry)  
XX  
DE DNA encoding human receptor for advanced glycosylation end product.  
XX  
KW Receptor for advanced glycation end product; RAGE; receptor;  
KW amyloid beta peptide; blood-brain barrier; neurovascular stress;  
KW cerebral vasoconstriction suppressor; cerebral blood flow enhancer;  
KW cerebral amyloid angiopathy; transgenic animal; amyloid beta precursor;  
KW Alzheimer's disease; Down's syndrome; head trauma; stroke; human; gene;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1215  
FT /tag= a  
FT /product= "RAGE"  
FT /note= "Receptor for advanced glycation end product"  
FT /partial  
FT /note= "No start codon given"  
XX  
PN W0200214519-A1.  
XX  
PD 21-FEB-2002.  
XX  
PF 14-AUG-2001; 2001WO-US025416.  
XX  
PR 14-AUG-2000; 2000US-00638648.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Stern DM, Schmidt AM, Yan SD, Zlokovic B;  
XX  
DR WPI: 2002-257610/30.  
DR P-PSDB; AAU7543.  
XX  
PT Ameliorating neurovascular stress and decreasing cerebral  
PT vasoconstriction in subject suffering from chronic/acute cerebral amyloid  
PT angiopathy, by administering inhibitor of receptor for advanced glycation  
PT endproduct.  
XX  
PS Disclosure; Page 16-17; 68pp; English.  
XX  
CC The invention describes a method of ameliorating neurovascular stress,  
CC and decreasing cerebral vasoconstriction in subject suffering from  
CC chronic or acute cerebral amyloid angiopathy, comprising administering an  
CC inhibitor (I) of receptor for advanced glycation end product (RAGE). (I)  
CC inhibits transcytosis of amyloid beta peptides across blood-brain  
CC barrier, thus decreasing cerebral vasoconstriction and increasing

CC cerebral blood flow. (I) is useful for treating amyloid angiopathy in a  
CC subject, decreasing cerebral vasoconstriction in a transgenic non-human  
CC animal (preferably, transgenic mouse overexpressing mutant human amyloid  
CC beta precursor protein) or a human, suffering from chronic or acute  
CC cerebral amyloid angiopathy, preferably, Alzheimer's disease, and for  
CC ameliorating neurovascular stress comprising cerebral amyloid angiopathy  
CC in a subject, where the neurovascular stress is caused by Alzheimer's  
CC disease, aging, Down's syndrome, head trauma or stroke. This sequence  
CC encodes the human receptor for advanced glycation end product (RAGE)  
CC described in the invention  
XX  
SQ Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;

Query Match 99.0%; Score 1009.8; DB 6; Length 1391;  
Best Local Similarity 99.8%; Pred. No. 2.1e-259;  
Matches 1011; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCAGCCGGAACAGCAGCTTGGAGCCCTGGGTGCTGTGGTCTCAGTCTGTGGGGGCGCAGTAGT 62  
Dd |||||||  
3 GGCAGCCGGAACAGCAGCTTGGAGCCCTGGGTGCTGTGGTCTCAGTCTGTGGGGGCGCAGTAGT 62  
QY 63 AGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACCTGGTGTCTGAACTGTAAGGGGCG 122  
Dd |||||||  
63 AGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACCTGGTGTCTGAACTGTAAGGGGCG 122  
QY 123 CCCCAGAAACCAACCCAGCGCTGGAATGGAACCTGAAACAGAGCCCGACAGAACCTTG 182  
Dd |||||||  
123 CCCCAGAAACCAACCCAGCGCTGGAATGGAACCTGAAACAGAGCCCGACAGAACCTTG 182  
QY 183 GAAGTCTCTCTCTCCCGAGGAGGCGCCCTGGGACAGCTGGTCTGCTTCCCTCCCAA 242  
Dd |||||||  
183 GAAGTCTCTCTCTCCCGAGGAGGCGCCCTGGGACAGCTGGTCTGCTTCCCTCCCAA 242  
QY 243 CGGCTCCCTCTCTCTCCCGCTGTGGGATCAGAGATGAGGGGATTTCCGGTGCACGCG 302  
Dd |||||||  
243 CGGCTCCCTCTCTCTCCCGCTGTGGGATCAGAGATGAGGGGATTTCCGGTGCACGCG 302  
QY 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCCAGTCCGCTGTACAGATTCC 362  
Dd |||||||  
303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCCAGTCCGCTGTACAGATTCC 362  
QY 363 TGGGAGCCAGAAATTTGATATTCTGCTCTCAACTCACGGCTGGTGTCCCAATAGGT 422  
Dd |||||||  
363 TGGGAGCCAGAAATTTGATATTCTGCTCTCAACTCACGGCTGGTGTCCCAATAGGT 422  
QY 423 GGGGACATGTGTGTGAGGGAGGAGTACCTCGAGGAGCTTTAGTCTGCACCTTGGATGG 482  
Dd |||||||  
423 GGGGACATGTGTGTGAGGGAGGAGTACCTCGAGGAGGAGTCTTGTGCTGACCTTGGATGG 482  
QY 483 GAAGCCCTGTGTCTTCAATGAGAGGGAGTATCTGTGAAGGAAACAGACAGGAGACACCC 542  
Dd |||||||  
483 GAAGCCCTGTGTGTCTTCAATGAGAGGGAGTATCTGTGAAGGAAACAGACAGGAGACACCC 542  
QY 543 TGAGACAGGGCTCTTCACTGAGCTCGAGCTAATGTTGACCCCGCCGCGGGGAGGAG 602  
Dd |||||||  
543 TGAGACAGGGCTCTTCACTGAGCTCGAGCTAATGTTGACCCCGCCGCGGGGAGGAG 602  
QY 603 TCCCGTCCCGCTCTCTCTGTAGCTTACGCCAGCGCTTCCCGACACCGCGGCTTGG 662  
Dd |||||||  
603 TCCCGTCCCGCTCTCTCTGTAGCTTACGCCAGCGCTTCCCGACACCGCGGCTTGG 662  
QY 663 CACAGCCCCCATCCAGCCCCCGTGTCTGGAGGCTGTGGCTCTGGAGGAGGTCCAATTGGT 722  
Dd |||||||  
663 CACAGCCCCCATCCAGCCCCCGTGTCTGGAGGCTGTGGCTCTGGAGGAGGTCCAATTGGT 722  
QY 723 GGTGAGCCAGAAAGGTGGAGCAGTAGTCTCTGGTGAACCGTAACCTGACCTGTGAAGT 782  
Dd |||||||  
723 GGTGAGCCAGAAAGGTGGAGCAGTAGTCTCTGGTGAACCGTAACCTGACCTGTGAAGT 782  
QY 783 CCTGCGCCAGCCCTCTCTCAATCCACTGGAATGAGGATGGTGTGCTCTGCGCCCTTCC 842  
Dd |||||||  
783 CCTGCGCCAGCCCTCTCTCAATCCACTGGAATGAGGATGGTGTGCTCTGCGCCCTTCC 842

QY 843 CCCAGCCCTGTGCTGATCTCCCTGAGATAGGSCCTCAGGACCAGGGAACCTACAGCTG 902  
Db 843 CCCAGCCCTGTGCTGATCTCCCTGAGATAGGSCCTCAGGACCAGGGAACCTACAGCTG 902  
QY 903 TGTGGCCACCCATTCCAGCACCGGGCCCGGAAAGCCGTGCTGTCAGCATCAGCATAT 962  
Db 903 TGTGGCCACCCATTCCAGCACCGGGCCCGGAAAGCCGTGCTGTCAGCATCAGCATAT 962  
QY 963 CGAACACGAGGAGGAGGGCCAACTCAGGCTCTGTGGGAGGATCAGGCTGG 1015  
Db 963 CGAACACGAGGAGGAGGGCCAACTCAGGCTCTGTGGGAGGATCAGGCTGG 1015  
RESULT 14  
ABK84114  
ID ABK84114 standard; cDNA; 1391 BP.  
XX AC ABK84114;  
XX DT 14-AUG-2002 (first entry)  
XX DE Human cDNA differentially expressed in granulocytic cells #685.  
XX KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
KW viral infection; parasitic infection; protozoal infection;  
KW fungal infection; sterile inflammatory disease; psoriasis;  
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
KW adult respiratory distress syndrome; inflammatory bowel disease;  
KW Crohn's disease; ulcerative colitis; periodontal disease;  
KW granulocyte activation; chronic inflammation; allergy.  
XX OS Homo sapiens.  
XX PN WO200228999-A2.  
XX PD 11-APR-2002.  
XX PF 03-OCT-2001; 2001WO-US030821.  
XX PR 03-OCT-2000; 2000US-0237189P.  
XX PA (GENE-) GENE LOGIC INC.  
XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
XX DR WPI; 2002-435328/46.  
XX PT Detecting granulocyte activation by detecting differential expression of  
PT genes associated with granulocyte activation, which serves as diagnostic  
PT markers that is useful for monitoring disease states and drug toxicity.  
XX PS Claim 1; SEQ ID NO 685; 114pp; English.  
XX CC The invention relates to detecting (M1) granulocyte (GC) activation  
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
CC DNA chip analysis as given in the specification, and comparing the  
CC expression level to an expression level in an unactivated GC, where  
CC differential expression of Gs is indicative of GCA. Also included are  
CC modulating (M2) GA by contacting GC with an agent that alters the  
CC expression of at least one gene in Gs; (2) screening (M3) for an agent  
CC capable of modulating GCA or an inflammation (especially chronic) in a  
CC tissue, an allergic response in a subject, exposure of a subject to a  
CC pathogen or sterile inflammatory disease using the gene expression  
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a  
CC tissue, an allergic response in a subject, exposure of a subject to a  
CC pathogen or sterile inflammatory disease, by detecting the level of  
CC of expression of the gene in the tissue of gene(s) from Gs, where the level  
CC of expression of the gene is indicative of inflammation; (4) treating  
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic  
CC response in a subject, exposure of a subject to a pathogen or sterile  
CC inflammatory disease, by contacting a tissue having inflammation with an  
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1

CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful  
CC for screening an agent capable of modulating GCA preferably in an  
CC inflammation in a tissue; M4 is useful for detecting an inflammation  
CC (especially chronic) in a tissue, an allergic response in a subject,  
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.  
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,  
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult  
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's  
CC disease, ulcerative colitis, periodontal disease; also bacterial  
CC infection, viral infection, parasitic infection, protozoal infection,  
CC fungal infection and M5 is useful for treating one of the above  
CC conditions. The present sequence represents a gene differentially  
CC expressed in granulocytes. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;  
Query Match 99.0%; Score 1009.8; DB 6; Length 1391;  
Best Local Similarity 99.8%; Pred. No. 2.1e-259;  
Matches 1011; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GGCAGCCGGAACAGCAGTTGGAGCCTGGGTGCTGCTCCTCAGTCTGTGGGGGCGAGTAGT 62  
Db 3 GGCAGCCGGAACAGCAGTTGGAGCCTGGGTGCTGCTCCTCAGTCTGTGGGGGCGAGTAGT 62  
QY 63 AGGTCTCTAAACATCAGACCCCGGATTTGGGAGCCACTGGTGTGTAAGTGTAAAGGGGCG 122  
Db 63 AGGTCTCTAAACATCAGACCCCGGATTTGGGAGCCACTGGTGTGTAAGTGTAAAGGGGCG 122  
QY 123 CCCCAAGAAACACACCCAGCGGCTGGAATGAAACTGAACACAGGCCGACAGAAAGCTTG 182  
Db 123 CCCCAAGAAACACACCCAGCGGCTGGAATGAAACTGAACACAGGCCGACAGAAAGCTTG 182  
QY 183 GAAGTCTCTGCTCTCCAGGAGGAGGCCCTTGGGACAGTGTGGTCTGTGCTTCCCAA 242  
Db 183 GAAGTCTCTGCTCTCCAGGAGGAGGCCCTTGGGACAGTGTGGTCTGTGCTTCCCAA 242  
QY 243 CGGCTCCCTCTCTTCCGCTGTCGGGATCCAGATGAGGGGATTTCCGGTGCCAGGC 302  
Db 243 CGGCTCCCTCTCTTCCGCTGTCGGGATCCAGATGAGGGGATTTCCGGTGCCAGGC 302  
QY 303 AATGAACAGGAATGAAAGAGAGACCAAGTCCAACTACCGAGTCCCTGTCTACAGATTCC 362  
Db 303 AATGAACAGGAATGAAAGAGAGACCAAGTCCAACTACCGAGTCCCTGTCTACAGATTCC 362  
QY 363 TGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCAGCGTGTGTCTCCCAATAAGGT 422  
Db 363 TGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCAGCGTGTGTCTCCCAATAAGGT 422  
QY 423 GGGGACATGTGTTCAGAGGGAAGCTACCTGCGAGGACTCTTAGCTGCACCTTGGATGG 482  
Db 423 GGGGACATGTGTTCAGAGGGAAGCTACCTGCGAGGACTCTTAGCTGCACCTTGGATGG 482  
QY 483 GAAAGCCCTGTGCTGCTTAATGAGAGGGAGATCTCTGAAGAAACAGACAGGAGACACCC 542  
Db 483 GAAAGCCCTGTGCTGCTTAATGAGAGGGAGATCTCTGAAGAAACAGACAGGAGACACCC 542  
QY 543 TGAGACAGGGCTCTTTCACATCTGAGTCCGAGCTAATGTGACCCCGCGGGAGGAGA 602  
Db 543 TGAGACAGGGCTCTTTCACATCTGAGTCCGAGCTAATGTGACCCCGCGGGAGGAGA 602  
QY 603 TCCCGTCCCACTTCTCTCTAGTCTCAGCCCGAGGCTTCCCGACACCCGGGCTTGGG 662  
Db 603 TCCCGTCCCACTTCTCTCTAGTCTCAGCCCGAGGCTTCCCGACACCCGGGCTTGGG 662  
QY 663 CACAGCCCCCATCCAGCCCCCGTGTCTGGAGGCTGTGCTCTGGAGGAGGTCATTTGGT 722  
Db 663 CACAGCCCCCATCCAGCCCCCGTGTCTGGAGGCTGTGCTCTGGAGGAGGTCATTTGGT 722  
QY 723 GGTGAGCCAGAAAGTGTGAGCAGTAGCTCTGTGGTGGAAACCGGTAAACCTGCTGAAGT 782  
Db 723 GGTGAGCCAGAAAGTGTGAGCAGTAGCTCTGTGGTGGAAACCGGTAAACCTGCTGAAGT 782

Db 723 GGTGGAGCCAGAGGTGGAGCAGTACTCTGTGTGGAAACGGTAACCCCTGACCTGTGAAGT 782  
 Qy 783 CCTGGCCCGCCCTCTCTCAATCCATCGGATGAAGAGTGTGTGCCCTTGCCCTTCC 842  
 Db 783 CCTGGCCCGCCCTCTCTCAATCCATCGGATGAAGAGTGTGTGCCCTTGCCCTTCC 842  
 Qy 843 CCCAGCCCTGTGCTGATCTCTCTAGATAGGCGCTCAGGACCGAGGAACCTACAGCTG 902  
 Db 843 CCCAGCCCTGTGCTGATCTCTCTAGATAGGCGCTCAGGACCGAGGAACCTACAGCTG 902  
 Qy 903 TGTGGCCACCCATTCACAGCCAGCGGCCCCAGGAAAGCCGTGTCTCAGCATCAGCATCAT 962  
 Db 903 TGTGGCCACCCATTCACAGCCAGCGGCCCCAGGAAAGCCGTGTCTCAGCATCAGCATCAT 962  
 Qy 963 CGAACAGCGGAGGAGGCGCAACTCAGGCTCTGTGGAGGATCAGGCGTGG 1015  
 Db 963 CGAACAGCGGAGGAGGCGCAACTCAGGCTCTGTGGAGGATCAGGCGTGG 1015

## RESULT 15

AAD36952  
 ID AAD36952 standard; cDNA; 1391 BP.  
 AC AAD36952;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Human receptor for advanced glycosylation end product (RAGE) cDNA.  
 KW Human; Receptor for advanced glycosylation end product; RAGE; cardiatic;  
 KW tissue growth; neointimal formation; blood vessel; restenosis; diabetes;  
 KW myocardial infarction; angioplasty; peripheral vascular surgery; angina;  
 KW transgenic animal; acute thrombotic stroke; venous thrombosis; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..1215  
 FT /\*tag= a  
 FT /product= "Human RAGE protein"  
 FT /notes= "CDS does not include start codon"  
 FT /partial  
 FT polyA\_signal 1368..1373  
 FT /\*tag= b  
 FT polyA\_site 1391  
 FT /\*tag= c

XX WO200230889-A2.  
 PN  
 XX  
 XX 18-APR-2002.  
 PD  
 XX  
 XX 12-OCT-2001; 2001WO-US032036.  
 PF  
 XX  
 XX 13-OCT-2000; 2000US-00687528.  
 PR  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 XX Stern DM, Schmidt A, Marso S, Topol E, Lincoff AM;  
 PI  
 XX WPI; 2002-426260/45.  
 DR P-PSDB; AAE23219.  
 DR  
 XX  
 XX Inhibiting new tissue growth or neointimal formation in blood vessels of  
 PT subject suffering from diabetes, stroke and preventing restenosis,  
 PT comprises administering inhibitor of receptor for advance glycation end  
 PT product.  
 PT  
 XX  
 PS Disclosure; Page 16-17; 43pp; English.  
 XX  
 XX The invention relates to a method for inhibiting new tissue growth or  
 CC neointimal formation in blood vessels in a subject that has experienced  
 CC blood vessel injury and preventing exaggerated restenosis in a diabetic  
 CC subject. The method comprises administering an inhibitor of receptor

CC advanced glycation/glycosylation end product (RAGE), so as to inhibit new  
 CC tissue growth or neointimal formation in subject's blood vessels and  
 CC preventing restenosis in the subject. The method is useful for inhibiting  
 CC new tissue growth or neointimal formation in blood vessels in a subject  
 CC like non-human animal, a transgenic non-human animal or a human suffering  
 CC from diabetes, acute thrombotic stroke, venous thrombosis, unstable  
 CC angina, myocardial infarction, abrupt closure following angioplasty or  
 CC stent placement, or thrombosis as a result of peripheral vascular surgery  
 CC The method is also useful for preventing restenosis and for determining  
 CC whether a compound inhibits new tissue growth in a blood vessel in a  
 CC subject. The present sequence is human receptor for advanced  
 CC glycosylation end product (RAGE) cDNA  
 XX

SQ Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;

Query Match 99.0%; Score 1009.8; DB 6; Length 1391;  
 Best Local Similarity 99.8%; Pred. No. 2.1e-259;  
 Matches 1011; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGCCGGAACAGCAGTTGGAGCCTGGGTCTCTCAGTCTGTGGGGGCGCAGTAGT 62  
 Db 3 GGAGCCGGAACAGCAGTTGGAGCCTGGGTCTCTCAGTCTGTGGGGGCGCAGTAGT 62  
 Qy 63 AGGTCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAAGTAAAGGGGC 122  
 Db 63 AGGTCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAAGTAAAGGGGC 122  
 Qy 123 CCCCAGAAACACACCCAGCGCTGGAATGGAACCTGAAACACAGGCGCGACAGAAGCTTG 182  
 Db 123 CCCCAGAAACACACCCAGCGCTGGAATGGAACCTGAAACACAGGCGCGACAGAAGCTTG 182  
 Qy 183 GAAGTCTCTGTCTCCCCAGGAGGAGGCCCTTGGGACAGTGTGGTCTGTCTTCCCAA 242  
 Db 183 GAAGTCTCTGTCTCCCCAGGAGGAGGCCCTTGGGACAGTGTGGTCTGTCTTCCCAA 242  
 Qy 243 CGGCTCCCTCTCTTCCCTCGGCTGTGGGATCAGGATGAGGGGATTTCCGGTGCCAGGC 302  
 Db 243 CGGCTCCCTCTCTTCCCTCGGCTGTGGGATCAGGATGAGGGGATTTCCGGTGCCAGGC 302  
 Qy 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 362  
 Db 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 362  
 Qy 363 TGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAACTCAGCGCTGGTGTCTCCAAATAGGT 422  
 Db 363 TGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAACTCAGCGCTGGTGTCTCCAAATAGGT 422  
 Qy 423 GGGGACATGTGTCTCAGAGGAGTACCTCTCAGCGGACTCTAGCTGGCAGCTTGGATGG 482  
 Db 423 GGGGACATGTGTCTCAGAGGAGTACCTCTCAGCGGAGTCTTAGCTGGCAGCTTGGATGG 482  
 Qy 483 GAAGCCCTGTGTCTTAATGAGAAGGAGTATCTGTGAAGGAACACAGCCAGGAGACACC 542  
 Db 483 GAAGCCCTGTGTCTTAATGAGAAGGAGTATCTGTGAAGGAACACAGCCAGGAGACACC 542  
 Qy 543 TGAGACAGGGCTCTTTCACACTCGAGTCGAGCTAATGTGTGACCCAGCCCGGGAGAGA 602  
 Db 543 TGAGACAGGGCTCTTTCACACTCGAGTCGAGCTAATGTGTGACCCAGCCCGGGAGAGA 602  
 Qy 603 TCCCGTCCACCTTCTCTGTAGTTTCCAGCCAGCGCTTCCCGACACCGGGCCTTGG 662  
 Db 603 TCCCGTCCACCTTCTCTGTAGTTTCCAGCCAGCGCTTCCCGACACCGGGCCTTGG 662  
 Qy 663 CACAGCCCCCATCCAGCCCCCGTGTGGGAGCTGTGCTCTGGAGAGGTCCAATTGGT 722  
 Db 663 CACAGCCCCCATCCAGCCCCCGTGTGGGAGCTGTGCTCTGGAGAGGTCCAATTGGT 722  
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 Qy 783 CCTGCCAGCCCTCTCTCAAAATCACTGATGAAGGATGTGTGCTTCCCTTCCCTTCC 842

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Db 903 TGTGGCCACCCATTCCAGCCACCGGGCCCCAGGAAAGCCGTGTGTCTGATCAGCATCATCAT 962  
Qy 963 CGAACACGCGAGGAGGGCCAACTGAGGCTCTGTGGAGGATCAGGGCTGG 1015  
Db 963 CGAACACGCGAGGAGGGCCAACTGAGGCTCTGTGGAGGATCAGGGCTGG 1015

Search completed: March 14, 2005, 18:41:03  
Job time : 646.487 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 18:05:33 ; Search time 693.244 Seconds  
(without alignments)  
8752.331 Million cell updates/sec

Title: US-10-091-019-2

Perfect score: 1020

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1020	100.0	1020	16	US-10-091-019-2
2	1015	99.5	1415	18	US-10-115-635-351
3	1013.4	99.4	1217	17	US-10-309-290-95
4	1013	99.3	1351	16	US-10-091-019-1
5	992	97.3	1223	19	US-10-472-507A-1
6	986.8	96.7	1405	8	US-08-905-709-3
7	986.8	96.7	1405	8	US-08-755-235-3
8	986.8	96.7	1405	18	US-10-850-861-3
9	957	93.8	1463	18	US-10-115-635-352
10	921	90.3	1173	17	US-10-309-290-99
11	919.4	90.1	1226	17	US-10-309-290-97
					Sequence 2, Appli
					Sequence 351, App
					Sequence 95, Appl
					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 352, App
					Sequence 99, Appl
					Sequence 97, Appl

12	717.6	70.4	1438	8	US-08-905-709-1	Sequence 1, Appli
13	717.6	70.4	1438	8	US-08-755-235-1	Sequence 1, Appli
14	717.6	70.4	1438	18	US-10-850-861-1	Sequence 1, Appli
15	336	32.9	336	16	US-10-091-019-4	Sequence 4, Appli
16	197	19.3	203	16	US-10-029-386-16362	Sequence 16362, A
17	197	19.3	485	13	US-10-027-632-257559	Sequence 257559, A
18	197	19.3	485	17	US-10-027-632-257559	Sequence 257559, A
19	197	19.3	553	16	US-10-029-386-2662	Sequence 2662, Ap
20	197	19.3	62944	9	US-09-954-456-2257	Sequence 2257, Ap
21	197	19.3	62944	11	US-09-968-007A-129	Sequence 129, App
22	144.2	14.1	582	16	US-10-029-386-9526	Sequence 9526, Ap
23	134.4	13.2	142	16	US-10-029-386-23226	Sequence 23226, A
24	128.6	12.6	610	9	US-09-954-456-906	Sequence 906, App
25	128.6	12.6	610	9	US-09-880-107-3595	Sequence 3595, Ap
26	120.2	11.8	3673778	16	US-10-312-841-2	Sequence 2, Appli
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28	108.6	10.6	1842	13	US-10-027-632-98444	Sequence 98444, A
29	108.6	10.6	1842	13	US-10-027-632-98445	Sequence 98445, A
30	108.6	10.6	1842	17	US-10-027-632-98444	Sequence 98444, A
31	108.6	10.6	1842	17	US-10-027-632-98445	Sequence 98445, A
32	49	4.8	65	10	US-09-908-975-3464	Sequence 3464, Ap
33	48.4	4.7	727	13	US-10-027-632-17391	Sequence 17391, A
34	48.4	4.7	727	17	US-10-027-632-17391	Sequence 17391, A
35	41	4.0	790	14	US-10-123-155-204	Sequence 204, App
36	41	4.0	790	15	US-10-146-731-204	Sequence 204, App
37	41	4.0	790	15	US-10-140-472-204	Sequence 204, App
38	41	4.0	790	15	US-10-141-761-204	Sequence 204, App
39	41	4.0	790	16	US-10-142-885-204	Sequence 204, App
40	41	4.0	790	16	US-10-158-790-204	Sequence 204, App
41	41	4.0	790	17	US-10-137-871-204	Sequence 204, App
42	41	4.0	790	17	US-10-140-923-204	Sequence 204, App
43	41	4.0	790	17	US-10-141-756-204	Sequence 204, App
44	41	4.0	790	17	US-10-141-759-204	Sequence 204, App
45	41	4.0	790	17	US-10-140-805-204	Sequence 204, App

#### ALIGNMENTS

#### RESULT 1

US-10-091-019-2  
; Sequence 2, Application US/10091019  
; Publication No. US20030166063A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Robert B.  
; APPLICANT: Shen, Jane M.  
; APPLICANT: Shabbaz, Manouchehr M.  
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins  
; FILE REFERENCE: 41305-270555  
; CURRENT APPLICATION NUMBER: US/10/091,019  
; CURRENT FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/273,418  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 1020  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1020)  
; OTHER INFORMATION:  
US-10-091-019-2

Query Match 100.0%; Score 1020; DB 16; Length 1020;  
Best Local Similarity 100.0%; Pred. No. 3.2e-286;  
Matches 1020; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAGCCGGAACAGCAGTGGAGCCTGGTGTCTGCTCAGTCTGTGGGGGCGAGTA 60  
DB 1 ATGGCAGCCGGAACAGCAGTGGAGCCTGGTGTCTGCTCAGTCTGTGGGGGCGAGTA 60



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QY 61 GTAGTGTCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTCTGAAGTGTAAAGGG 120
Db 61 GTAGTGTCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTCTGAAGTGTAAAGGG 120
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QY 181 TGAAGGTCTGTCTCTCCCGAGGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCCTCC 240
Db 181 TGAAGGTCTGTCTCTCCCGAGGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCCTCC 240
QY 241 AACGGCTCCCTCTTCTCCCTTCGGCTGTCCGGATCCAGGATCAGGGGATTTCCGGTGCAG 300
Db 241 AACGGCTCCCTCTTCTCCCTTCGGCTGTCCGGATCCAGGATCAGGGGATTTCCGGTGCAG 300
QY 301 GCATGAACAGGAATGAAGAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGTT 360
Db 301 GCATGAACAGGAATGAAGAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGTT 360
QY 361 CCTGGGAAGCCAGAAATTTGTAGATTCTGCTCTGAACTCACGGCTGGTGTCTCCCAATAG 420
Db 361 CCTGGGAAGCCAGAAATTTGTAGATTCTGCTCTGAACTCACGGCTGGTGTCTCCCAATAG 420
QY 421 GTGGGACATGTGTGTCTAGAGGAGGAGTACCTCTGAGGAGTCTTAGCTGGCACTTGGAT 480
Db 421 GTGGGACATGTGTGTCTAGAGGAGGAGTACCTCTGAGGAGTCTTAGCTGGCACTTGGAT 480
QY 481 GGGAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540
Db 481 GGGAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540
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Db 541 CCTGAGACAGGGCTCTTTCACATGCGAGTCCGAGCTAATGTGTAACCCAGCCGGGAGGA 600
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Db 601 GATCCCGTCCCACTTCTCTGTAGCTTTCAGCCAGGCTTCCCGGACACCGGGGCTTG 660
QY 661 CGCACAGCCCACTCAGCCCGCTGTCTGGAGCTTGGCTGTGGAGAGGTCCCAATTG 720
Db 661 CGCACAGCCCACTCAGCCCGCTGTCTGGAGCTTGGCTGTGGAGAGGTCCCAATTG 720
QY 721 GTGGTGGAGCAGAGGTGAGCAGTAGCTCTCTGTGGAACCGTAAACCTGACCTGTGAA 780
Db 721 GTGGTGGAGCAGAGGTGAGCAGTAGCTCTCTGTGGAACCGTAAACCTGACCTGTGAA 780
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGATGTGTGCTTGCCTTGCCTTT 840
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## RESULT 2

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US-10-115-635-351
; Sequence 351, Application US/10115635
; Publication No. US2004013743A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle

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; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 797CON
; CURRENT APPLICATION NUMBER: US/10/115,635
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/714,936
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 362
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 351
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1239)
US-10-115-635-351

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Query Match 99.5%; Score 1015; DB 18; Length 1415;
Best Local Similarity 100.0%; Pred. No. 9.5e-285;
Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 CCTGGGAAGCCAGAAATTTGTAGATTCTGCTCTGAACTCACCGGCTGGTGTTCCTCAATAAG 420
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RESULT 3

US-10-309-290-95  
; Sequence 95, Application US/10309290  
; Publication No. US20040023241A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsebrook II, John P.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Chillakuru, Rajeev A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Gould-Rothberg, Bonnie E.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Jeffers, Michael E.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Li, Li  
; APPLICANT: Malvankar, Uriel M.  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Murphey, Ryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Peyman, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Starling, Gary  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Voss, Edward Z.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-502A  
; CURRENT APPLICATION NUMBER: US/10/309,290  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/336,600  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,285  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/341,346  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/341,477  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/341,540  
; PRIOR FILING DATE: 2001-12-17

; PRIOR APPLICATION NUMBER: 60/342,592  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/344,297  
; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/344,903  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/373,288  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 60/380,981  
; PRIOR FILING DATE: 2002-05-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 95  
; LENGTH: 1217  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)..(1214)  
US-10-309-290-95  
  
Query Match 99.4%; Score 1013.4; DB 17; Length 1217;  
Best Local Similarity 99.9%; Pred. No. 2.7e-284;  
Matches 1014; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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Qy 61 GTAGTGTCTCAAAACATCAGAGCCCGGATTTGGCGAGCCACTGCTGCTGAAGTGTAAAGGG 120  
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Qy 121 GCGCCCAAGAAACACACCCCGGCTGGAATGGAACCTGAACACAGCCGCGGACAGAGCT 180  
Db 123 GCGCCCAAGAAACACACCCCGGCTGGAATGGAACCTGAACACAGCCGCGGACAGAGCT 182  
Qy 181 TGGAAAGTCTCTGCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTGCTGCTTCCC 240  
Db 183 TGGAAAGTCTCTGCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTGCTGCTTCCC 242  
Qy 241 AACGCTCTCTCTCTCCCGCTGTGGGATTCAGGATCAGGAGGATTTTCGGTGGCCAG 300  
Db 243 AACGCTCTCTCTCTCCCGCTGTGGGATTCAGGATCAGGAGGATTTTCGGTGGCCAG 302  
Qy 301 GCAATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAATT 360  
Db 303 GCAATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAATT 362  
Qy 361 CCTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACCGCTGGTGTTCCTCAATAAG 420  
Db 363 CCTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACCGCTGGTGTTCCTCAATAAG 422  
Qy 421 GTGGGACATGTGTCTCAGAGGAAAGTACCTCTCAGGAGCTCTTAGCTGGCACTTTGGAT 480  
Db 423 GTGGGACATGTGTCTCAGAGGAAAGTACCTCTCAGGAGCTCTTAGCTGGCACTTTGGAT 482  
Qy 481 GGGAGCCCTCTGCTCTTAATGAGAGGAGTATCTGTGAAGGAACAGACACAGGAGACAC 540  
Db 483 GGGAGCCCTCTGCTCTTAATGAGAGGAGTATCTGTGAAGGAACAGACACAGGAGACAC 542  
Qy 541 CCTGAGACAGGCTCTTTCACACTGCAGTCCGAGCTAAATGGTGCACCCAGCCGGGAGGA 600  
Db 543 CCTGAGACAGGCTCTTTCACACTGCAGTCCGAGCTAAATGGTGCACCCAGCCGGGAGGA 602  
Qy 601 GATCCCGTCCACCTTCTCTGTAGTTCAGCCAGGCTTTCCTCCGACACCCGGGCTTTG 660  
Db 603 GATCCCGTCCACCTTCTCTGTAGTTCAGCCAGGCTTTCCTCCGACACCCGGGCTTTG 662  
Qy 661 CGCACAGCCCCCATCCAGCCCGCTGTCTGGAGCCTGTGCTCTGGAGAGGTCCAATTG 720  
Db 663 CGCACAGCCCCCATCCAGCCCGCTGTCTGGAGCCTGTGCTCTGGAGAGGTCCAATTG 722



NAME/KEY: CDS  
LOCATION: (25) ... (1068)  
US-10-472-507A-1

Query Match 97.3%; Score 992; DB 19; Length 1223;  
Best Local Similarity 100.0%; Pred. No. 4.5e-278; Indels 0; Gaps 0;  
Matches 992; Conservative 0; Mismatches 0;

QY 1 ATGGCAGCGGAAACAGCAGTTGGAGCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTA 60  
DB 25 ATGGCAGCGGAAACAGCAGTTGGAGCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTA 84  
QY 61 GTAGTGTCTAAAACATCAAGCCCGGATTTGGAGCCACTGGTGTGAAGTGTAAAGGG 120  
DB 85 GTAGTGTCTAAAACATCAAGCCCGGATTTGGAGCCACTGGTGTGAAGTGTAAAGGG 144  
QY 121 GCCCCCAAGAAACCCAGCGGCTGGAACTGAACTGAACACAGCCGCGACAGAGCT 180  
DB 145 GCCCCCAAGAAACCCAGCGGCTGGAACTGAACTGAACACAGCCGCGACAGAGCT 204  
QY 181 TGGAGGTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTGCTTCTCC 240  
DB 205 TGGAGGTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTGCTTCTCC 264  
QY 241 AAGCGTCTCTCTCTCCCGGCTGTGGGATCCAGGATGAGGGATTTCCGGTCCAG 300  
DB 265 AAGCGTCTCTCTCTCCCGGCTGTGGGATCCAGGATGAGGGATTTCCGGTCCAG 324  
QY 301 GCAATGAACAGAAATGGAAGGAGCAAGTCCAACTACCGAGTCCGTCTACCAAGAT 360  
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QY 361 CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCAGCGCTGGTGTCCCAATAG 420  
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QY 421 GTGGGACATGTGTGTCAGAGGAAAGTACCTTCAGGAGACTTTAGCTGGCACTTGGAT 480  
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QY 481 GGGAGCCCTGTGCTTAATGAGGAGGATCTGTGAAGGAAACAGACACAGGAGAC 540  
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QY 541 CTGAGACAGGGCTCTTCACTGTCAGTGGAGCTAATGTGACCCAGCCCGGGGAGGA 600  
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DB 625 GATCCCGTCCCACTTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGCTTTG 684  
QY 661 CGCAGAGCCCTCATCCAGCCCGTGTCTGGAGCTGTGCTGAGAGGCTCAATTTG 720  
DB 685 CGCAGAGCCCTCATCCAGCCCGTGTCTGGAGCTGTGCTGAGAGGCTCAATTTG 744  
QY 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGGTGAACCGTAACCTGACCTGTGAA 780  
DB 745 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGGTGAACCGTAACCTGACCTGTGAA 804  
QY 781 GTCCCTGCGCAGCCCTCTCTCAATCCATCTGATGAAGATGTTGTGCTTCCCTTT 840  
DB 805 GTCCCTGCGCAGCCCTCTCTCAATCCATCTGATGAAGATGTTGTGCTTCCCTTT 864  
QY 841 CCCCCAGCCCTGTGTGATCTCTCCCTGATAGAGGCTTCAGGACAGGAACTTACAGC 900  
DB 865 CCCCCAGCCCTGTGTGATCTCTCCCTGATAGAGGCTTCAGGACAGGAACTTACAGC 924  
QY 901 TGTGTGGCCACCCATTTCCAGCCACCGGCCCCAGGAAAGCGTGTCTCAGCATCAGCATC 960  
DB 925 TGTGTGGCCACCCATTTCCAGCCACCGGCCCCAGGAAAGCGTGTCTCAGCATCAGCATC 984  
QY 961 ATCGAACAGGCGAGGAGGGGCCAACTGCAGG 992

DB 985 ATCGAACAGGCGAGGAGGGGCCAACTGCAGG 1016

RESULT 6

US-08-905-709-3  
; Sequence 3, Application US/08905709  
; Publication NO. US20010039256A1  
; GENERAL INFORMATION:  
; APPLICANT: Steirn, David  
; APPLICANT: Schmidt, Ann M.  
; TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED  
; TITLE OF INVENTION: ATHEROSCLEROSIS USING (SRAGE) SOLUBLE RECEPTOR FOR  
; TITLE OF INVENTION: ADVANCED GLYCATION ENDPRODUCTS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/905,709  
; FILING DATE: 05-AUG-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/52876  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0526  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1405 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-905-709-3

Query Match 96.7%; Score 986.8; DB 8; Length 1405;  
Best Local Similarity 99.6%; Pred. No. 1.5e-276;  
Matches 1010; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 3 GGCAGCCGGAACAGCAGTTGGAGCCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTAGT 62  
DB 3 GGCAGCCGGAACAGCAGTTGGAGCCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTAGT 62  
QY 63 AGGTGCTCAAAACATCAAGCCCGGATTTGGAGCCACTGGTGTGAAGTGTAAAGGGGC 122  
DB 63 AGGTGCTCAAAACATCAAGCCCGGATTTGGAGCCACTGGTGTGAAGTGTAAAGGGGC 122  
QY 123 CCCCAGAAACACCCAGCCGCTGGAACTGAACTGAACACAGCCGCGACAGAGCTTG 182  
DB 123 CCCCAGAAACACCCAGCCGCTGGAACTGAACTGAACACAGCCGCGACAGAGCTTG 182  
QY 183 GAAGTGTCTCTCTCCCGAGGAGGCGCTGGGACAGTGTGGCTGTGCTTCTCCCAA 242  
DB 183 GAAGTGTCTCTCTCCCGAGGAGGCGCTGGGACAGTGTGGCTGTGCTTCTCCCAA 242  
QY 243 CGGCTCCCTCTTCTTCCGGCTGTGGGATCAGAGTGAAGGGATTTTCCGTTGCCAGGC 302  
DB 243 CGGCTCCCTCTTCTTCCGGCTGTGGGATCAGAGTGAAGGGATTTTCCGTTGCCAGGC 302  
QY 303 AATGAACAGGAATGAAGAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCC 362



APPLICANT: Schmidt, Ann Marie  
APPLICANT: Wu, Jun  
TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES  
FILE REFERENCE: 0575/50159  
CURRENT APPLICATION NUMBER: US/10/850,861  
CURRENT FILING DATE: 2004-05-20  
PRIOR APPLICATION NUMBER: US/08/755,235  
PRIOR FILING DATE: 1996-11-22  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 1405  
TYPE: DNA  
ORGANISM: Human  
US-10-850-861-3

Query Match 96.7%; Score 986.8; DB 18; Length 1405;  
Best Local Similarity 99.6%; Pred. No. 1.5e-276;  
Matches 1010; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 3 GGCAGCGGAAACAGCAGTTGGAGCCTGGGTCTGGTCTCCTCAGTCTCTGTGGGGGCGAGTAGT 62  
DB 3 GGCAGCGGAAACAGCAGTTGGAGCCTGGGTCTGGTCTCCTCAGTCTCTGTGGGGGCGAGTAGT 62

QY 63 AGGTGCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGGTCTGAAAGTGAAGGGGGC 122  
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QY 123 CCCAAGAACACCCCGGCTGGATTTGAATGAACTGAAACAGGCGCGAGAGCTTG 182  
DB 123 CCCAAGAACACCCCGGCTGGATTTGAATGAACTGAAACAGGCGCGAGAGCTTG 182

QY 183 GAAGTCTCTGCTCTCCCGAGGAGGAGCCCTGGGACAGTGGTCTGCTCTCCCAA 242  
DB 183 GAAGTCTCTGCTCTCCCGAGGAGGAGCCCTGGGACAGTGGTCTGCTCTCCCAA 242

QY 243 CGGCTCCCTCTTCCCTCGGCTGTGGGATTCAGGATGAGGGGATTTTCGGTGCAGGC 302  
DB 243 CGGCTCCCTCTTCCCTCGGCTGTGGGATTCAGGATGAGGGGATTTTCGGTGCAGGC 302

QY 303 AATGACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGCTCTACAGATTCC 362  
DB 303 AATGACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGCTCTACAGATTCC 362

QY 363 TGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAGGT 422  
DB 363 TGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAGGT 422

QY 423 GGGGACATGTGTCTCAGAGGAAGCTACCTCGAGGAGCTCTTTAGCTGGCACTTGGATGG 482  
DB 423 GGGGACATGTGTCTCAGAGGAAGCTACCTCGAGGAGCTCTTTAGCTGGCACTTGGATGG 482

QY 483 GAAGCCCTGGTCTTAATGAGAGGAGTATCTGTGAAGGACACAGCAGGAGACCC 542  
DB 483 GAAGCCCTGGTCTTAATGAGAGGAGTATCTGTGAAGGACACAGCAGGAGACCC 542

QY 543 TGAGACAGGGCTCTTCACTGTCAGTTCGAGCTAAATGGTGACCCAGCCCGGGGAGAGA 602  
DB 543 TGAGACAGGGCTCTTCACTGTCAGTTCGAGCTAAATGGTGACCCAGCCCGGGGAGAGA 602

QY 603 TCCCGTCCCACTCTTCTCTGTAGCTTACGCCAGGCTTTCCCGACACCGGCGCTTGG 662  
DB 603 TCCCGTCCCACTCTTCTCTGTAGCTTACGCCAGGCTTTCCCGACACCGGCGCTTGG 662

QY 663 CACAGCCCCATCAGCCCCGTGTCTGGAGCTTGTGCTCTGAGGAGTCCAATT-GG 721  
DB 663 CACAGCCCCATCAGCCCCGTGTCTGGAGCTTGTGCTCTGAGGAGTCCAATTGGG 722

QY 722 TGGTGGAGCCAGAGGTGGAGTAGTCTCTGGTGAACCGTAAACCTGACCTGTGAAG 781  
DB 722 TGGTGGAGCCAGAGGTGGAGTAGTCTCTGGTGAACCGTAAACCTGACCTGTGAAG 782

QY 782 TCCTGCCCAGCCCTCTCTCTCAAACTCAACTGAGTGAAGGATGGTGTGCCCTTGCCTTC 841

DB 783 TCCTGCCCAGCCCTCTCTCAAACTCAACTGAGTGAAGGATGGTGTGCC-TGCCCTTC 841  
QY 842 CCCCAGCCCTGTGCTGATCTCTCCCTGAGTAGGGCTCAGGACCGAGGAACTACAGCT 901  
DB 842 CCCCAGCCCTGTGCTGATCTCTCCCTGAGTAGGGCTCAGGACCGAGGAACTACAGCT 901

QY 902 GTGTGGCCACCATTCACGCCACGGGCCCCAGGAAAGCGTGTGTGAGATCAGATCA 961  
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QY 962 TCGAACCCAGCGAGGAGGGGCCCACTGTCAGGCTCTGTGGAGGATCAGGGCTGG 1015  
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RESULT 9  
US-10-115-635-352  
; Sequence 352, Application US/10115635  
; Publication No. US20040137434A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 797CON  
; CURRENT APPLICATION NUMBER: US/10/115,635  
; CURRENT FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: 09/714,936  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 362  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 352  
; LENGTH: 1463  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(1287)  
US-10-115-635-352

Query Match 93.8%; Score 957; DB 18; Length 1463;  
Best Local Similarity 95.5%; Pred. No. 7e-268;  
Matches 1015; Conservative 0; Mismatches 0; Indels 48; Gaps 1;

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QY 61 GTAGTGTCTCAAAACATCATCAGCCCGGATTTGGGAGCCACTGGTGTGAAGTGAAGGG 120  
DB 85 GTAGTGTCTCAAAACATCATCAGCCCGGATTTGGGAGCCACTGGTGTGAAGTGAAGGG 144

QY 121 GCCCCCAAGAAACCCAGCGGCTGGAAATGAAACTGAACACAGCCGCGACAGAGCT 180  
DB 145 GCCCCCAAGAAACCCAGCGGCTGGAAATGAAACTGAACACAGCCGCGACAGAGCT 204

QY 181 TGAAGTCTCTCTCTCCCGAGGAGGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCC 240  
DB 205 TGAAGTCTCTCTCTCCCGAGGAGGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCC 264

QY 241 AACGGTCTCTCTCTCTCCCGGATTCAGGATGAGGGGATTTTCGGTTCGCG 300





Result No.	Query			ID	Description
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LOCUS  
DEFINITION Pan troglodytes AGER gene, VIRUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION  
AY421474

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VERSION AV421474.1 GI:39748336  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
REFERENCE 1 (bases 1 to 1163)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1163)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source Location/Qualifiers  
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/mol_type="genomic DNA"  
/db_xref="taxon:9598"  
gene <1..>1163  
/gene="AGER"  
/locus_tag="HCM7569"  
ORIGIN  
Query Match 93.5%; Score 953.8; DB 9; Length 1163;  
Best Local Similarity 99.2%; Pred. No. 6e-235;  
Matches 955; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Qy 53 GGGCAGTAGTAGTGTCTCAAAACATCAGCCCGGATTGGCGAGCCTGTGTCTGAAGT 112  
Db 1 GGGCAGTAGTAGTGTCTCAAAACATCAGCCCGGATTGGCGAGCCTGTGTCTGAAGT 60  
Qy 113 GTAAGGGGGCCCCCAAGAAACCCACCCAGCGCTCGAATGGAATGAACTGAACACAGCCGGA 172  
Db 61 GTAAGGGGGCCCCCAAGAAACCCACCCAGCGCTCGAATGGAATGGAATGAACTGAACACAGCCGGA 120  
Qy 173 CAGAAAGCTTGAAGTCTCTGTCTCCCAAGGAGGAGGCCCTTGGACAGTGTGGCTCGTG 232  
Db 121 CAGAAAGCTTGAAGTCTCTGTCTCCCAAGGAGGAGGCCCTTGGACAGTGTGGCTCGTG 180  
Qy 233 TCCTTCCCAACGGCTCCCTCTCTCCGCTGTCCGGATCCAGATCAGGAGATTTTCC 292  
Db 181 TCCTTCCCAACGGCTCCCTCTCTCTCCGCTGTCCGGATCCAGATCAGGAGATTTTCC 240  
Qy 293 GGTGCAGGCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCT 352  
Db 241 GGTGCAGGCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCT 300  
Qy 353 ACCAGATTCTGGGAAGCCAGAAATTTAGATTTCCTCTGAACTCAACGCTGTGTTC 412  
Db 301 ACCAGATTCTGGGAAGCCAGAAATTTAGATTTCCTCTGAACTCAACGCTGTGTTC 360  
Qy 413 CCAATAAGGTGGGACATGTGTGTGACAGGAGGAGTACCTGACAGGACTCTTACGTGC 472  
Db 361 CCAATAAGGTGGGACATGTGTGTGNNNNNNGAAGTACCTGACAGGACTCTTACGTGC 420  
Qy 473 ACTTGGATGGGAAGCCCTGTGTGCTTAATGAAAGGAGTATCTGTGAAGGAACAGACCA 532  
Db 421 ACTTGGATGGGAGCCCTGTGTGCTTAATGAAAGGAGTATCTGTGAAGGAACAGACCA 480  
Qy 533 GGAGACACCTTGAGACAGGGCTTTTCACTGTGCACTCGGAGCTAATGTGACCCAGGCC 592  
Db 533 GGAGACACCTTGAGACAGGGCTTTTCACTGTGCACTCGGAGCTAATGTGACCCAGGCC 592
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2005, 02:38:05 ; Search time 80 Seconds  
(without alignments)  
1638.897 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 339

Sequence: 1 MAAGTAGVAGWVLVLSWGA.....IIEPGEGETAGVGSGSLV 339

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

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2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	338	99.7	340	2	AAM44199 Human sol
3	338	99.7	340	2	AAM33753 Human RAG
4	338	99.7	391	8	ADP19666 Human LP2
5	338	99.7	402	7	ADP95564 Human NOV
6	338	99.7	404	4	AAB81925 Extracorp
7	338	99.7	404	5	ADP65011 Human pro
8	338	99.7	404	5	ADP31292 Human rec
9	338	99.7	404	8	ADf42983 Human RAG
10	338	99.7	404	8	ADK00129 Human RAG
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13	331	97.6	347	5	ABB82298 Human sol
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15	331	97.6	352	8	ADP19656 Human LP2
16	316	93.2	318	2	AAM44200 Human mat
17	316	93.2	318	2	AAM33754 Human RAG
18	275	81.1	360	8	ADP19664 Human LP2
19	274	80.8	298	8	ADP19658 Human LP2
20	274	80.8	325	8	ADM80782 Human CAD
21	271	79.9	390	7	ADP95566 Human NOV
22	271	79.9	390	7	ADP95568 Human NOV
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26	241	71.1	332	3	AAy52130	Human Rec
27	238	70.2	404	5	AAU77543	Human rec
28	238	70.2	404	5	AAE23219	Human rec
29	238	70.2	404	7	AAE39510	Human RAG
30	238	70.2	404	7	ADG32004	Human hom
31	230	67.8	250	6	ABR43202	Human REM
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33	198	58.4	420	5	ABP65012	Human pro
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35	191	56.3	368	8	ADP19662	Human LP2
36	172	50.7	585	8	ADK00127	Human RAG
37	119	35.1	128	6	ABR43201	Human REM
38	114	33.6	127	8	ADP19668	Human LP2
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ALIGNMENTS

RESULT 1

ABB82164  
ID ABB82164 standard; protein; 339 AA.  
XX  
AC ABB82164;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Human soluble RAGE (sRAGE).  
XX  
KW Receptor for Advanced Glycated end product; RAGE; recombinant; nontropic;  
KW antihypertensive; antidiabetic; cytotatic; nephrotropic; vasotropic;  
KW neuroprotective; antiinflammatory; gene therapy; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200270667-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 05-MAR-2002; 2002WO-US006881.  
XX  
PR 05-MAR-2001; 2001US-0273418P.  
XX  
PA (TRAN-) TRANSTECH PHARMA INC.  
XX  
PI Harris R, Shen J, Shabbaz M;  
XX  
DR WPI; 2002-713443/77.  
DR N-PSDB; ABQ79956.  
XX  
PT High level expression of recombinant Receptors for Advanced Glycated end products (RAGE) proteins for treating increased levels of advanced glycosylation end products, comprises infecting cells with a high titer recombinant virus.  
PT  
PT Example; Fig 2B; 51pp; English.  
XX  
XX The invention relates to a method for high level expression of recombinant forms of the Receptor for Advanced Glycated end products (RAGE) or its fragments. The method involves (i) subcloning a nucleotide sequence encoding RAGE or its fragment into a virus; (ii) preparing a high titer stock of recombinant virus; and (iii) infecting host cells with the high titer recombinant virus under conditions such that predetermined levels of RAGE or its fragment is produced, where the predetermined levels of RAGE comprises at least 25 mg recombinant protein per liter of culture. The method is useful for high level expression of recombinant RAGE polypeptide or its fragment which may be useful in



XX DR WPI; 1997-526458/48.  
 XX DR N-PSDB; AAV06517.  
 XX PT New soluble advanced glycosylation end-product receptor polypeptide -  
 XX PT used for reducing vascular permeability, complications of diabetes etc.,  
 XX PT also for purification and to screen for modulators.  
 XX PS Claim 3; Fig 1A; 91pp; English.  
 XX PS This is a human advanced glycosylation end-product receptor (RAGE)  
 CC polypeptide (340 amino acid residues). The RAGE polypeptides and its  
 CC active fragments or their mimetics, inhibit interaction between advanced  
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
 CC are used to treat diseases associated with AGE/RAGE interaction, such as  
 CC increased vascular permeability, diabetes mellitus (particularly  
 CC complications such as micro- or macro- vasculopathy or occlusive vascular  
 CC disorders such as neuropathy, nephropathy, retinopathy or  
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation  
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
 CC age-related disorders such as oxidative stress. These RAGE polypeptides  
 CC are also used, when immobilised, to purify AGE from a protein mixture and  
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
 CC interaction. They can also be used diagnostically to detect abnormal  
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
 CC interaction between AGE and RAGE or other receptors and for purification  
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
 CC used to express recombinant RAGE and as probes for isolating related  
 CC genes  
 XX SQ Sequence 340 AA;  
 Query Match 99.7%; Score 338; DB 2; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-308;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGTAVGAWVLVLSLWAGVGAQNTARIGEPVLKCKGAPKPPQRLWKLTGRTGA 60  
 DB 1 MAAGTAVGAWVLVLSLWAGVGAQNTARIGEPVLKCKGAPKPPQRLWKLTGRTGA 60  
 QY 61 WKVLSQQGGPNDVSARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETSRYRVYQI 120  
 DB 61 WKVLSQQGGPNDVSARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETSRYRVYQI 120  
 QY 121 PGKPEIVDSASELTAGVPNKVGTVCSEGSYPAGTILSWHLDDGKPLVNEKGVSKETRRH 180  
 DB 121 PGKPEIVDSASELTAGVPNKVGTVCSEGSYPAGTILSWHLDDGKPLVNEKGVSKETRRH 180  
 QY 181 PETGLFTLQSELMTVPARGGDPRTFTSCFSPLGPRHRLRTAPIQRYWEPVPLEEVQL 240  
 DB 181 PETGLFTLQSELMTVPARGGDPRTFTSCFSPLGPRHRLRTAPIQRYWEPVPLEEVQL 240  
 QY 241 VVEPEGAVAPGTTVLTCEVPAQPSQIHKMKDGVPLPSPVLILPEIGPDQGTYS 300  
 DB 241 VVEPEGAVAPGTTVLTCEVPAQPSQIHKMKDGVPLPSPVLILPEIGPDQGTYS 300  
 QY 301 CVATHSSHGPQESRAVYSIIEBGERGPTAGSVGGSL 338  
 DB 301 CVATHSSHGPQESRAVYSIIEBGERGPTAGSVGGSL 338  
 RESULT 4  
 ID ADP19666  
 XX ADP19666 standard; protein; 391 AA.  
 AC ADP19666;  
 XX 12-AUG-2004 (first entry)  
 DT Human LP2005 protein SEQ ID.NO:12.  
 DE human; LP2005; antidiabetic; neuroprotective; nootropic;  
 KW antinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;  
 immunosuppressive; nephrotropic; dermatologic; gene therapy; diabetes;  
 Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
 autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
 systemic lupus erythematosus.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide 1..23  
 FT /label= signal  
 FT Protein 24..391  
 FT /label= LP2005  
 XX WO2004044126-A2.  
 XX 27-MAY-2004.  
 XX 05-NOV-2003; 2003WO-US032734.  
 XX 14-NOV-2002; 2002US-0426253P.  
 XX (ELIL ) LILLY & CO ELI.  
 XX Na S, Perkins DR;  
 XX WPI; 2004-411705/38.  
 XX N-PSDB; ADP19665.  
 XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or  
 LP2003) for diagnosing or treating disorders associated with aberrant  
 levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome  
 identification.  
 Claim 9; SEQ ID NO 12; 111pp; English.  
 The present sequence represents human LP2005, which is used in the  
 exemplification of the present invention. The present invention  
 describes: (1) an isolated nucleic acid (I) comprising DNA having at  
 least 95% sequence identity to a polynucleotide selected from the group  
 consisting of: (a) a polynucleotide having a nucleotide sequence as shown  
 in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a  
 polypeptide or mature form of a polypeptide having the amino acid  
 sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide  
 fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide  
 having a nucleotide sequence which is complementary to the nucleotide  
 sequence of a polynucleotide as in (a), (b) or (c); (2) a vector  
 comprising (1); (3) a host cell comprising the vector; (4) producing an  
 LP polypeptide; (5) an isolated polypeptide produced by the above method  
 and comprising an amino acid sequence comprising about 95% sequence  
 identity to a sequence of amino acid residues comprising LP2001, LP2003,  
 LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric  
 molecule comprising an LP polypeptide fused to a heterologous amino acid  
 sequence; (7) an antibody which specifically binds to an LP polypeptide  
 described above; (8) a composition (C) comprising a therapeutic amount of  
 an active agent selected from an LP polypeptide, an agonist to an LP  
 polypeptide, an antagonist to an LP polypeptide, an LP polypeptide  
 antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a  
 polynucleotide in combination with a pharmaceutical carrier; and (9)  
 diagnosing or treating a mammal suffering from a disease, condition or  
 disorder associated with aberrant levels of an LP-polypeptide. (C) has  
 antidiabetic, neuroprotective, nootropic, antiinflammatory,  
 antirheumatic, antiarthritic, vulnery, cytostatic, immunosuppressive,  
 nephrotropic and dermatological activities, and can be used in gene  
 therapy. The compositions (C) and methods are useful for diagnosing or  
 treating disorders associated with aberrant levels of an LP polypeptide,  
 such as diabetes and its complications, Alzheimer's disease,  
 inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple  
 sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
 can also be used for chromosome identification. The LP polypeptide can  
 also be used in manufacturing a medicament for the treatment of the above  
 mentioned diseases, conditions or disorders associated with aberrant  
 levels of the LP polypeptide.

XX antinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;  
 immunosuppressive; nephrotropic; dermatologic; gene therapy; diabetes;  
 Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
 autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
 systemic lupus erythematosus.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide 1..23  
 FT /label= signal  
 FT Protein 24..391  
 FT /label= LP2005  
 XX WO2004044126-A2.  
 XX 27-MAY-2004.  
 XX 05-NOV-2003; 2003WO-US032734.  
 XX 14-NOV-2002; 2002US-0426253P.  
 XX (ELIL ) LILLY & CO ELI.  
 XX Na S, Perkins DR;  
 XX WPI; 2004-411705/38.  
 XX N-PSDB; ADP19665.  
 XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or  
 LP2003) for diagnosing or treating disorders associated with aberrant  
 levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome  
 identification.  
 Claim 9; SEQ ID NO 12; 111pp; English.  
 The present sequence represents human LP2005, which is used in the  
 exemplification of the present invention. The present invention  
 describes: (1) an isolated nucleic acid (I) comprising DNA having at  
 least 95% sequence identity to a polynucleotide selected from the group  
 consisting of: (a) a polynucleotide having a nucleotide sequence as shown  
 in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a  
 polypeptide or mature form of a polypeptide having the amino acid  
 sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide  
 fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide  
 having a nucleotide sequence which is complementary to the nucleotide  
 sequence of a polynucleotide as in (a), (b) or (c); (2) a vector  
 comprising (1); (3) a host cell comprising the vector; (4) producing an  
 LP polypeptide; (5) an isolated polypeptide produced by the above method  
 and comprising an amino acid sequence comprising about 95% sequence  
 identity to a sequence of amino acid residues comprising LP2001, LP2003,  
 LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric  
 molecule comprising an LP polypeptide fused to a heterologous amino acid  
 sequence; (7) an antibody which specifically binds to an LP polypeptide  
 described above; (8) a composition (C) comprising a therapeutic amount of  
 an active agent selected from an LP polypeptide, an agonist to an LP  
 polypeptide, an antagonist to an LP polypeptide, an LP polypeptide  
 antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a  
 polynucleotide in combination with a pharmaceutical carrier; and (9)  
 diagnosing or treating a mammal suffering from a disease, condition or  
 disorder associated with aberrant levels of an LP-polypeptide. (C) has  
 antidiabetic, neuroprotective, nootropic, antiinflammatory,  
 antirheumatic, antiarthritic, vulnery, cytostatic, immunosuppressive,  
 nephrotropic and dermatological activities, and can be used in gene  
 therapy. The compositions (C) and methods are useful for diagnosing or  
 treating disorders associated with aberrant levels of an LP polypeptide,  
 such as diabetes and its complications, Alzheimer's disease,  
 inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple  
 sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
 can also be used for chromosome identification. The LP polypeptide can  
 also be used in manufacturing a medicament for the treatment of the above  
 mentioned diseases, conditions or disorders associated with aberrant  
 levels of the LP polypeptide.

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XX SQ Sequence 391 AA;
Query Match          99.7%; Score 338; DB 8; Length 391;
Best Local Similarity 100.0%; Pred. No. 3.9e-308;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGEPLVLKCKGAPKPPORLEWKLNTGRTGA 60
Db 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGEPLVLKCKGAPKPPORLEWKLNTGRTGA 60

QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRVRVYQI 120
Db 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRVRVYQI 120

QY 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLGDKPLVNEKGVSKVEQTRRH 180
Db 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLGDKPLVNEKGVSKVEQTRRH 180

QY 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
Db 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240

QY 241 VVEPEGAVAPGGTIVLTCEVPAQPSQIHWMDGVLPLPPSPVLLPIGPDQGTYS 300
Db 241 VVEPEGAVAPGGTIVLTCEVPAQPSQIHWMDGVLPLPPSPVLLPIGPDQGTYS 300

QY 301 CVATHSHGQESRAVSISIIIEGEGTPTAGSVGGSL 338
Db 301 CVATHSHGQESRAVSISIIIEGEGTPTAGSVGGSL 338

RESULT 5
ADE95564
ID ADE95564 standard; protein; 402 AA.
XX AC ADE95564;
XX AC ADE95564;
DT 12-FEB-2004 (first entry)
XX DE Human NOVX16c protein.
XX KW NOVX protein; biochemical stimulation; physiological stimulation;
KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;
KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
KW nootropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;
KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
KW Depression; allergy; fertility disorder; NOVX16c.
XX OS Homo sapiens.
XX OS Homo sapiens.
XX PN W02003050245-A2.
XX PD 19-JUN-2003.
XX PF 03-DEC-2002; 2002WO-US038594.
XX PR 05-DEC-2001; 2001US-0336600P.
XX PR 07-DEC-2001; 2001US-0338285P.
XX PR 12-DEC-2001; 2001US-0341346P.
XX PR 17-DEC-2001; 2001US-0341477P.
XX PR 20-DEC-2001; 2001US-0341540P.
XX PR 27-DEC-2001; 2001US-0342592P.
XX PR 31-DEC-2001; 2001US-0344297P.
XX PR 17-APR-2002; 2001US-0344903P.
XX PR 15-MAY-2002; 2002US-0373288P.
XX PR 17-MAY-2002; 2002US-0381495P.

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PR 28-MAY-2002; 2002US-0383534P.
PR 28-MAY-2002; 2002US-0383744P.
PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-0384024P.
PR 07-AUG-2002; 2002US-0401788P.
PR 26-AUG-2002; 2002US-0406353P.
PR 31-OCT-2002; 2002US-0401788.
PR 02-DEC-2002; 2002US-0406353.
XX (CURA-) CURAGEN CORP.
XX PA
XX PI Albrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;
PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
PI Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphy R;
PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;
PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
XX WPI; 2003-513974/48.
DR N-PSDB; ADE95563.
DR N-PSDB; ADE95563.
XX PT
XX PT New NOVX polypeptides and nucleic acids, useful for preventing or
XX PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
XX PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
XX PT pharmacogenomics.
PS Claim 2; SEQ ID NO 96; 211pp; English.
XX CC
XX CC This invention relates to novel NOVX proteins, and the DNA sequence which
XX CC encode them, having properties related to stimulation of biochemical or
XX CC physiological responses in a cell, a tissue, an organ or an organism.
XX CC Compounds which modulate the proteins of the invention may have cardiant,
XX CC antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,
XX CC antiarthritic, antidiabetic, nephrotropic, dermatological,
XX CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
XX CC nootropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
XX CC antidepressant, antiallergic or gynaecological activities. The DNA
XX CC sequences of the invention may be useful for gene therapy whilst the
XX CC protein sequences may allow the development of a vaccine. The protein is
XX CC useful in the manufacture of a medicament for treating a syndrome
XX CC associated with a human disease. The invention may be useful in
XX CC diagnosing, treating or preventing NOVX-associated disorders, for example
XX CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
XX CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
XX CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
XX CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
XX CC fertility disorders. The nucleic acids may further be used as
XX CC hybridisation probes, in chromosome mapping, tissue typing, preventive
XX CC medicine, and pharmacogenomics. The present sequence is the amino acid
XX CC sequence of the human NOVX16c protein of the invention.
XX SQ Sequence 402 AA;
Query Match          99.7%; Score 338; DB 7; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-308;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGEPLVLKCKGAPKPPORLEWKLNTGRTGA 60
Db 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGEPLVLKCKGAPKPPORLEWKLNTGRTGA 60

QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRVRVYQI 120
Db 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRVRVYQI 120

QY 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLGDKPLVNEKGVSKVEQTRRH 180
Db 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLGDKPLVNEKGVSKVEQTRRH 180

QY 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
Db 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240

QY 241 VVEPEGAVAPGGTIVLTCEVPAQPSQIHWMDGVLPLPPSPVLLPIGPDQGTYS 300

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Db 241 VVEPEGAVAGGTVTLTCEVPAQSPQIHMMKDGVLPLPPSPVLILPEIGPDQGTYS 300  
QY 301 CVATHSHGQPSRAVSISIIEREGEGTAGSVGGSL 338  
Db 301 CVATHSHGQPSRAVSISIIEREGEGTAGSVGGSL 338  
RESULT 6  
AAB81925  
ID AAB81925 standard; protein; 404 AA.  
XX AAB81925;  
AC AAB81925;  
DT 15-JUN-2001 (first entry)  
DE Extracorporeal circulation material receptor protein.  
KW Extracorporeal circulation; carbonyl stress product; receptor; diabetes;  
KW vascular lesion; excretory dysfunction.  
XX Unidentified.  
OS  
KW WC200118060-A1.  
XX  
XX 15-MAR-2001.  
PD  
PF 08-SEP-2000; 2000MO-JP006172.  
XX  
XX 08-SEP-1999; 99JP-00254463.  
PR  
XX (TORA ) TORAY IND INC.  
PA  
XX Shimizu S, Kubota M, Akiyama H, Usui M;  
XX WPI; 2001-290314/30.  
DR  
XX Material for extracorporeal circulation, applicable in selective  
PT elimination of diabetic complication factors such as carbonyl stress  
PT products caused by abnormally promoted carbonyl stress from excretory  
PT dysfunction in vascular lesions.  
XX  
PS Claim 1; Page 31-32; 36pp; Japanese.  
XX  
XX The present invention describes a material for extracorporeal circulation  
CC which is made from a water-insoluble carrier immobilized with a protein  
CC having the sequence shown here. The materials of the invention, including  
CC adsorbents, are for extracorporeal circulation, which are applicable in  
CC the selective elimination of diabetic complication factors from a body  
CC fluid, and are therefore useful in treating vascular lesions like  
CC arteriosclerosis due to carbonyl stress products caused by abnormally  
CC promoted carbonyl stress from excretory dysfunction  
XX  
SQ Sequence 404 AA;  
Query Match 99.7%; Score 338; DB 4; Length 404;  
Best Local Similarity 100.0%; Pred. No. 46-308;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGTAGAWVLVLSLWGA VVGAVGQNTARIGELVLKCKGAPKPPORLEWKLNTGRTEA 60  
Db 1 MAAGTAGAWVLVLSLWGA VVGAVGQNTARIGELVLKCKGAPKPPORLEWKLNTGRTEA 60  
QY 61 WKVLSFGGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTSNRYRVYQI 120  
Db 61 WKVLSFGGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTSNRYRVYQI 120  
QY 121 PKRPEIVDSASELTAGVPNKVGTGCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQETRRH 180  
Db 121 PKRPEIVDSASELTAGVPNKVGTGCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQETRRH 180  
QY 181 PETGLFTLQSELMTVPARGDPRPTSCSPGLPHRALRTAPIQPRVWEPVPLEVQL 240

Db 181 PETGLFTLQSELMTVPARGDPRPTSCSPGLPHRALRTAPIQPRVWEPVPLEVQL 240  
QY 241 VVEPEGAVAGGTVTLTCEVPAQSPQIHMMKDGVLPLPPSPVLILPEIGPDQGTYS 300  
Db 241 VVEPEGAVAGGTVTLTCEVPAQSPQIHMMKDGVLPLPPSPVLILPEIGPDQGTYS 300  
QY 301 CVATHSHGQPSRAVSISIIEREGEGTAGSVGGSL 338  
Db 301 CVATHSHGQPSRAVSISIIEREGEGTAGSVGGSL 338  
RESULT 7  
ABP65011  
ID ABP65011 standard; protein; 404 AA.  
XX  
AC ABP65011;  
DT 25-FEB-2003 (first entry)  
DE Human protein SEQ ID 671.  
XX  
XX Human; expressed sequence tag; EST; haematopoietic disorder;  
KW central nervous system disease; viral infection;  
KW peripheral nervous system disease; non-healing wound; infectious disease;  
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;  
KW fungal infection; autoimmune disorder; coagulation disorder; neuropathic;  
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;  
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;  
KW immunostimulant; cerebroprotective.  
XX  
OS Homo sapiens.  
XX  
XX WO200259260-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 16-NOV-2001; 2001WO-US042950.  
XX  
PR 17-NOV-2000; 2000US-00714936.  
XX  
XX (HYSE-) HYSEQ INC.  
PA  
XX  
XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QH;  
PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
XX  
XX WPI; 2002-590824/63.  
DR N-PSDB; ABQ99597.  
XX  
XX New isolated polynucleotide, useful in research, diagnostic or  
PT therapeutic methods, e.g. preventing or treating disorders involving  
PT aberrant protein expression or biological activity.  
XX  
PS Claim 20; SEQ ID NO 671; 394pp; English.  
XX  
XX The present invention relates to novel human coding sequences (ABQ99268-  
CC ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in  
CC therapeutic, diagnostic and research methods. The polynucleotides may be  
CC used in the field of molecular biology as hybridisation probes, primers  
CC for PCR, for chromosome and gene mapping, for the recombinant production  
CC of protein, or in generation of anti-sense DNA or RNA. The  
CC polynucleotides are useful in diagnostics as expressed sequence tags  
CC (ESTs) for identifying expressed genes or for physical mapping of the  
CC human genome. The proteins may be used as molecular weight markers, or as  
CC nutritional sources or supplements. The proteins may be used to maintain  
CC and expand cell population in a totipotent or pluripotent state,  
CC useful for re-engineering damaged or diseased tissues, transplantation,  
CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The  
CC polynucleotides and proteins are useful for preventing, treating or  
CC ameliorating disorders involving aberrant protein expression or  
CC biological activity, e.g. haematopoietic disorders, central/peripheral  
CC nervous system diseases, mechanical and traumatic disorders, non-healing  
CC wounds, immune deficiencies and disorders, infectious diseases caused by  
CC viral, bacterial or fungal infection, autoimmune disorders, allergic



CC reactions and conditions, coagulation disorders, or cancer. The  
 CC polynucleotide sequences of the invention were assembled from ESTs  
 CC isolated mainly by sequencing by hybridisation, and in some cases,  
 CC sequences obtained from one or more public databases. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 404 AA;

Query Match 99.7%; Score 338; DB 5; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 4e-308;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGAWLVLSLWGAVGVAQNIITARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60  
 DB 1 MAAGTAGAWLVLSLWGAVGVAQNIITARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60  
 QY 61 WKVLSPOGGPMDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVYQI 120  
 DB 61 WKVLSPOGGPMDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVYQI 120  
 QY 121 PGKPEIVDSASLTAGVKNKVTGCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKVKEQTRRH 180  
 DB 121 PGKPEIVDSASLTAGVKNKVTGCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKVKEQTRRH 180  
 QY 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240  
 DB 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240  
 QY 241 VVEPEGGA VAPGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLILPEIGPDQGTYS 300  
 DB 241 VVEPEGGA VAPGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLILPEIGPDQGTYS 300  
 QY 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338  
 DB 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338

RESULT 8  
 ADF31292  
 ID ADF31292 standard; protein; 404 AA.  
 XX  
 AC ADF31292;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human receptor of advanced glycation end products (RAGE).  
 XX  
 KW human; receptor; advanced glycation end product; RAGE;  
 KW receptor of advanced glycation end product; high yield; high purity.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP2003306500-A.  
 XX  
 PD 28-OCT-2003.  
 XX  
 PF 05-FEB-2003; 2003JP-00027992.  
 XX  
 PR 15-FEB-2002; 2002JP-00038380.  
 XX  
 PA (TORA ) TORAY IND INC.  
 XX  
 DR WPI; 2004-015267/02.  
 XX  
 PT Purifying receptor of advanced glycation end products derivative  
 PT containing Igv domain of receptor of advanced glycation end product using  
 PT one or more affinity columns.  
 XX  
 PS Disclosure; SEQ ID NO 1; 13pp; Japanese.  
 XX  
 CC The invention relates to a method of purifying a receptor of advanced

CC Glycation end products (RAGE) derivative. The method is useful for  
 CC purifying receptor of advanced glycation end product derivative. The  
 CC method enables simple, rapid with high yield and high purity manufacture  
 CC of RAGE derivative. The present sequence represents the amino acid  
 CC sequence of human receptor of advanced glycation end products (RAGE).  
 XX  
 SQ Sequence 404 AA;

Query Match 99.7%; Score 338; DB 8; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 4e-308;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGAWLVLSLWGAVGVAQNIITARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60  
 DB 1 MAAGTAGAWLVLSLWGAVGVAQNIITARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60  
 QY 61 WKVLSPOGGPMDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVYQI 120  
 DB 61 WKVLSPOGGPMDSVARVLPNGSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVYQI 120  
 QY 121 PGKPEIVDSASLTAGVKNKVTGCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKVKEQTRRH 180  
 DB 121 PGKPEIVDSASLTAGVKNKVTGCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKVKEQTRRH 180  
 QY 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240  
 DB 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240  
 QY 241 VVEPEGGA VAPGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLILPEIGPDQGTYS 300  
 DB 241 VVEPEGGA VAPGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLILPEIGPDQGTYS 300  
 QY 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338  
 DB 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338

RESULT 9  
 ADF42983  
 ID ADF42983 standard; protein; 404 AA.  
 XX  
 AC ADF42983;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human receptor of advanced glycation (RAGE) protein.  
 XX  
 KW diabetic complication factor; receptor of advanced glycation end product;  
 KW RAGE binding substance adsorption ligand; water-insoluble carrier;  
 KW biological evaluation; diabetic complication; renal disease; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP2003306499-A.  
 XX  
 PD 28-OCT-2003.  
 XX  
 PF 05-FEB-2003; 2003JP-00027991.  
 XX  
 PR 15-FEB-2002; 2002JP-00038378.  
 XX  
 PA (TORA ) TORAY IND INC.  
 XX  
 DR WPI; 2004-015266/02.  
 XX  
 PT Obtaining diabetic complication factor comprises contacting biological  
 PT fluid with adsorbent, and immobilizing receptor of advanced glycation end  
 PT products binding substance ligand on carrier.  
 XX  
 PS Disclosure; SEQ ID NO 1; 18pp; Japanese.  
 XX  
 CC This invention relates to a novel method of obtaining a diabetic  
 CC complication factor which comprises contacting liquid from a biological

CC fluid with an adsorbent which immobilises a receptor of advanced  
 CC glycation end products (RAGE) binding substance adsorption ligand on a  
 CC water-insoluble carrier, cleaning the adsorbent in an aqueous solution,  
 CC separating and recovering the diabetically complicated factor by contacting  
 CC the adsorbent with the aqueous solution. The method is useful for  
 CC carrying out biological evaluation which involves determining advanced  
 CC degree of diabetic complication or degree of a renal-disease.  
 XX  
 SQ Sequence 404 AA;

Query Match 99.7%; Score 338; DB 8; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 4e-308;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEA 60  
 DB 1 MAAGTAVGAWLVLSLWGVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEA 60  
 QY 61 WKVLSFQGGPWDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120  
 DB 61 WKVLSFQGGPWDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120  
 QY 121 PGKPEIVDSASELTAGVPKNVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180  
 DB 121 PGKPEIVDSASELTAGVPKNVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180  
 QY 181 PETGLFTLQSELMVTPARGGDRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240  
 DB 181 PETGLFTLQSELMVTPARGGDRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240  
 QY 241 VVEPEGGA VAPGTVTLTCEVPAQSPQIHMMKDGVPPLPPLPSPVLLILPEIGPDQGTYS 300  
 DB 241 VVEPEGGA VAPGTVTLTCEVPAQSPQIHMMKDGVPPLPPLPSPVLLILPEIGPDQGTYS 300  
 QY 301 CVATHSSHGQPSRAVSISIIPEEGEGTAGSVGGSGL 338  
 DB 301 CVATHSSHGQPSRAVSISIIPEEGEGTAGSVGGSGL 338

RESULT 10  
 ADK00129  
 ID ADK00129 standard; protein; 404 AA.  
 AC  
 AC ADK00129;  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human RAGE protein.  
 XX  
 KW Advanced Glycation End Product Ligand Binding Element; RAGE-LBE;  
 KW Cytostatic; Antidiabetic; Nootropic; Antiarthritic; Osteopathic;  
 KW Neuroprotective; Antiinflammatory; Dermatological; Immunosuppressive;  
 KW Vasotropic; Antiporiatic; Antibacterial; Antiartherosclerotic;  
 KW amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;  
 KW chronic inflammatory disease; osteoarthritis; irritable bowel disease;  
 KW multiple sclerosis; psoriasis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO2004016229-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 18-AUG-2003; 2003WO-US025996.  
 XX  
 PR 16-AUG-2002; 2002US-0404205P.  
 XX  
 PA (AMHP ) WYETH.  
 XX  
 PI Pittman DD, Clancy B, Larsen G, Trepicchio WL, Breinan FM;  
 PI Feldmann M, Foxwell BJM, Feldman JL;

DR WPI; 2004-192067/18.  
 XX N-PSDB; ADK00130.  
 XX  
 PT New fusion protein comprising a Receptor for Advanced Glycation End  
 PT Product Ligand Binding Element (RAGE-LBE) and an Immunoglobulin element,  
 PT useful for preparing a composition for treating e.g., Alzheimer's  
 PT disease.  
 XX  
 PS Disclosure; SEQ ID NO 43; 100pp; English.  
 XX  
 CC The present invention relates to a new fusion protein comprises a  
 CC Receptor for Advanced Glycation End Product Ligand Binding Element (RAGE-  
 CC LBE) and an immunoglobulin element. The fusion protein is useful for  
 CC preparing a composition for treating RAGE-associated disorders such as  
 CC amyloidosis, cancer, Crohn's disease, diabetes, complications of  
 CC diabetes, prion-related disorders, vasculitis, nephropathies,  
 CC retinopathies and/or neuropathies; Alzheimer's disease, chronic  
 CC inflammatory disease e.g., rheumatoid arthritis, osteoarthritis,  
 CC irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute  
 CC inflammatory disease e.g., sepsis, or cardiovascular disease, e.g.,  
 CC atherosclerosis or restenosis. The present sequence represents human RAGE  
 CC protein.  
 XX  
 SQ Sequence 404 AA;

Query Match 99.7%; Score 338; DB 8; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 4e-308;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEA 60  
 DB 1 MAAGTAVGAWLVLSLWGVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEA 60  
 QY 61 WKVLSFQGGPWDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120  
 DB 61 WKVLSFQGGPWDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120  
 QY 121 PGKPEIVDSASELTAGVPKNVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180  
 DB 121 PGKPEIVDSASELTAGVPKNVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180  
 QY 181 PETGLFTLQSELMVTPARGGDRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240  
 DB 181 PETGLFTLQSELMVTPARGGDRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240  
 QY 241 VVEPEGGA VAPGTVTLTCEVPAQSPQIHMMKDGVPPLPPLPSPVLLILPEIGPDQGTYS 300  
 DB 241 VVEPEGGA VAPGTVTLTCEVPAQSPQIHMMKDGVPPLPPLPSPVLLILPEIGPDQGTYS 300  
 QY 301 CVATHSSHGQPSRAVSISIIPEEGEGTAGSVGGSGL 338  
 DB 301 CVATHSSHGQPSRAVSISIIPEEGEGTAGSVGGSGL 338

RESULT 11  
 AAM48746  
 ID AAM48746 standard; protein; 339 AA.  
 XX  
 AC AAM48746;  
 XX  
 DT 02-APR-2002 (first entry)  
 XX  
 DE Human BRAGE protein SEQ ID NO 2.  
 XX  
 KW Human; RAGE; receptor for advanced glycosylated endproduct; receptor;  
 KW antidiabetic; neuroprotective; cytostatic; antiinflammatory; vasotropic;  
 KW nephrotropic; dermatological; antiarteriosclerotic; nootropic; diabetes;  
 KW Alzheimer's disease; cancer; inflammation; kidney failure;  
 KW systemic lupus; nephritis; erectile dysfunction; atherosclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192892-A2.

XX PD 06-DEC-2001.  
 XX PF 30-MAY-2001; 2001WO-US017447.  
 XX PR 30-MAY-2000; 2000US-0207342P.  
 XX FR 05-MAR-2001; 2001US-00799152.  
 XX PA (TRAN-) TRANS TECH PHARMA.  
 XX PI Shahbaz M;  
 XX DR WPI; 2002-114372/15.  
 XX PT Detecting a receptor for advanced glycosylated endproducts (RAGE) modulators,  
 PT for treating e.g., cancer, diabetes or inflammation, comprises measuring  
 PT the amount of bound anti-RAGE antibody.  
 XX PS Claim 2; Fig 2; 49pp; English.  
 XX CC The invention relates to detecting receptor for advanced glycosylated  
 CC endproducts (RAGE) modulators comprising determining the amount of RAGE  
 CC protein or its fragment bound to the pre-adsorbed ligand by measuring the  
 CC amount of anti-RAGE antibody bound to the solid surface. The method is  
 CC useful for rapid, high-throughput identification of compounds that  
 CC modulate RAGE. The compounds are useful for treating symptoms of diabetes  
 CC and symptoms of diabetic late complications, amyloidosis, Alzheimer's  
 CC disease, cancer, inflammation, kidney failure, systemic lupus nephritis  
 CC or inflammatory lupus nephritis, erectile dysfunction and atherosclerosis  
 XX Sequence 339 AA;  
 XX  
 Query Match 99.4%; Score 337; DB 5; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 3e-307;  
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAM 61  
 DB 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAM 61  
 QY 62 KVLSPQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQIP 121  
 DB 62 KVLSPQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQIP 121  
 QY 122 GKPEIVDSASELTAGVPNKVGTCSVSGSYPA GTLSWHL DCKPLVPNEKGVSKQETRRHP 181  
 DB 122 GKPEIVDSASELTAGVPNKVGTCSVSGSYPA GTLSWHL DCKPLVPNEKGVSKQETRRHP 181  
 QY 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQIV 241  
 DB 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQIV 241  
 QY 242 VEPEGGA VAPGGVTTLTCEVPAQPSQIHWMDGVLPPLPPSPVLLIPGPDQGTYS 301  
 DB 242 VEPEGGA VAPGGVTTLTCEVPAQPSQIHWMDGVLPPLPPSPVLLIPGPDQGTYS 301  
 QY 302 VATHSHGPOESRAVSIISIEPEGEGPTAGSVGSGSL 338  
 DB 302 VATHSHGPOESRAVSIISIEPEGEGPTAGSVGSGSL 338  
 RESULT 12  
 AAM48745  
 ID AAM48745 standard; protein; 404 AA.  
 AC AAM48745;  
 XX  
 DT 02-APR-2002 (first entry)  
 XX Human RAGE protein SEQ ID NO 1.  
 XX Human; RAGE; receptor for advanced glycosylated endproduct; receptor;  
 KW antidiabetic; neuroprotective; cytosolic; antiinflammatory; vasotropic;  
 KW

KW nephrotropic; dermatological; antiarteriosclerotic; nootropic; diabetes;  
 KW Alzheimer's disease; cancer; inflammation; kidney failure;  
 KW systemic lupus; nephritis; erectile dysfunction; atherosclerosis.  
 OS Homo sapiens.  
 XX WO200192892-A2.  
 PN 06-DEC-2001.  
 PD 30-MAY-2001; 2001WO-US017447.  
 PF 30-MAY-2000; 2000US-0207342P.  
 PR 05-MAR-2001; 2001US-00799152.  
 XX (TRAN-) TRANS TECH PHARMA.  
 PA Shahbaz M;  
 PI WPI; 2002-114372/15.  
 DR Detecting a receptor for advanced glycosylated endproducts (RAGE) modulators,  
 XX for treating e.g., cancer, diabetes or inflammation, comprises measuring  
 XX the amount of bound anti-RAGE antibody.  
 PS Claim 1; Fig 2; 49pp; English.  
 XX The invention relates to detecting receptor for advanced glycosylated  
 CC endproducts (RAGE) modulators comprising determining the amount of RAGE  
 CC protein or its fragment bound to the pre-adsorbed ligand by measuring the  
 CC amount of anti-RAGE antibody bound to the solid surface. The method is  
 CC useful for rapid, high-throughput identification of compounds that  
 CC modulate RAGE. The compounds are useful for treating symptoms of diabetes  
 CC and symptoms of diabetic late complications, amyloidosis, Alzheimer's  
 CC disease, cancer, inflammation, kidney failure, systemic lupus nephritis  
 CC or inflammatory lupus nephritis, erectile dysfunction and atherosclerosis  
 XX Sequence 404 AA;  
 XX

Query Match 99.4%; Score 337; DB 5; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-307;  
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAM 61  
 DB 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAM 61  
 QY 62 KVLSPQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQIP 121  
 DB 62 KVLSPQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQIP 121  
 QY 122 GKPEIVDSASELTAGVPNKVGTCSVSGSYPA GTLSWHL DCKPLVPNEKGVSKQETRRHP 181  
 DB 122 GKPEIVDSASELTAGVPNKVGTCSVSGSYPA GTLSWHL DCKPLVPNEKGVSKQETRRHP 181  
 QY 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQIV 241  
 DB 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQIV 241  
 QY 242 VEPEGGA VAPGGVTTLTCEVPAQPSQIHWMDGVLPPLPPSPVLLIPGPDQGTYS 301  
 DB 242 VEPEGGA VAPGGVTTLTCEVPAQPSQIHWMDGVLPPLPPSPVLLIPGPDQGTYS 301  
 QY 302 VATHSHGPOESRAVSIISIEPEGEGPTAGSVGSGSL 338  
 DB 302 VATHSHGPOESRAVSIISIEPEGEGPTAGSVGSGSL 338  
 RESULT 13  
 ABB82298  
 ID ABB82298 standard; protein; 347 AA.  
 XX  
 AC ABB82298;

XX 08-JAN-2003 (first entry)  
XX Human soluble RAGE protein.  
XX RAGE; receptor; advanced glycation endproduct; antidiabetic; nootropic;  
XX neuroprotective; antiarteriosclerotic; antiulcer; human.  
XX Homo sapiens.  
XX WO200274805-A1.  
XX 26-SEP-2002.  
XX 19-MAR-2002; 2002WO-JP002623.  
XX 19-MAR-2001; 2001JP-00078409.  
XX 10-AUG-2001; 2001JP-00243114.  
XX 25-FEB-2002; 2002JP-00048182.  
XX (UYKA-) UNIV JAPAN KANAZAWA.  
XX Yamamoto H, Yonekura H, Yamamoto Y, Sakurai S, Watanabe T;  
XX WPI; 2002-740851/80.  
XX N-PSDB; ABV73151.  
XX Soluble advanced glycation endproduct receptor polypeptides and  
XX substances modifying their activity for treatment and prevention of  
XX disorders associated with diabetes and aging.  
XX Claim 1; Page 118-120; 127pp; Japanese.  
XX The invention relates to soluble receptor polypeptides for advanced  
XX glycation endproducts (soluble RAGE) and encoding polynucleotides. The  
XX soluble RAGE protein can be prepared by standard recombinant methodology.  
XX The protein, polynucleotide and modulators can be used for the  
XX prevention, treatment and diagnosis of diabetic complications, diseases  
XX of aging, disorders of glycation of metabolic proteins, Alzheimer's  
XX disease, arteriosclerosis and ulceration, and study of the mechanism and  
XX pathology of these diseases. The present sequence represents the human  
XX soluble RAGE protein  
XX Sequence 347 AA;  
Query Match 97.6%; Score 331; DB 5; Length 347;  
Best Local Similarity 100.0%; Pred. No. 1.3e-301;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGBPLVLKCKGAPKPPQRLWKLNTGRTEA 60  
DB 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGBPLVLKCKGAPKPPQRLWKLNTGRTEA 60  
QY 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120  
DB 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120  
QY 121 PGKPEIVDSASLTAGVKNKVGTCVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180  
DB 121 PGKPEIVDSASLTAGVKNKVGTCVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180  
QY 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVQL 240  
DB 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVQL 240  
QY 241 VVEPEGGAAPGCTVTLTCEVPAQPSQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300  
DB 241 VVEPEGGAAPGCTVTLTCEVPAQPSQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300  
QY 301 CVATHSSHGPQESRAVSIISIEPGBEGPTAG 331  
DB 301 CVATHSSHGPQESRAVSIISIEPGBEGPTAG 331

RESULT 14  
ADG37044  
ID ADG37044 standard; protein; 347 AA.  
XX  
AC ADG37044;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Receptor for advanced glycation endproducts (RAGE).  
XX receptor for advanced glycation endproducts; RAGE; diabetic complication;  
XX glycosuria nephropathy; glycosuria retinopathy; Alzheimer's disease;  
XX atherosclerosis; Down's syndrome; multiple sclerosis; amyloidosis;  
XX autoimmune disease; inflammation; cancer; wound healing; human; receptor.  
XX Homo sapiens.  
XX JP2003230382-A.  
XX 19-AUG-2003.  
XX 08-FEB-2002; 2002JP-00032155.  
XX 08-FEB-2002; 2002JP-00032155.  
XX (KANA-) KANAZAWA DAIGAKUCHO.  
XX WPI; 2003-820207/77.  
XX N-PSDB; ADG37043.  
XX New advanced glycation endproducts-receptor for advanced glycation  
XX endproducts antagonist useful for treating or preventing diabetic  
XX complication, glycosuria nephropathy, and glycosuria retinopathy.  
XX Example 1; SEQ ID NO 2; 23pp; Japanese.  
XX The invention relates to a receptor for advanced glycation endproducts  
XX (RAGE). An AGE-RAGE antagonist composition is useful for treating or  
XX preventing diabetic complication (e.g., glycosuria nephropathy,  
XX glycosuria retinopathy), Alzheimer's disease, atherosclerosis, Down's  
XX syndrome, multiple sclerosis, amyloidosis, autoimmune disease,  
XX inflammation, cancer, wound healing, etc. The present sequence represents  
XX the amino acid sequence of the receptor for advanced glycation  
XX endproducts (RAGE).  
XX Sequence 347 AA;  
Query Match 97.6%; Score 331; DB 7; Length 347;  
Best Local Similarity 100.0%; Pred. No. 1.3e-301;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGBPLVLKCKGAPKPPQRLWKLNTGRTEA 60  
DB 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGBPLVLKCKGAPKPPQRLWKLNTGRTEA 60  
QY 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120  
DB 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120  
QY 121 PGKPEIVDSASLTAGVKNKVGTCVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180  
DB 121 PGKPEIVDSASLTAGVKNKVGTCVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180  
QY 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVQL 240  
DB 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVQL 240  
QY 241 VVEPEGGAAPGCTVTLTCEVPAQPSQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300  
DB 241 VVEPEGGAAPGCTVTLTCEVPAQPSQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300  
QY 301 CVATHSSHGPQESRAVSIISIEPGBEGPTAG 331

Db 301 CVATHSHGPOESRAVSIIIEPGEETAG 331

RESULT 15  
ADP19656  
ID ADP19656 standard; protein; 352 AA.

AC ADP19656;

DT 12-AUG-2004 (first entry)

DE Human LP2000 protein SEQ ID NO:2.

XX human; LP2000; antidiabetic; neuroprotective; neurotropic;  
XX antiinflammatory; antirheumatic; antiarthritic; vulnary; cytosstatic;  
KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;  
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
KW systemic lupus erythematosus.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1. .23  
FT /label= signal  
FT Protein 24. .352  
FT /label= LP2000

XX W0200404126-A2.

XX 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US032734.

XX 14-NOV-2002; 2002US-0426253P.

XX (ELIL) LILLY & CO ELI.

XX Na S, Perkins DR;

XX WPI; 2004-411705/38.

XX N-PSDB; ADP19655.

XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or  
PT LP2003) for diagnosing or treating disorders associated with aberrant  
PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome  
PT identification.

XX Disclosure; SEQ ID NO 2; 11pp; English.

XX The present sequence represents human LP2000, which is used in the  
CC exemplification of the present invention. The present invention  
CC describes: (1) an isolated nucleic acid (I) comprising DNA having at  
CC least 95% sequence identity to a polynucleotide selected from the group  
CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown  
CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a  
CC polypeptide or mature form of a polypeptide having the amino acid  
CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide  
CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide  
CC having a nucleotide sequence which is complementary to the nucleotide  
CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector  
CC comprising (I); (3) a host cell comprising the vector; (4) producing an  
CC LP polypeptide; (5) an isolated polypeptide produced by the above method  
CC and comprising an amino acid sequence comprising about 95% sequence  
CC identity to a sequence of amino acid residues comprising LP2001, LP2003,  
CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric  
CC molecule comprising an LP polypeptide fused to a heterologous amino acid  
CC sequence; (7) an antibody which specifically binds to an LP polypeptide  
CC described above; (8) a composition (C) comprising a therapeutic amount of  
CC an active agent selected from an LP polypeptide, an agonist to an LP  
CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide, and a  
CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a

CC polynucleotide in combination with a pharmaceutical carrier; and (9)  
CC diagnosing or treating a mammal suffering from a disease, condition or  
CC disorder associated with aberrant levels of an LP-polypeptide. (C) has  
CC antidiabetic, neuroprotective, neurotropic, antiinflammatory,  
CC antirheumatic, antiarthritic, vulnary, cytosstatic, immunosuppressive,  
CC nephrotropic and dermatological activities, and can be used in gene  
CC therapy. The compositions (C) and methods are useful for diagnosing or  
CC treating disorders associated with aberrant levels of an LP polypeptide,  
CC such as diabetes and its complications, Alzheimer's disease,  
CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple  
CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
CC may also be used for chromosome identification. The LP polypeptide can  
CC also be used in manufacturing a medicament for the treatment of the above  
CC mentioned diseases, conditions or disorders associated with aberrant  
CC levels of the LP polypeptide.

XX SQ Sequence 352 AA;

Query Match 97.6%; Score 331; DB 8; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.3e-301; Indels 0; Gaps 0;

Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGEPVLKCKGAPKPPQRLKWLNTGRTEA 60

Db 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGEPVLKCKGAPKPPQRLKWLNTGRTEA 60

QY 61 WKVLSPOGGGPMDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNYRVVYQI 120

Db 61 WKVLSPOGGGPMDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNYRVVYQI 120

QY 121 PGKPEIVDSASLITAGVFNKVGTCVSEGSYPAGTSLSHLDGKPLVPNEKGSVKQETRRH 180

Db 121 PGKPEIVDSASLITAGVFNKVGTCVSEGSYPAGTSLSHLDGKPLVPNEKGSVKQETRRH 180

QY 181 PETGLFTLQSELMVTPARGDPRPTFSCSPGLPRHRLARTAPIQPRVWEPVPLEEVOL 240

Db 181 PETGLFTLQSELMVTPARGDPRPTFSCSPGLPRHRLARTAPIQPRVWEPVPLEEVOL 240

QY 241 VVEPEGGAAPGVTTLTCEVPAQPSQIHWKDGVPPLPSPVLILPEIGPODQGTYS 300

Db 241 VVEPEGGAAPGVTTLTCEVPAQPSQIHWKDGVPPLPSPVLILPEIGPODQGTYS 300

QY 301 CVATHSSHGPOESRAVSIIIEPGEETAG 331

Db 301 CVATHSSHGPOESRAVSIIIEPGEETAG 331

Search completed: March 16, 2005, 06:03:30  
Job time : 83 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	338	99.7	340	2	US-08-633-148-2	Sequence 2, Appli	
2	338	99.7	404	4	US-09-949-016-11025	Sequence 11025, A	
3	316	93.2	318	2	US-08-633-148-4	Sequence 4, Appli	
4	316	93.2	332	4	US-09-062-365-1	Sequence 1, Appli	
5	238	70.2	404	4	US-09-638-649-3	Sequence 3, Appli	
6	238	70.2	404	4	US-09-638-648-3	Sequence 3, Appli	
7	216	63.7	405	4	US-08-755-235-4	Sequence 4, Appli	
8	207	61.1	278	2	US-08-432-016-5	Sequence 5, Appli	
9	207	61.1	278	2	US-08-684-594-5	Sequence 5, Appli	
10	30	8.8	30	4	US-09-062-365-5	Sequence 5, Appli	
11	30	8.8	30	4	US-08-948-131-1	Sequence 1, Appli	
12	26	7.7	403	4	US-09-638-649-5	Sequence 5, Appli	
13	26	7.7	403	4	US-09-638-648-5	Sequence 5, Appli	
14	24	7.1	416	4	US-09-638-649-1	Sequence 1, Appli	
15	24	7.1	416	4	US-08-755-235-2	Sequence 2, Appli	
16	24	7.1	416	4	US-09-638-648-1	Sequence 1, Appli	
17	22	6.5	22	2	US-09-062-365-2	Sequence 2, Appli	
18	16	4.7	16	2	US-08-633-148-18	Sequence 18, Appli	
19	15	4.4	15	2	US-08-633-148-12	Sequence 12, Appli	
20	13	3.8	30	4	US-08-948-131-2	Sequence 2, Appli	
21	11	3.2	11	2	US-08-633-148-9	Sequence 9, Appli	
22	11	3.2	11	2	US-08-633-148-15	Sequence 15, Appli	
23	11	3.2	30	4	US-08-948-131-3	Sequence 3, Appli	
24	10	2.9	10	2	US-08-633-148-5	Sequence 5, Appli	
25	10	2.9	10	2	US-08-633-148-7	Sequence 7, Appli	
26	10	2.9	10	2	US-08-633-148-8	Sequence 8, Appli	
27	10	2.9	10	2	US-08-633-148-11	Sequence 11, Appli	

QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNYRVYQI 120  
DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNYRVYQI 120  
QY 121 PKPEIVDSASELTAGVPNKVGTGCVSEGSYPAGTLSHWLDGKPLVPNEKGVSKQTRRH 180  
DB 121 PKPEIVDSASELTAGVPNKVGTGCVSEGSYPAGTLSHWLDGKPLVPNEKGVSKQTRRH 180  
QY 181 PETGLFTLQSELMVTARGDPRFTFSCSPGLPRHRLRTAPIQPRVWPEVPLEEVOL 240  
DB 181 PETGLFTLQSELMVTARGDPRFTFSCSPGLPRHRLRTAPIQPRVWPEVPLEEVOL 240  
QY 241 VVEPEGGAAPGGTVTTLTCEVPAQSPQIHWKMDGVPPLPSPSVLILPEIGPDQGTYS 300  
DB 241 VVEPEGGAAPGGTVTTLTCEVPAQSPQIHWKMDGVPPLPSPSVLILPEIGPDQGTYS 300  
QY 301 CVATHSSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338  
DB 301 CVATHSSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338  
RESULT 2  
US-09-949-016-11025  
; Sequence 11025, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949, 016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11025  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11025  
Query Match 99.7%; Score 338; DB 4; Length 404;  
Best Local Similarity 100.0%; Pred. No. 1.2e-310; Mismatches 0; Indels 0; Gaps 0;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAGTAGAWLVLSLWGA VVGAQNTARIGBPLVLKCKGAPKPPQRLWKLTGRTEA 60  
DB 1 MAAGTAGAWLVLSLWGA VVGAQNTARIGBPLVLKCKGAPKPPQRLWKLTGRTEA 60  
QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNYRVYQI 120  
DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNYRVYQI 120  
QY 121 PKPEIVDSASELTAGVPNKVGTGCVSEGSYPAGTLSHWLDGKPLVPNEKGVSKQTRRH 180  
DB 121 PKPEIVDSASELTAGVPNKVGTGCVSEGSYPAGTLSHWLDGKPLVPNEKGVSKQTRRH 180  
QY 181 PETGLFTLQSELMVTARGDPRFTFSCSPGLPRHRLRTAPIQPRVWPEVPLEEVOL 240  
DB 181 PETGLFTLQSELMVTARGDPRFTFSCSPGLPRHRLRTAPIQPRVWPEVPLEEVOL 240  
QY 241 VVEPEGGAAPGGTVTTLTCEVPAQSPQIHWKMDGVPPLPSPSVLILPEIGPDQGTYS 300  
DB 241 VVEPEGGAAPGGTVTTLTCEVPAQSPQIHWKMDGVPPLPSPSVLILPEIGPDQGTYS 300  
QY 301 CVATHSSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338  
DB 301 CVATHSSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338

DB 301 CVATHSSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338  
RESULT 3  
US-08-633-148-4  
; Sequence 4, Application US/08633148  
; Patent No. 5864018  
; GENERAL INFORMATION:  
; APPLICANT: MORSE, MICHAEL J.  
; APPLICANT: NAGASHIMA, MARIKO  
; APPLICANT: HOLLANDER, DORIS A.  
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
; END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,148  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY ESQ., MATTHEW B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 014618-0056000US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 318 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-633-148-4  
Query Match 93.2%; Score 316; DB 2; Length 318;  
Best Local Similarity 100.0%; Pred. No. 5.4e-290;  
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 23 AQNTARIGEPVLKCKGAPKPPQRLWKLTGRTEAWKLVSPQGGPWSVARVLPNG 82  
DB 1 AQNTARIGEPVLKCKGAPKPPQRLWKLTGRTEAWKLVSPQGGPWSVARVLPNG 60  
QY 83 SLFLPAVGIDEGIFRCQAMNRNGKTKSNYRVYQIPKPEIVDSASELTAGVPNKVG 142  
DB 61 SLFLPAVGIDEGIFRCQAMNRNGKTKSNYRVYQIPKPEIVDSASELTAGVPNKVG 120  
QY 143 TCVSEGSYPAGTLSHWLDGKPLVPNEKGVSKQTRRHPTGLTLOSELMVTARGGDP 202  
DB 121 TCVSEGSYPAGTLSHWLDGKPLVPNEKGVSKQTRRHPTGLTLOSELMVTARGGDP 180  
QY 203 RPTFSCSPGLPRHRLRTAPIQPRVWPEVPLEEVOLVVEPEGGAAPGGTVTTLTCEVP 262  
DB 181 RPTFSCSPGLPRHRLRTAPIQPRVWPEVPLEEVOLVVEPEGGAAPGGTVTTLTCEVP 240  
QY 263 AQSPQIHWKMDGVPPLPSPSVLILPEIGPDQGTYSVCVATHSSHGPOESRAVSISIIIE 322  
DB 241 AQSPQIHWKMDGVPPLPSPSVLILPEIGPDQGTYSVCVATHSSHGPOESRAVSISIIIE 300  
QY 323 PGEPTAGSVGGSL 338  
DB 301 PGEPTAGSVGGSL 316



RESULT 4  
US-09-062-365-1  
; Sequence 1, Application US/09062365  
; Patent No. 6465422  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David  
; APPLICANT: Schmidt, Ann Marie  
; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A  
; TITLE OF INVENTION: SUBJECT  
; FILE REFERENCE: 55424  
; CURRENT APPLICATION NUMBER: US/09/062,365  
; CURRENT FILING DATE: 1998-04-17  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Human  
US-09-062-365-1

Query Match 93.2%; Score 316; DB 4; Length 332;  
Best Local Similarity 100.0%; Pred. No. 5.6e-290;  
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 23 AQNITARIGEPLVKCKGAPKPPQRLKWLKLTGRTEAMKVLSPQGGPMDVARVLPNG 82  
DB 1 AQNITARIGEPLVKCKGAPKPPQRLKWLKLTGRTEAMKVLSPQGGPMDVARVLPNG 60  
QY 83 SLPLPAVGTDGIFRCQAMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPKNVG 142  
DB 61 SLPLPAVGTDGIFRCQAMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPKNVG 120  
QY 143 TCVSEGSYPAGTSLWHLCKPLVPNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDP 202  
DB 121 TCVSEGSYPAGTSLWHLCKPLVPNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDP 180  
QY 203 RTFSCSFSGPLPRHRLATPIQPRVWEPVPLEEVLVVEPGGAVAPGGTTLTCEVP 262  
DB 181 RTFSCSFSGPLPRHRLATPIQPRVWEPVPLEEVLVVEPGGAVAPGGTTLTCEVP 240  
QY 263 AQPSPQIHMWDGVPPLPSPVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIIIE 322  
DB 241 AQPSPQIHMWDGVPPLPSPVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIIIE 300  
QY 323 PGEEGTAGSVGSGSL 338  
DB 301 PGEEGTAGSVGSGSL 316

RESULT 5  
US-09-638-649-3  
; Sequence 3, Application US/09638649  
; Patent No. 6563015  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED  
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND  
; FILE REFERENCE: 0575/62175  
; CURRENT APPLICATION NUMBER: US/09/638,649  
; CURRENT FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Human  
US-09-638-649-3

Query Match 70.2%; Score 238; DB 4; Length 404;  
Best Local Similarity 100.0%; Pred. No. 2.8e-216;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 101 AMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPKNVGTCVSEGSYPAGTSLWHL 160  
DB 101 AMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPKNVGTCVSEGSYPAGTSLWHL 160  
QY 161 GKPLVPNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDPRTFSCSFSGPLPRHRL 220  
DB 161 GKPLVPNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDPRTFSCSFSGPLPRHRL 220  
QY 221 RTAPIQPRVWEPVPLEEVLVVEPGGAVAPGGTTLTCEVPAQSPQIHMWDGVPPL 280  
DB 221 RTAPIQPRVWEPVPLEEVLVVEPGGAVAPGGTTLTCEVPAQSPQIHMWDGVPPL 280  
QY 281 PPSVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIIIEPGEETAGSVGSGSL 338  
DB 281 PPSVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIIIEPGEETAGSVGSGSL 338

RESULT 6  
US-09-638-648-3  
; Sequence 3, Application US/09638648  
; Patent No. 6825164  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Yan, Shi Du  
; APPLICANT: Zlokovic, Berislav  
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID  
; TITLE OF INVENTION: ANGIOPATHY  
; FILE REFERENCE: 0575/62097  
; CURRENT APPLICATION NUMBER: US/09/638,648  
; CURRENT FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Human  
US-09-638-648-3

Query Match 70.2%; Score 238; DB 4; Length 404;  
Best Local Similarity 100.0%; Pred. No. 2.8e-216;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 101 AMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPKNVGTCVSEGSYPAGTSLWHL 160  
DB 101 AMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPKNVGTCVSEGSYPAGTSLWHL 160  
QY 161 GKPLVPNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDPRTFSCSFSGPLPRHRL 220  
DB 161 GKPLVPNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDPRTFSCSFSGPLPRHRL 220  
QY 221 RTAPIQPRVWEPVPLEEVLVVEPGGAVAPGGTTLTCEVPAQSPQIHMWDGVPPL 280  
DB 221 RTAPIQPRVWEPVPLEEVLVVEPGGAVAPGGTTLTCEVPAQSPQIHMWDGVPPL 280  
QY 281 PPSVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIIIEPGEETAGSVGSGSL 338  
DB 281 PPSVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIIIEPGEETAGSVGSGSL 338

RESULT 7  
US-08-755-235-4  
; Sequence 4, Application US/08755235  
; Patent No. 6790443  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Wu, Jun  
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES

FILE REFERENCE: 0575/50159  
CURRENT APPLICATION NUMBER: US/08/755,235  
CURRENT FILING DATE: 1996-11-22  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 4  
LENGTH: 405  
TYPE: PRT  
ORGANISM: Human  
US-08-755-235-4

Query Match 63.7%; Score 216; DB 4; Length 405;  
Best Local Similarity 100.0%; Pred. No. 1.6e-195;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	101	AMNRNGKETKSNRYRVVYQIPGKPEIVDSASELTAGVKNKVTGTCVSGSYPAAGTLSWHL	160
Db	101	AMNRNGKETKSNRYRVVYQIPGKPEIVDSASELTAGVKNKVTGTCVSGSYPAAGTLSWHL	160
QY	161	GKPLVNEKGVSVKQTRRHHPETGLFTLQSELMVTPARGDPRPTFCSPGLPRHRL	220
Db	161	GKPLVNEKGVSVKQTRRHHPETGLFTLQSELMVTPARGDPRPTFCSPGLPRHRL	220
QY	221	RTAPIQPRVWEPVPLEEVQVVEEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL	280
Db	221	RTAPIQPRVWEPVPLEEVQVVEEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL	280
QY	281	PPSPVLLILPEIGPODQGTYSVATHSSHGPOESRAV	316
Db	281	PPSPVLLILPEIGPODQGTYSVATHSSHGPOESRAV	316

RESULT 8  
US-08-432-016-5  
Sequence 5, Application US/08432016  
Patent No. 5968768  
GENERAL INFORMATION:  
APPLICANT: HAYNES, BARTON F.  
APPLICANT: ARUFFO, ALEJANDRO  
APPLICANT: PATEL, DHAVALKUMAR  
APPLICANT: BOWEN, MICHAEL A.  
APPLICANT: MARQUARDT, HANS  
TITLE OF INVENTION: CD6 LIGAND  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,016  
FILING DATE: 01-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/333,350  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/143,903  
FILING DATE: 02-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1579-95  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 278 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-432-016-5

Query Match 61.1%; Score 207; DB 2; Length 278;  
Best Local Similarity 100.0%; Pred. No. 3.5e-187;  
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	101	AMNRNGKETKSNRYRVVYQIPGKPEIVDSASELTAGVKNKVTGTCVSGSYPAAGTLSWHL	160
Db	72	AMNRNGKETKSNRYRVVYQIPGKPEIVDSASELTAGVKNKVTGTCVSGSYPAAGTLSWHL	131
QY	161	GKPLVNEKGVSVKQTRRHHPETGLFTLQSELMVTPARGDPRPTFCSPGLPRHRL	220
Db	132	GKPLVNEKGVSVKQTRRHHPETGLFTLQSELMVTPARGDPRPTFCSPGLPRHRL	191
QY	221	RTAPIQPRVWEPVPLEEVQVVEEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL	280
Db	192	RTAPIQPRVWEPVPLEEVQVVEEGGAVAPGGTTLTCEVPAQPSQIHHMKDGVPLPL	251
QY	281	PPSPVLLILPEIGPODQGTYSVATHSS	307
Db	252	PPSPVLLILPEIGPODQGTYSVATHSS	278

RESULT 9  
US-08-684-594-5  
Sequence 5, Application US/08684594  
Patent No. 5998172  
GENERAL INFORMATION:  
APPLICANT: HAYNES, BARTON F.  
APPLICANT: ARUFFO, ALEJANDRO  
APPLICANT: PATEL, DHAVALKUMAR  
APPLICANT: BOWEN, MICHAEL A.  
APPLICANT: MARQUARDT, HANS  
TITLE OF INVENTION: CD6 LIGAND  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/684,594  
FILING DATE: 18-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,016  
FILING DATE: 01-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/333,350  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/143,903  
FILING DATE: 02-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1579-112  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 278 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-684-594-5

Query Match 61.1%; Score 207; DB 2; Length 278;  
Best Local Similarity 100.0%; Pred. No. 3.5e-187; Indels 0; Gaps 0;  
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 ANNRKGTSTNRYRVRVYIQPKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTILSWHLD 160  
DB 72 ANNRKGTSTNRYRVRVYIQPKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTILSWHLD 131

QY 161 GKPLVNEKGVSKQTRRHPTGLTLOSELMTVPARGDPRPTFSCFSGLPRHRL 220  
DB 132 GKPLVNEKGVSKQTRRHPTGLTLOSELMTVPARGDPRPTFSCFSGLPRHRL 191

QY 221 RTAPIQPRVWEVPLVEEVOLVVEPEGVAVPGTTLTCEVPAQSPQIHHMKDGVPLPL 280  
DB 192 RTAPIQPRVWEVPLVEEVOLVVEPEGVAVPGTTLTCEVPAQSPQIHHMKDGVPLPL 251

QY 281 PPSVLLPEIGPDQGTYSVCVATHSS 307  
DB 252 PPSVLLPEIGPDQGTYSVCVATHSS 278

RESULT 10  
US-09-062-365-5  
; Sequence 5, Application US/09062365  
; Patent No. 6465422  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Stern, David  
; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A  
; FILE REFERENCE: 55424  
; CURRENT APPLICATION NUMBER: US/09/062,365  
; CURRENT FILING DATE: 1998-04-17  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Human  
US-09-062-365-5

Query Match 8.8%; Score 30; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.9e-21; Indels 0; Gaps 0;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLCKGAPKPPQRLWK 52  
DB 1 AQNITARIGEPLVLCKGAPKPPQRLWK 30

RESULT 11  
US-08-948-131-1  
; Sequence 1, Application US/08948131  
; Patent No. 6555651  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David  
; APPLICANT: Yan, Shi Du  
; APPLICANT: Schmidt, Ann Marie  
; TITLE OF INVENTION: Ligand Binding Site of Rage and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham

STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICANT: US/08/948,131  
FILING DATE: 09-OCT-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 53447  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-948-131-1

Query Match 8.8%; Score 30; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.9e-21; Indels 0; Gaps 0;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12  
US-09-638-649-5  
; Sequence 5, Application US/09638649  
; Patent No. 6563015  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED  
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND  
; FILE REFERENCE: 0575/62175  
; CURRENT APPLICATION NUMBER: US/09/638,649  
; CURRENT FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 403  
; TYPE: PRT  
; ORGANISM: Murine  
US-09-638-649-5

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QY 137 VPKVGTCTVSEGSYPAGTILSWHLDGK 162  
DB 136 VPKVGTCTVSEGSYPAGTILSWHLDGK 161

RESULT 13  
US-09-638-648-5  
; Sequence 5, Application US/09638648

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; Patent No. 6825164
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; APPLICANT: Zlokovic, Berislav
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
; TITLE OF INVENTION: ANGIOPATHY
; FILE REFERENCE: 0575/62097
; CURRENT APPLICATION NUMBER: US/09/638,648
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mouse
US-09-638-648-5

Query Match          7.7%; Score 26; DB 4; Length 403;
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 136 VPKNVGTCSVSEGSYPAGTSLSWHLGK 161

RESULT 14
US-09-638-649-1
; Sequence 1, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Bos Taurus
US-09-638-649-1

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Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 247 EVQLVVEPPEGGAVAPGGITVLTCE 270

RESULT 15
US-08-755-235-2
; Sequence 2, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Bovine
US-08-755-235-2

Query Match          7.1%; Score 24; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPPEGGAVAPGGITVLTCE 260
Db 247 EVQLVVEPPEGGAVAPGGITVLTCE 270

Search completed: March 16, 2005, 06:04:32
Job time : 28 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2005, 06:04:08 ; Search time 326 Seconds  
(without alignments)  
343.722 Million cell updates/sec

Title: US-10-091-019-3  
Perfect score: 339  
Sequence: 1 MAAGTAGAWLVLSLWGA.....IIEPGEGETAGVGSGGLV 339

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Gapop 60.0 , Gapext 60.0

Searched: 1401741 seqs, 330541175 residues

Word size : 0 1401741

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

- Database : Published Applications\_AA.\*
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  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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  - 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
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  - 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	339	100.0	339	14	US-10-091-019-3
2	338	99.7	404	15	US-10-309-290-96
3	331	97.6	347	17	US-10-472-507A-2
4	316	93.2	332	9	US-09-872-185B-2
5	316	93.2	332	9	US-09-851-071-1
6	271	79.9	390	15	US-10-309-290-98
7	271	79.9	390	15	US-10-309-290-100
8	216	63.7	405	8	US-08-755-235-4
9	207	61.1	342	16	US-10-408-765A-641
10	112	33.0	112	9	US-09-872-185B-1
11	30	8.8	30	8	US-08-948-131-1
12	30	8.8	30	9	US-09-872-185B-3
13	30	8.8	30	9	US-09-872-185B-7

14	30	8.8	30	9	US-09-851-071-5	Sequence 5, Appli
15	24	7.1	416	8	US-08-755-235-2	Sequence 2, Appli
16	22	6.5	22	9	US-09-851-071-2	Sequence 2, Appli
17	13	3.8	30	8	US-08-948-131-2	Sequence 4, Appli
18	13	3.8	30	9	US-09-872-185B-4	Sequence 4, Appli
19	11	3.2	30	8	US-08-948-131-3	Sequence 3, Appli
20	11	3.2	30	9	US-09-872-185B-5	Sequence 5, Appli
21	10	2.9	10	8	US-08-948-131-5	Sequence 5, Appli
22	10	2.9	10	9	US-09-872-185B-8	Sequence 8, Appli
23	10	2.9	10	9	US-09-851-071-6	Sequence 6, Appli
24	10	2.9	30	8	US-08-948-131-4	Sequence 4, Appli
25	10	2.9	30	9	US-09-872-185B-6	Sequence 6, Appli
26	9	2.7	25	16	US-10-327-598-238	Sequence 238, App
27	9	2.7	25	16	US-10-327-598-241	Sequence 241, App
28	9	2.7	25	16	US-10-327-598-243	Sequence 243, App
29	9	2.7	25	16	US-10-327-598-244	Sequence 244, App
30	9	2.7	89	17	US-10-872-932A-28	Sequence 28, Appl
31	9	2.7	89	17	US-10-872-932A-29	Sequence 29, Appl
32	9	2.7	98	15	US-10-308-817-118	Sequence 118, App
33	9	2.7	98	15	US-10-308-817-119	Sequence 119, App
34	9	2.7	98	15	US-10-308-817-120	Sequence 120, App
35	9	2.7	98	15	US-10-453-698-118	Sequence 118, App
36	9	2.7	98	15	US-10-453-698-119	Sequence 119, App
37	9	2.7	98	15	US-10-453-698-120	Sequence 120, App
38	9	2.7	105	14	US-10-029-386-33917	Sequence 33917, A
39	9	2.7	108	10	US-09-848-798-51	Sequence 51, Appl
40	9	2.7	108	10	US-09-848-798-52	Sequence 52, Appl
41	9	2.7	108	10	US-09-848-798-53	Sequence 53, Appl
42	9	2.7	108	10	US-09-848-798-166	Sequence 166, App
43	9	2.7	112	16	US-10-327-598-809	Sequence 809, App
44	9	2.7	118	16	US-10-327-598-1106	Sequence 1106, App
45	9	2.7	119	15	US-10-291-265-720	Sequence 720, App

ALIGNMENTS

RESULT 1  
US-10-091-019-3  
; Sequence 3, Application US/10091019  
; Publication No. US20030166063A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Robert B.  
; APPLICANT: Shen, Jane M.  
; APPLICANT: Shahbaz, Manouchehr M.  
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins  
; FILE REFERENCE: 41305-270555  
; CURRENT APPLICATION NUMBER: US/10/091,019  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/273,418  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-091-019-3

Query Match	100.0%	Score 339;	DB 14;	Length 339;
Best Local Similarity	100.0%	Pred. No. 3.3e-309;		
Matches 339;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	61	WKVLSPPQGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNRYRVYQI	120	
Db	61	WKVLSPPQGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNRYRVYQI	120	
QY	121	PKPDIIVSASLITAGVPKNVGTCTVSEGSYPAGTISWHLDGKPLVPNEKGVSKVQETRRH	180	

Db 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 180  
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Db 181 PETGLFTLQSELMVTPARGGDPRTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVOL 240  
QY 241 VVEPEGGAVAGGTGVTTLTCEVPAQSPQIHMMKDGVPFLPLPSPVLLPEIGPDQGTYS 300  
Db 241 VVEPEGGAVAGGTGVTTLTCEVPAQSPQIHMMKDGVPFLPLPSPVLLPEIGPDQGTYS 300  
QY 301 CVATHSHGPQESRAVSIISIEPGEETAGSVGGSLV 339  
Db 301 CVATHSHGPQESRAVSIISIEPGEETAGSVGGSLV 339

RESULT 2

US-10-309-290-96  
; Sequence 96, Application US/10309290  
; Publication No. US20040023241A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook II, John P.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Chilikuru, Rajeev A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Gould-Rothberg, Bonnie E.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Jeffers, Michael E.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Li, Li  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Murphey, Ryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Peyman, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Starling, Gary  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Voss, Edward Z.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-502A  
; CURRENT APPLICATION NUMBER: US/10/309,290  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/336,600  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,285  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/341,346  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/341,477  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/341,540  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/342,592  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/344,297  
; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/344,903  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/373,288  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 60/380,981  
; PRIOR FILING DATE: 2002-05-15  
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; NUMBER OF SEQ ID NOS: 274

; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 96  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-290-96  
  
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Best Local Similarity 100.0%; Pred. No. 3.3e-308;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 61 WKVLSPOGGPMDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVYQI 120  
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Db 301 CVATHSHGPQESRAVSIISIEPGEETAGSVGGSL 338

RESULT 3

US-10-472-507A-2  
; Sequence 2, Application US/10472507A  
; Publication No. US20050033017A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamamoto, Hiroshi  
; APPLICANT: Yonekura, Hideto  
; APPLICANT: Yamamoto, Yasuhiko  
; APPLICANT: Sakurai, Shigeru  
; APPLICANT: Watanabe, Takuo  
; TITLE OF INVENTION: Soluble Rage Protein  
; FILE REFERENCE: 026350-089  
; CURRENT APPLICATION NUMBER: US/10/472,507A  
; CURRENT FILING DATE: 2003-09-22  
; PRIOR APPLICATION NUMBER: PCT/JP02,02623  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: JP 2001-78409  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: JP 2001-243114  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: JP 2002-48182  
; PRIOR FILING DATE: 2002-02-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 347  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-472-507A-2

Query Match 97.6%; Score 331; DB 17; Length 347;  
Best Local Similarity 100.0%; Pred. No. 1.1e-301;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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RESULT 4  
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; Patent No. US20020122799A1  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Herold, Kevin  
; APPLICANT: Yan, Shi Du  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Lamster, Ira  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION  
; FILE REFERENCE: 0575/64080  
; CURRENT APPLICATION NUMBER: US/09/872,185B  
; CURRENT FILING DATE: 2001-06-01  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Human  
US-09-872-185B-2

Query Match 93.2%; Score 316; DB 9; Length 332;  
Best Local Similarity 100.0%; Pred. No. 1.2e-287;  
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLCCKGAPKPPQORLEWKLNTGRTEAMKVLSPQGGPWSVARVLPNG 82  
Db 1 AQNITARIGEPLVLCCKGAPKPPQORLEWKLNTGRTEAMKVLSPQGGPWSVARVLPNG 60  
QY 83 SLFLPVGIDEGIFRCQAMNRNGKTKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 142  
Db 61 SLFLPVGIDEGIFRCQAMNRNGKTKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 120  
QY 143 TCVSEGSYPAGTLSWHLDDGKPLVNEKGVSKQETRRHPETGLFTLQSELMTVPARGGDP 202  
Db 121 TCVSEGSYPAGTLSWHLDDGKPLVNEKGVSKQETRRHPETGLFTLQSELMTVPARGGDP 180  
QY 203 RPTFCSPFGLPRHRLRTAPIQPRVWEPVPLEEVOLVVEPEGAVAGGTVTLTCEVP 262  
Db 181 RPTFCSPFGLPRHRLRTAPIQPRVWEPVPLEEVOLVVEPEGAVAGGTVTLTCEVP 240  
QY 263 AQPSQIHHMKDGVPLPSPVLILPEIGPDQGTYS CVATHSSHGPOESRAVSISIIIE 322  
Db 241 AQPSQIHHMKDGVPLPSPVLILPEIGPDQGTYS CVATHSSHGPOESRAVSISIIIE 300  
QY 323 PCEEGPTAGSVGSGSL 338  
Db 301 PCEEGPTAGSVGSGSL 316

RESULT 5  
US-09-851-071-1  
; Sequence 1, Application US/09851071  
; Patent No. US20020177550A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Anne Marie  
; APPLICANT: Stern, David  
; TITLE OF INVENTION: A METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A SUBJECT  
; FILE REFERENCE: 0575/55424-Z/JPW/SHS/MVM  
; CURRENT APPLICATION NUMBER: US/09/851,071  
; CURRENT FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Human  
US-09-851-071-1

Query Match 93.2%; Score 316; DB 9; Length 332;  
Best Local Similarity 100.0%; Pred. No. 1.2e-287;  
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLCCKGAPKPPQORLEWKLNTGRTEAMKVLSPQGGPWSVARVLPNG 82  
Db 1 AQNITARIGEPLVLCCKGAPKPPQORLEWKLNTGRTEAMKVLSPQGGPWSVARVLPNG 60  
QY 83 SLFLPVGIDEGIFRCQAMNRNGKTKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 142  
Db 61 SLFLPVGIDEGIFRCQAMNRNGKTKSNYRVVYQIPGKPEIVDSASELTAGVPNKVG 120  
QY 143 TCVSEGSYPAGTLSWHLDDGKPLVNEKGVSKQETRRHPETGLFTLQSELMTVPARGGDP 202  
Db 121 TCVSEGSYPAGTLSWHLDDGKPLVNEKGVSKQETRRHPETGLFTLQSELMTVPARGGDP 180  
QY 203 RPTFCSPFGLPRHRLRTAPIQPRVWEPVPLEEVOLVVEPEGAVAGGTVTLTCEVP 262  
Db 181 RPTFCSPFGLPRHRLRTAPIQPRVWEPVPLEEVOLVVEPEGAVAGGTVTLTCEVP 240  
QY 263 AQPSQIHHMKDGVPLPSPVLILPEIGPDQGTYS CVATHSSHGPOESRAVSISIIIE 322  
Db 241 AQPSQIHHMKDGVPLPSPVLILPEIGPDQGTYS CVATHSSHGPOESRAVSISIIIE 300  
QY 323 PCEEGPTAGSVGSGSL 338  
Db 301 PCEEGPTAGSVGSGSL 316

RESULT 6  
US-10-309-290-98  
; Sequence 98, Application US/10309290  
; Publication No. US20040023241A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsbrook II, John P.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Chillakuru, Rajeev A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Gould-Rothberg, Bonnie E.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Jeffers, Michael E.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Li, Li  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Murphey, Ryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Peyman, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.



```

; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2001-12-05
; PRIOR FILING DATE: 2001-12-07
; PRIOR FILING DATE: 2001-12-07
; PRIOR FILING DATE: 2001-12-12
; PRIOR FILING DATE: 2001-12-17
; PRIOR FILING DATE: 2001-12-17
; PRIOR FILING DATE: 2001-12-17
; PRIOR FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2001-12-27
; PRIOR FILING DATE: 2001-12-27
; PRIOR FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2002-04-17
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 98
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-98
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Query Match      79.9%; Score 271; DB 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.2e-245;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 GGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIV 127
Db 54 GGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIV 113

Qy 128 DSASELTAGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRHPTGLFT 187
Db 114 DSASELTAGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRHPTGLFT 173

Qy 188 LQSELMVTPARGDPRPTSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVVVEPEGG 247
Db 174 LQSELMVTPARGDPRPTSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVVVEPEGG 233

Qy 248 AVAPGGTTLTCEVPAQPSQIHHMKDGVPLPLPSPVLILPEIGPQDQGYSCVATHSS 307
Db 234 AVAPGGTTLTCEVPAQPSQIHHMKDGVPLPLPSPVLILPEIGPQDQGYSCVATHSS 293

Qy 308 HGPQESRAVSIITIEPGEEGPTAGSVGGSL 338
Db 294 HGPQESRAVSIITIEPGEEGPTAGSVGGSL 324
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## RESULT 7

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US-10-309-290-100
; Sequence 100, Application US/10309290
; Publication No. US20040023241a1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
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; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2001-12-05
; PRIOR FILING DATE: 2001-12-05
; PRIOR FILING DATE: 2001-12-07
; PRIOR FILING DATE: 2001-12-07
; PRIOR FILING DATE: 2001-12-12
; PRIOR FILING DATE: 2001-12-17
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; PRIOR FILING DATE: 2001-12-17
; PRIOR FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2001-12-27
; PRIOR FILING DATE: 2001-12-27
; PRIOR FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2002-04-17
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 100
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-100
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Query Match      79.9%; Score 271; DB 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.2e-245;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 GGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIV 127
Db 54 GGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIV 113

Qy 128 DSASELTAGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRHPTGLFT 187
Db 114 DSASELTAGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRHPTGLFT 173

Qy 188 LQSELMVTPARGDPRPTSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVVVEPEGG 247
Db 174 LQSELMVTPARGDPRPTSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVVVEPEGG 233
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QY 248 AVAPGGTTLTCEVPAQSPQIHHMKDGVPLPLPSPVLILPEIGPDQDGTSCVATHSS 307
Db 234 AVAPGGTTLTCEVPAQSPQIHHMKDGVPLPLPSPVLILPEIGPDQDGTSCVATHSS 293
QY 308 HGPQESRAVSISITIEPGEPTAGSVGGGSL 338
Db 294 HGPQESRAVSISITIEPGEPTAGSVGGGSL 324

RESULT 8
US-08-755-235-4
; Sequence 4, Application US/08755235
; Publication No. US20030059423A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Human
US-08-755-235-4

Query Match 63.7%; Score 216; DB 8; Length 405;
Best Local Similarity 100.0%; Pred. No. 8.7e-194;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 AMNRNGKTSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSEGSYPAGTILSWHLD 160
Db 101 AMNRNGKTSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSEGSYPAGTILSWHLD 160
QY 161 GKPLVNEKGVSKVETRRHPETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRL 220
Db 161 GKPLVNEKGVSKVETRRHPETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRL 220
QY 221 RTAPIQPRVWEVPVLEEVQVWEPEGAVAPGGTTLTCEVPAQSPQIHHMKDGVPLPL 280
Db 221 RTAPIQPRVWEVPVLEEVQVWEPEGAVAPGGTTLTCEVPAQSPQIHHMKDGVPLPL 280
QY 281 PPSVLILPEIGPDQDGTSCVATHSSHGQPSRAV 316
Db 281 PPSVLILPEIGPDQDGTSCVATHSSHGQPSRAV 316

RESULT 9
US-10-408-765A-641
; Sequence 641, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-408-765A-641
Query Match 61.1%; Score 207; DB 16; Length 342;
Best Local Similarity 100.0%; Pred. No. 2.1e-185;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNRYRVYQIPGKPEIV 127
Db 54 GGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNRYRVYQIPGKPEIV 113
QY 128 DSASELTAGVPNKVGTCSVSEGSYPAGTILSWHLDGKPLVNEKGVSKVETRRHPETGLFT 187
Db 114 DSASELTAGVPNKVGTCSVSEGSYPAGTILSWHLDGKPLVNEKGVSKVETRRHPETGLFT 173
QY 188 LQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEVPVLEEVQVWEPEGG 247
Db 174 LQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEVPVLEEVQVWEPEGG 233
QY 248 AVAPGGTTLTCEVPAQSPQIHHMKD 274
Db 234 AVAPGGTTLTCEVPAQSPQIHHMKD 260

RESULT 10
US-09-872-185B-1
; Sequence 1, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Human
US-09-872-185B-1

Query Match 33.0%; Score 112; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 9.4e-97;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVKCKGAPKPPQRLWKLTNGRTEAMKVLSPQGGPWDSVARVLPNG 82
Db 1 AQNITARIGEPLVKCKGAPKPPQRLWKLTNGRTEAMKVLSPQGGPWDSVARVLPNG 60
QY 83 SLFLPAVGIQDEGIFRCQAMNRNGKTSNRYRVYQIPGKPEIVDSASELT 134
Db 61 SLFLPAVGIQDEGIFRCQAMNRNGKTSNRYRVYQIPGKPEIVDSASELT 112

RESULT 11
US-08-948-131-1
; Sequence 1, Application US/08948131
; Publication No. US20010053357A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: Ligand Binding Site of Rage and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
```

; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/948,131  
 ; FILING DATE: 09-OCT-1997  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 53447  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-278-0400  
 ; TELEFAX: 212-391-0526  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 30 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-948-131-1

Query Match 8.8%; Score 30; DB 8; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-20;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52  
 Db 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 12  
 US-09-872-185B-3  
 ; Sequence 3, Application US/09872185B  
 ; Patent No. US20020122799A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stern, David M.  
 ; APPLICANT: Herold, Kewan  
 ; APPLICANT: Yan, Shi Du  
 ; APPLICANT: Schmidt, Anne Marie  
 ; APPLICANT: Lamster, Ira  
 ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION  
 ; FILE REFERENCE: 0575/64080  
 ; CURRENT APPLICATION NUMBER: US/09/872,185B  
 ; CURRENT FILING DATE: 2001-06-01  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 30  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-872-185B-3

Query Match 8.8%; Score 30; DB 9; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-20;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52  
 Db 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 13  
 US-09-872-185B-7  
 ; Sequence 7, Application US/09872185B  
 ; Patent No. US20020122799A1  
 ; GENERAL INFORMATION:

; APPLICANT: Stern, David M.  
 ; APPLICANT: Herold, Kewan  
 ; APPLICANT: Yan, Shi Du  
 ; APPLICANT: Schmidt, Anne Marie  
 ; APPLICANT: Lamster, Ira  
 ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION  
 ; FILE REFERENCE: 0575/64080  
 ; CURRENT APPLICATION NUMBER: US/09/872,185B  
 ; CURRENT FILING DATE: 2001-06-01  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 30  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-872-185B-7

Query Match 8.8%; Score 30; DB 9; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-20;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52  
 Db 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 14  
 US-09-851-071-5  
 ; Sequence 5, Application US/09851071  
 ; Patent No. US2002017550A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmidt, Anne Marie  
 ; APPLICANT: Stern, David  
 ; TITLE OF INVENTION: A METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A SUBJECT  
 ; FILE REFERENCE: 0575/55424-Z/JPW/SHS/MVM  
 ; CURRENT APPLICATION NUMBER: US/09/851,071  
 ; CURRENT FILING DATE: 2001-05-08  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 5  
 ; LENGTH: 30  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-851-071-5

Query Match 8.8%; Score 30; DB 9; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-20;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52  
 Db 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 15  
 US-08-755-235-2  
 ; Sequence 2, Application US/08755235  
 ; Publication No. US20030059423A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stern, David M.  
 ; APPLICANT: Schmidt, Anne Marie  
 ; APPLICANT: Wu, Jun  
 ; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES  
 ; FILE REFERENCE: 0575/50159  
 ; CURRENT APPLICATION NUMBER: US/08/755,235  
 ; CURRENT FILING DATE: 1996-11-22  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 416  
 ; TYPE: PRT  
 ; ORGANISM: Bovine  
 ; US-08-755-235-2

Query Match 7.1%; Score 24; DB 8; Length 416;  
Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPEGGAVAPGGTVLTCE 260  
DB 247 EVQLVVEPEGGAVAPGGTVLTCE 270

Search completed: March 16, 2005, 08:08:47  
Job time : 326 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 16, 2005, 02:39:20 ; Search time 24 Seconds  
(without alignments)  
1359.062 Million cell updates/sec

Title: US-10-091-019-3  
Perfect score: 339  
Sequence: 1 MAAGTAGAWLVLSWGA.....IIIEGEGTAGSGVGSGLV 339

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	26	7.7	402	2	T09062
3	24	7.1	416	1	A42879
4	9	2.7	97	2	S36066
5	9	2.7	98	2	S36063
6	9	2.7	98	2	S36062
7	9	2.7	110	2	S57465
8	9	2.7	112	2	S26655
9	9	2.7	116	2	C27390
10	9	2.7	117	1	LVH2
11	9	2.7	117	2	S04526
12	9	2.7	120	2	S30528
13	9	2.7	136	2	S42610
14	9	2.7	235	2	S25749
15	8	2.4	357	1	K1EBBR
16	8	2.4	359	1	K1EBBT
17	8	2.4	394	2	D70674
18	8	2.4	410	2	T13531
19	8	2.4	549	2	JC5926
20	8	2.4	550	2	G70597
21	8	2.4	599	2	G86204
22	8	2.4	643	2	I50539
23	8	2.4	745	2	TJ5170
24	8	2.4	1012	2	JC5925
25	8	2.4	1089	2	T31583
26	8	2.4	6831	2	A88852
27	8	2.4	6839	2	S57242
28	8	2.4	7160	2	T27935
29	7	2.1	89	2	G96958

30	7	2.1	105	2	E75360
31	7	2.1	106	2	I48862
32	7	2.1	125	2	C72579
33	7	2.1	144	2	S23655
34	7	2.1	182	2	C90141
35	7	2.1	187	2	H87376
36	7	2.1	215	2	T36448
37	7	2.1	223	2	H64065
38	7	2.1	236	2	T35095
39	7	2.1	242	2	AG2283
40	7	2.1	253	2	B83332
41	7	2.1	257	2	G87285
42	7	2.1	258	2	A96013
43	7	2.1	259	2	A87377
44	7	2.1	263	2	S59380
45	7	2.1	267	2	I72882

ALIGNMENTS

RESULT 1

I61596  
advanced glycosylation end-products receptor precursor - human  
N;Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence revision 07-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: I61596; B42879; S27968  
R:Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, H.;  
Genomics 23, 408-419, 1994  
A>Title: Three genes in the human MHC class III region near the junction with the class I  
nterpart of mouse mammary tumor gene int-3.  
A:Reference number: A55562; MUID:95137587; PMID:7835890  
A:Accession: I61596  
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBI  
A:Molecule type: DNA  
A:Residues: 1-404 <RES>  
A:Cross-references: UNIPROT:Q15109; GB:D28769; NID:G561657; PIDN:BAA05958.1; PID:G561659  
R:Neepser, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; Ste  
J. Biol. Chem. 267, 14998-15004, 1992  
A>Title: Cloning and expression of a cell surface receptor for advanced glycosylation en  
A:Reference number: A42879; MUID:92340547; PMID:1378843  
A:Accession: B42879  
A:Molecule type: mRNA  
A:Residues: 'G', '2-99', 'R', '101-404' <NEE>  
A:Cross-references: EMBL:M91211; NID:G190845; PIDN:AAA03574.1; PID:G190846  
A:Experimental source: lung  
A>Note: sequence extracted from NCBI backbone (NCBIP:109438)  
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosy  
cellular function, thus contributing to tissue lesions in diabetes.  
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on r  
ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.  
C:Genetics:  
A:Gene: GDB:AGER  
A:Cross-references: GDB:306354; OMIM:600214  
A:Map position: 6p21.3-6p21.3  
A:Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2  
C:Function:  
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neurit  
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology  
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-404/Product: advanced glycosylation end products receptor #status predicted <MAT>  
F:23-344/Domain: extracellular #status predicted <EXT>  
F:31-101/Domain: immunoglobulin homology <IM1>  
F:137-210/Domain: immunoglobulin homology <IM2>  
F:252-303/Domain: immunoglobulin homology <IM3>  
F:345-362/Domain: transmembrane #status predicted <TMW>  
F:363-404/Domain: intracellular #status predicted <INT>  
F:25, 81/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:38-99, 144-208, 259-301/Disulfide bonds: #status predicted

Query Match 99.7% Score 338 DB 1 Length 404;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGAAGVVLVSLGAVVGAQNTARIGEPVLVCKGAPKPPORLEWKLNTGRTEA 60  
Db 1 MAAGTAGAAGVVLVSLGAVVGAQNTARIGEPVLVCKGAPKPPORLEWKLNTGRTEA 60

QY 61 WKVLSPOGGFWDVSARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120  
Db 61 WKVLSPOGGFWDVSARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120

QY 121 PKRPEIIVDSASELTAGVNPKNVGTVCSEGSYPAGTILSHWLDGKPLVNEKGVSKVQETRRH 180  
Db 121 PKRPEIIVDSASELTAGVNPKNVGTVCSEGSYPAGTILSHWLDGKPLVNEKGVSKVQETRRH 180

QY 181 PETGLFTLQSELMTVPARGDPRPTFSCSPGLPRHRLRTAPIOPRVWEPVLEEVOL 240  
Db 181 PETGLFTLQSELMTVPARGDPRPTFSCSPGLPRHRLRTAPIOPRVWEPVLEEVOL 240

QY 241 VVPEGGAVAPGGTIVLTCEVPAQSPQIHMKDGVPLPLPPSPVLILPEIGPDQGTYS 300  
Db 241 VVPEGGAVAPGGTIVLTCEVPAQSPQIHMKDGVPLPLPPSPVLILPEIGPDQGTYS 300

QY 301 CVATHSHGPOEGRANVSISIEPGERGPTAGSVGGSL 338  
Db 301 CVATHSHGPOEGRANVSISIEPGERGPTAGSVGGSL 338

RESULT 2  
T09062  
Probable advanced glycosylation end-products receptor precursor - mouse  
N;Alternate names: RAGE  
C;Species: Mus musculus (house mouse)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T09062  
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Schmitt, J.; et al. 1997. The RAGE (Receptor for Advanced Glycosylation End-Product) gene encodes a type I transmembrane protein that binds to advanced glycosylation end-products and mediates the effects of amyloid beta peptide on neuronal function. J. Biol. Chem. 272:14987-14997, 1997.  
A;Description: Sequence of the mouse major histocompatibility locus class III region. submitted to the EMBL Data Library, October 1997  
A;Reference number: Z16543  
A;Accession: T09062  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-402 <ROW>  
A;Cross-references: UNIPROT:Q35444; EMBL:AF030001; NID:g2564945; PID:g2564950  
C;Gene: RAGE  
A;Map position: 17  
A;Intons: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2  
C;Superfamily: advanced glycosylation end-products receptor; immunoglobulin homology  
C;Keywords: receptor; transmembrane protein  
F;31-100/Domain: immunoglobulin homology <IMM>

Query Match 7.7%; Score 26; DB 2; Length 402;  
Best Local Similarity 100.0%; Pred. No. 9.4e-18;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKVGTCTVSEGSYPAGTILSHWLDGK 162  
Db 136 VPKVGTCTVSEGSYPAGTILSHWLDGK 161

RESULT 3  
A42879  
Advanced glycosylation end-products receptor precursor - bovine  
N;Alternate names: advanced glycosylation end-product-binding protein, 35K; glycoprotein  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 04-Mar-1993 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: A42879; A42878; S27949  
R;Neepser, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; Schmitt, J.; et al. 1998. Cloning and expression of a cell surface receptor for advanced glycosylation end-products. J. Biol. Chem. 273:14998-15004, 1998.  
A;Title: Cloning and expression of a cell surface receptor for advanced glycosylation end-products. J. Biol. Chem. 273:14998-15004, 1998.  
A;Reference number: A42879; PMID:92340547; PMID:1378843  
A;Accession: A42879

A;Molecule type: mRNA  
A;Residues: 1-416 <NEE>  
A;Cross-references: UNIPROT:Q28173; GB:M91212; NID:gl63650; PIDN:AAA03575.1; PID:gl63651  
A;Experimental source: lung  
A;Note: sequence extracted from NCBI backbone (NCBIP:109436)  
A;Note: parts of this sequence, including the amino end of the mature protein, were determined by Schmidt, A.M.; Viana, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; Hejblum, L.; et al. 1997. Isolation and characterization of two binding proteins for advanced glycosylation end-products. J. Biol. Chem. 272:14987-14997, 1997.  
A;Title: Isolation and characterization of two binding proteins for advanced glycosylation end-products. J. Biol. Chem. 272:14987-14997, 1997.  
A;Reference number: A42878; PMID:92340546; PMID:1321822  
A;Accession: A42878  
A;Molecule type: protein  
A;Residues: 23-24,'X',26-37,'X',39-49,'XX',52-54 <SCH>  
A;Experimental source: endothelial cells  
A;Note: sequence extracted from NCBI backbone (NCBIP:109434)  
C;Comment: Advanced glycosylation end-products are heterogeneous nonenzymatically glycosylated cellular function, thus contributing to tissue lesions in diabetes.  
C;Comment: This receptor appears also to mediate the effects of amyloid beta peptide on neuronal function in the neurotoxic pathway that produces dementia in Alzheimer's disease.  
C;Function:  
A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neurite outgrowth.  
A;Superfamily: advanced glycosylation end-products receptor; immunoglobulin homology  
C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted <M>  
F;23-354/Domain: extracellular #status predicted <EXT>  
F;31-100/Domain: immunoglobulin homology <IM1>  
F;136-209/Domain: immunoglobulin homology <IM2>  
F;262-313/Domain: immunoglobulin homology <IM3>  
F;355-372/Domain: transmembrane #status predicted <TM>  
F;373-416/Domain: intracellular #status predicted <INT>  
F;25.80/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match 7.1%; Score 24; DB 1; Length 416;  
Best Local Similarity 100.0%; Pred. No. 9.8e-16;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPGGAVAPGGTIVLTCE 260  
Db 247 EVQLVVEPGGAVAPGGTIVLTCE 270

RESULT 4  
S36066  
Ig lambda chain - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 01-Dec-1995 #text\_change 09-May-1997  
C;Accession: S36066  
R;Williams, S.C.  
submitted to the EMBL Data Library, April 1993  
A;Reference number: S36046  
A;Accession: S36066  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-97 <WIL>  
A;Cross-references: EMBL:Z22210  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 2.7%; Score 9; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTIVLTTC 259  
Db 14 PGGTIVLTTC 22

RESULT 5  
S36063  
Ig lambda chain - human (fragment)  
C;Species: Homo sapiens (man)



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 16, 2005, 02:46:31 ; Search time 82 Seconds  
(without alignments)  
2117.010 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 339

Sequence: 1 MAAGTAVGAWLVLSLWGA.....IIEPGEGTAGSVGGSLV 339

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338	99.7	404	1	RAGE_HUMAN
2	331	97.6	347	2	Q86SN1
3	131	38.6	147	2	Q71BG7
4	30	8.8	50	2	Q71BB6
5	28	8.3	402	1	RAGE_RAT
6	28	8.3	402	2	Q6WG86
7	26	7.7	402	2	Q35444
8	26	7.7	403	1	RAGE_MOUSE
9	24	7.1	416	1	RAGE_BOVIN
10	21	6.2	119	2	Q6TVZ6
11	21	6.2	161	2	Q6UFY5
12	21	6.2	330	2	Q6QP58
13	19	5.6	23	2	Q6SA79
14	17	5.0	17	2	Q71UQ2
15	16	4.7	82	2	Q9UQR5
16	9	2.7	17	2	Q95794
17	9	2.7	32	2	Q9TRQ1
18	9	2.7	117	1	LV0A_HUMAN
19	9	2.7	219	2	Q880R7
20	9	2.7	246	2	Q9ANU6
21	9	2.7	259	2	Q92171
22	9	2.7	261	2	Q51496
23	9	2.7	270	2	Q93874
24	8	2.4	17	2	Q95795
25	8	2.4	173	2	Q9UFP6
26	8	2.4	220	2	Q9B4G8
27	8	2.4	224	2	Q75613
28	8	2.4	231	2	Q79494
29	8	2.4	231	2	Q7Y9Q9
30	8	2.4	231	2	Q6GNB8
31	8	2.4	233	2	Q6GNH3

32 8 2.4 250 2 Q69XD7  
33 8 2.4 253 2 Q9X5W5  
34 8 2.4 259 2 O52384  
35 8 2.4 259 2 Q9L5D0  
36 8 2.4 272 2 Q9LC88  
37 8 2.4 273 2 Q96KM5  
38 8 2.4 285 2 P78977  
39 8 2.4 299 2 Q6NUK6  
40 8 2.4 338 2 Q63IS8  
41 8 2.4 345 2 Q8WW19  
42 8 2.4 355 2 Q84YW6  
43 8 2.4 357 1 KITH\_BHV16  
44 8 2.4 359 1 KITH\_BHV1Q  
45 8 2.4 359 2 Q65560

#### ALIGNMENTS

RESULT 1  
RAGE\_HUMAN  
ID RAGE\_HUMAN STANDARD; PRT; 404 AA.  
AC Q15109; Q15279; Q9H2X7; Q9V3R3;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE Advanced glycosylation end product-specific receptor precursor  
DE (Receptor for advanced glycosylation end products).  
GN Name=AGER; Synonyms=RAGE;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Lung;  
RX MEDLINE=92340547; PubMed=1378843;  
RA Neepner M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,  
RA Elliston K., Stern D., Shaw A.;  
RT "Cloning and expression of a cell surface receptor for advanced  
RT glycosylation end products of proteins."  
RL J. Biol. Chem. 267:14998-15004(1992).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=95137587; PubMed=7835890;  
RA Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,  
RA Inoko H., Ikemura T.;  
RT "Three genes in the human MHC class III region near the junction with  
RT the class II: gene for receptor of advanced glycosylation end  
RT products, PBX2 homeobox gene and a notch homolog, human counterpart of  
RT mouse mammary tumor gene int-3."  
RL Genomics 23:408-419(1994).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,  
RA Banta A., Spies T., Hood L.;  
RT "Sequence determination of 300 kilobases of the human class III MHC  
RT locus."  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.  
RX Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,  
RA Yamamoto H.;  
RT "Molecular heterogeneity of the receptor for advanced glycation  
RT endproducts."  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RX Malherbe P., Richards J., Gaillard H., Thompson A., Diener C.,  
RA Schuler A., Huber G.;  
RT "cDNA cloning of a novel secreted isoform of the human receptor for  
RT advanced glycation end products (RAGE) and characterization of cells  
RT co-expressing cell-surface scavenger receptors and Swedish mutant

amyloid precursor protein." ;  
 Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 [6]  
 SEQUENCE FROM N.A. (ISOFORM 1).  
 TISSUE=Lung;  
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Ioquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.R., Hulyk S.W.,  
 Valladao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfard G.G.,  
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences." ;  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [7]  
 SEQUENCE OF 1-12 FROM N.A.  
 Hudson B.I., Futers T.S.;  
 "Novel polymorphisms in the receptor for advanced glycation end-  
 products (RAGE) gene." ;  
 Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 CC -I- FUNCTION: Mediates interactions of advanced glycosylation end  
 products (AGE). These are nonenzymatically glycosylated proteins  
 which accumulate in vascular tissue in aging and at an accelerated  
 rate in diabetes. Receptor for amyloid beta peptide.  
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).  
 CC -I- Secreted (isoform 2).  
 CC -I- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q15109-1; Sequence=Displayed;  
 CC Name=2; Synonyms=RAGESEC;  
 CC IsoId=Q15109-2; Sequence=VSP\_002551, VSP\_002552;  
 CC -I- TISSUE SPECIFICITY: Endothelial cells.  
 CC -I- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 -----  
 CC ENBL; M91211; AAA03574.1; -;  
 CC ENBL; D28769; BAA05958.1; -;  
 CC ENBL; U89336; AAB47491.1; -;  
 CC ENBL; AB036432; BAA89369.1; -;  
 CC ENBL; AJ133822; CAB43108.1; -;  
 CC ENBL; BC020669; AAH20669.1; -;  
 CC ENBL; AF208289; AAC35728.1; -;  
 CC FIR; I61596; I61596.  
 CC Genew; HGNC:320; AGER.  
 CC H-InVdb; HIX0005749; -;  
 CC MIM; 600214; -;  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0004888; P:transmembrane receptor activity; TAS.  
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
 CC GO; GO:0006954; P:inflammatory response; TAS.  
 CC InterPro; IPR007110; Ig-like.  
 CC InterPro; IPR003006; Ig MHC.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=22510265; PubMed=12495433; DOI=10.1042/BU20021371;  
RA Yonekura H., Yamamoto Y., Sakurai S., Petrova R.G., Abedin Md.J.,  
RA Li H., Yasui K., Takeuchi M., Makita Z., Takasawa S., Okamoto H.,  
RA Watanabe T., Yamamoto H.;  
RT "Novel splice variants of the receptor for advanced glycation end-  
RT products expressed in human vascular endothelial cells and pericytes,  
RT and their putative roles in diabetes-induced vascular injury.";  
RL Biochem. J. 370:1097-1109(2003).  
DR EMBL; AB061668; BAC65465.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig\_c2.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS00835; IG LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Receptor; Signal.  
FT SIGNAL 1 22  
SQ SEQUENCE 347 AA; 37050 MW; 519E377C4D6AC62C CRC64;  
  
Query Match 97.6%; Score 331; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MAAGTAGAVGLVLSLWGAVGAGQNTARIGELPLVKCKGAPKPPQRLWKLTGRTGA 60  
DB 1 MAAGTAGAVGLVLSLWGAVGAGQNTARIGELPLVKCKGAPKPPQRLWKLTGRTGA 60  
  
QY 61 WKVLSQGGGPDVSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120  
DB 61 WKVLSQGGGPDVSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120  
  
QY 121 PGKPEIVDSASELTAGVKNKVCSEGSYPAGTSLWHLGKPLVNEKGVSKETRRH 180  
DB 121 PGKPEIVDSASELTAGVKNKVCSEGSYPAGTSLWHLGKPLVNEKGVSKETRRH 180  
  
QY 181 PETGLFTLQSELNVTTPARGDPRPTSCSPGLPRHRALRTAPIQPRVWEPVPLEVOL 240  
DB 181 PETGLFTLQSELNVTTPARGDPRPTSCSPGLPRHRALRTAPIQPRVWEPVPLEVOL 240  
  
QY 241 VPEEGAVAPGGTTLTCEVPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300  
DB 241 VPEEGAVAPGGTTLTCEVPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300  
  
QY 301 CVATHSHGPOESRAVSISIIIEGEGPTAG 331  
DB 301 CVATHSHGPOESRAVSISIIIEGEGPTAG 331  
  
RESULT 3  
QY1BG7 PRELIMINARY; PRT; 147 AA.  
AC QY1BG7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Advanced glycosylation end product-specific receptor variant sRAGE2  
DE (Fragment).  
GN Name=AGER;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=22941919; PubMed=14580673; DOI=10.1016/j.bbaexp.2003.08.008;  
RA Schlueter C., Hauke S., Flohr A.M., Rogalla P., Bullerdiek J.;  
RT "Tissue-specific expression patterns of the RAGE receptor and its  
RT soluble forms-a result of regulated alternative splicing?";  
RL Biochim. Biophys. Acta 1630:1-6(2003).  
DR EMBL; AF536237; AAQ10686.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00409; Ig; 1.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Receptor.  
FT NON\_TER 1 1  
SQ SEQUENCE 147 AA; 15676 MW; F4D9D530B2EAC934 CRC64;  
  
Query Match 38.6%; Score 131; DB 2; Length 147;  
Best Local Similarity 100.0%; Pred. No. 5.3e-125;  
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 201 DPRPTFSCSPGLPRHRALRTAPIQPRVWEPVPLEVOLVPEEGAVAPGGTTLTCE 260  
DB 1 DPRPTFSCSPGLPRHRALRTAPIQPRVWEPVPLEVOLVPEEGAVAPGGTTLTCE 60  
  
QY 261 VPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYSVCVATHSHGPOESRAVSIS 320  
DB 61 VPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYSVCVATHSHGPOESRAVSIS 120  
  
QY 321 IEPGEGPTAG 331  
DB 121 IEPGEGPTAG 131  
  
RESULT 4  
QY1BB6 PRELIMINARY; PRT; 50 AA.  
ID QY1BB6;  
AC QY1BB6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Advanced glycosylation end product-specific receptor RAGE3 (Advanced  
DE glycosylation end product-specific receptor variant sRAGE1)  
DE (Fragment).  
GN Name=AGER;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast cancer;  
RX MEDLINE=22941919; PubMed=14580673; DOI=10.1016/j.bbaexp.2003.08.008;  
RA Schlueter C., Hauke S., Flohr A.M., Rogalla P., Bullerdiek J.;  
RT "Tissue-specific expression patterns of the RAGE receptor and its  
RT soluble forms-a result of regulated alternative splicing?";  
RL Biochim. Biophys. Acta 1630:1-6(2003).  
DR EMBL; AF537303; AAQ10782.1; -.  
DR EMBL; AF536236; AAQ10685.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 1 1  
SQ SEQUENCE 50 AA; 5708 MW; 71A023326D84AD9C CRC64;  
  
Query Match 8.8%; Score 30; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.9e-22;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 201 DPRPTFSCSPGLPRHRALRTAPIQPRVW 230  
|||||

Db 1 DRRFTSCSPGLPRHRLRTAFIQPRVW 30

RESULT 5  
RAGE RAT

ID \_RAGE\_RAT STANDARD; PRT; 402 AA.

AC Q63495;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Advanced glycosylation end product-specific receptor precursor  
DE (Receptor for advanced glycosylation end products).  
GN Name=Ager; Synonyms=RAGE;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Lung;  
RX MEDLINE=97368045; PubMed=9224812;  
RA Renard C., Chappoy O., Wautier M.P., Nagashima M., Lundh E.,  
RA Morser J., Zhao L., Schmidt A.M., Scherzmann J.M., Wautier J.L.;  
RT "Recombinant advanced glycation end product receptor pharmacokinetics  
in normal and diabetic rats.";  
RL Mol. Pharmacol. 52:54-62(1997).  
CC -!- FUNCTION: Mediates interactions of advanced glycosylation end  
CC products (AGE). These are nonenzymatically glycosylated proteins  
CC which accumulate in vascular tissue in aging and at an accelerated  
CC rate in diabetes.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Endothelial cells.  
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

-----  
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-----

EMBL; L33413; AAA2027.1; -;  
RSD; 69258; Ager.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR Pfam; PF00047; ig\_3.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Glycoprotein; Immunoglobulin domain; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 22 Potential.  
FT CHAIN 23 402 Advanced glycosylation end product-specific receptor.  
FT FT Extracellular (Potential).  
FT DOMAIN 23 341 Potential.  
FT TRANSMEM 342 362 Potential.  
FT DOMAIN 363 402 Cytoplasmic (Potential).  
FT DOMAIN 23 109 Ig-like V-type.  
FT DOMAIN 123 219 Ig-like C2-type 1.  
FT DOMAIN 233 315 Ig-like C2-type 2.  
FT DISULFID 38 98 Potential.  
FT DISULFID 143 206 Potential.  
FT DISULFID 257 299 Potential.  
FT CARBOHYD 25 25 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 402 AA; 42663 MW; 59448BC3A51E94E CRC64;

Query Match 8.3%; Score 28; DB 1; Length 402;  
Best Local Similarity 100.0%; Pred. No. 2e-19;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKVGTCTVSEGSYPAGTSLWHLDGKPL 164  
|||||  
Db 136 VPKVGTCTVSEGSYPAGTSLWHLDGKPL 163  
|||||

RESULT 6  
Q6MG86

ID Q6MG86 PRELIMINARY; PRT; 402 AA.  
AC Q6MG86;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Advanced glycosylation end product-specific receptor.  
GN Name=Ager;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Brown Norway;  
RX PubMed=15060004; DOI=10.1101/gr.1987704;  
RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shina T.,  
RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;  
RT "The genomic sequence and comparative analysis of the rat major  
RT histocompatibility complex.";  
RL Genome Res. 14:631-639(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Brown Norway;  
RA Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosiura A.,  
RA Lang N., Lehrach S., Thiel J., Sontag M., Hurt P., Himmelbauer H.,  
RA Sudbrak R., Reinhardt R.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; EX833044; CAE83960.1; -;  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; ig\_3;  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00408; IGC2; 2.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Receptor.  
SQ SEQUENCE 402 AA; 42644 MW; CEA49453C05E1CA1 CRC64;

Query Match 8.3%; Score 28; DB 2; Length 402;  
Best Local Similarity 100.0%; Pred. No. 2e-19;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKVGTCTVSEGSYPAGTSLWHLDGKPL 164  
|||||  
Db 136 VPKVGTCTVSEGSYPAGTSLWHLDGKPL 163  
|||||

RESULT 7  
O35444

ID O35444 PRELIMINARY; PRT; 402 AA.  
AC O35444;  
DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE RAGE (Advanced glycosylation end product-specific receptor).  
GN Name=RAGE; Synonyms=Ager;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=14656967; DOI=10.1101/gr.1736803;

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OM protein - protein search, using sw model

Run on: March 15, 2005, 09:02:00 ; Search time 79 Seconds  
(without alignments)  
1659.643 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 1806

Sequence: 1 MAAGTAGVAGNVLVLSWGA.....IIEPGEETAGSVGGSLV 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1806	100.0	339	5	AB882164 Human sol
2	1802	99.8	340	2	AAW44199 Human sol
3	1802	99.8	340	2	AAW33753 Human RAG
4	1802	99.8	391	8	ADP19666 Human LP2
5	1802	99.8	402	7	ADP95564 Human NOV
6	1802	99.8	404	4	AA881925 Extracorp
7	1802	99.8	404	5	ABP65011 Human pro
8	1802	99.8	404	8	ADF31292 Human rec
9	1802	99.8	404	8	ADF42983 Human rec
10	1802	99.8	404	8	ADK00129 Human RAG
11	1797	99.5	339	5	AAW48746 Human sRA
12	1797	99.5	404	5	AAW48745 Human RAG
13	1796	99.4	381	8	ADSI0986 Human the
14	1793	99.3	404	5	AAU77543 Human rec
15	1793	99.3	404	5	AAE23219 Human rec
16	1793	99.3	404	7	AAE39510 Human RAG
17	1793	99.3	404	7	ADG32004 Human hom
18	1784	98.8	420	5	ABP65012 Human pro
19	1784	98.8	425	8	ADP19660 Human LP2
20	1784	98.8	585	8	ADK00127 Human RAG
21	1768	97.9	347	7	AB882298 Human sol
22	1768	97.9	347	7	ADG37044 Receptor
23	1768	97.9	352	8	ADP19656 Human LP2
24	1750	96.9	368	8	ADP19662 Human LP2
25	1709	94.6	390	7	ADP95568 Human NOV

26	1709	94.6	390	8	ADP19670 Human LP2
27	1709	94.6	421	6	ABR43188 Human REM
28	1705	94.4	390	7	ADP95566 Human NOV
29	1690	93.6	318	2	AAW44200 Human mat
30	1690	93.6	318	2	AAW33754 Human RAG
31	1687	93.4	332	3	AAW52130 Human Rec
32	1482.5	82.1	360	8	ADP19664 Human LP2
33	1480	81.9	416	5	AAU77542 Bovine re
34	1480	81.9	416	5	AAE23218 Cow recep
35	1480	81.9	416	7	AAE39509 Bovine RA
36	1480	81.9	416	7	ADG32003 Cow lung-
37	1466	81.2	298	8	ADP19658 Human LP2
38	1466	81.2	325	8	ADM80782 Human CAD
39	1404.5	77.8	343	8	ADK00124 Murine so
40	1404.5	77.8	403	5	AAU77544 Murine re
41	1404.5	77.8	403	5	AAE23220 Mouse rec
42	1404.5	77.8	403	7	AAE39511 Murine RA
43	1379.5	76.4	342	7	ADJ68835 Human hea
44	1229	68.1	250	6	ABR43202 Human REM
45	633	35.0	128	6	ABR43201 Human REM

ALIGNMENTS

RESULT 1

AB882164

ID AB882164 standard; protein; 339 AA.

XX AC AB882164;

XX DT 23-DEC-2002 (first entry)

XX DE Human soluble RAGE (sRAGE).

XX KW Receptor for Advanced Glycated end product; RAGE; recombinant; nontropic;

KW antihyperosclerotic; antidiabetic; cytostatic; nephrotropic; vasotropic;

KW neuroprotective; antiinflammatory; gene therapy; human.

XX OS Homo sapiens.

XX PN WO200270667-A2.

XX PD 12-SEP-2002.

XX PF 05-MAR-2002; 2002WO-US0066881.

XX PR 05-MAR-2001; 2001US-0273418P.

XX PA (TRAN-) TRANSTECH PHARMA INC.

XX PI Harris R, Shen J, Shabbaz M;

XX DR WPI; 2002-713443/77.

XX DR N-PSDB; ABQ79956.

XX High level expression of recombinant Receptors for Advanced Glycated end

PT products (RAGE) proteins for treating increased levels of advanced

PT glycosylation end products, comprises infecting cells with a high titer

PT recombinant virus.

XX Example; Fig 2B; 51pp; English.

XX The invention relates to a method for high level expression of

CC recombinant forms of the Receptor for Advanced Glycated end products

CC (RAGE) or its fragments. The method involves (i) subcloning a nucleotide

CC sequence encoding RAGE or its fragment into a virus; (ii) preparing a

CC high titer stock of recombinant virus; and (iii) infecting host cells

CC with the high titer recombinant virus under conditions such that

CC predetermined levels of RAGE or its fragment is produced, where the

CC predetermined levels of RAGE comprises at least 25 mg recombinant protein

CC per liter of culture. The method is useful for high level expression of

CC recombinant RAGE polypeptide or its fragment which may be useful in

CC preventing, treating or ameliorating diseases associated with increased  
 CC levels of advanced glycosylation end products, such as atherosclerosis,  
 CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's  
 CC disease, inflammation, systemic lupus nephritis, inflammatory lupus  
 CC nephritis, cancer or erectile dysfunction. The present sequence  
 CC represents the amino acid sequence of human sRAGE (soluble, extracellular  
 CC portion of RAGE)  
 XX  
 SQ Sequence 339 AA;

Query Match 100.0%; Score 1806; DB 5; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-127;  
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGTAVGAWVLVLSLWGAVVGAQNITARIIGELVKCKGAPKPPQPLEWKLNTGTEA 60  
 DB 1 MAAGTAVGAWVLVLSLWGAVVGAQNITARIIGELVKCKGAPKPPQPLEWKLNTGTEA 60  
 QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVYQI 120  
 DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVYQI 120  
 QY 121 PKGPEIVDSASLTAGVKNKVTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKVKEQTRRH 180  
 DB 121 PKGPEIVDSASLTAGVKNKVTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKVKEQTRRH 180  
 QY 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240  
 DB 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240  
 QY 241 VVEPEGGAAPGGTTLTCEVPAQPSQIHHMKDGVLPPLPPSVLILPIGPDQGTYS 300  
 DB 241 VVEPEGGAAPGGTTLTCEVPAQPSQIHHMKDGVLPPLPPSVLILPIGPDQGTYS 300  
 QY 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSLV 339  
 DB 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSLV 339

RESULT 2  
 AAW44199  
 ID AAW44199 standard; protein; 340 AA.  
 AC AAW44199;  
 XX  
 XX  
 DT 14-MAY-1998 (first entry)  
 XX  
 DE Human soluble receptor to an advanced glycosylation end product.  
 XX  
 KW Human; soluble receptor; advanced glycosylation end product; RAGE; AGE;  
 KW antibody; vascular permeability; diabetes mellitus.  
 XX  
 OS Homo sapiens.  
 XX  
 EN WO9739125-A1.  
 XX  
 XX 23-OCT-1997.  
 XX  
 XX 11-APR-1997; 97WO-EP001834.  
 XX  
 XX 16-APR-1996; 96US-00633148.  
 XX  
 XX (SCHD ) SCHERING PATENTE AG.  
 XX  
 XX Morser MJ, Nagashima M, Hollander DA;  
 XX  
 XX WPI; 1997-558580/51.  
 XX  
 XX N-PSDB; AAV12394.  
 XX

Anti-advanced glycosylation end product polypeptide antibody - prevents  
 PT receptor binding and therefore reduces vascular permeability, useful to  
 PT treat diabetes mellitus.  
 XX  
 XX

PS  
 XX

Claim 2; Page 40-41; 90pp; English.

CC The present sequence represents a soluble human receptor to an advanced  
 CC glycosylation end product (RAGE) polypeptide. The present invention  
 CC describes an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are non-  
 CC enzymatically glycosylated proteins, which accumulate in vascular tissue  
 CC in ageing, and at an accelerated rate in individuals with diabetes. The  
 CC Ab, which prevents the interaction between an AGE and it's receptor  
 CC (RAGE), reduces vascular permeability. The Ab can be used to treat  
 CC diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular  
 CC disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated  
 CC amyloidosis or atherosclerosis. The Ab can also be used for the isolation  
 CC and purification of human RAGE polypeptide  
 XX  
 SQ Sequence 340 AA;

Query Match 99.8%; Score 1802; DB 2; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-127;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGTAVGAWVLVLSLWGAVVGAQNITARIIGELVKCKGAPKPPORLEWKLNTGTEA 60  
 DB 1 MAAGTAVGAWVLVLSLWGAVVGAQNITARIIGELVKCKGAPKPPORLEWKLNTGTEA 60  
 QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVYQI 120  
 DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVYQI 120  
 QY 121 PKGPEIVDSASLTAGVKNKVTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKVKEQTRRH 180  
 DB 121 PKGPEIVDSASLTAGVKNKVTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKVKEQTRRH 180  
 QY 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240  
 DB 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240  
 QY 241 VVEPEGGAAPGGTTLTCEVPAQPSQIHHMKDGVLPPLPPSVLILPIGPDQGTYS 300  
 DB 241 VVEPEGGAAPGGTTLTCEVPAQPSQIHHMKDGVLPPLPPSVLILPIGPDQGTYS 300  
 QY 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSL 338  
 DB 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSL 338

RESULT 3  
 AAW33753  
 ID AAW33753 standard; protein; 340 AA.  
 AC AAW33753;  
 XX  
 XX  
 DT 08-MAY-1998 (first entry)  
 XX  
 DE Human RAGE polypeptide (340 amino acid residues).  
 XX  
 KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
 KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 EN WO9739121-A1.  
 XX  
 XX 23-OCT-1997.  
 XX  
 XX 11-APR-1997; 97WO-EP001832.  
 XX  
 XX 16-APR-1996; 96US-00633147.  
 XX  
 XX (SCHD ) SCHERING AG.  
 XX  
 XX Morser MJ, Nagashima M;

XX WPI; 1997-526458/48.  
 DR N-PSDB; AAV06517.  
 XX  
 PT New soluble advanced glycosylation end-product receptor polypeptide -  
 PT used for reducing vascular permeability, complications of diabetes etc.,  
 PT also for purification and to screen for modulators.  
 XX  
 PS Claim 3; Fig 1A; 91pp; English.  
 XX  
 CC This is a human advanced glycosylation end-product receptor (RAGE)  
 CC polypeptide (340 amino acid residues). The RAGE polypeptides and its  
 CC active fragments or their mimetics, inhibit interaction between advanced  
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
 CC are used to treat diseases associated with AGE/RAGE interaction, such as  
 CC increased vascular permeability, diabetes mellitus (particularly  
 CC complications such as micro- or macro- vasculopathy or occlusive vascular  
 CC disorders such as neuropathy, nephropathy, retinopathy or  
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation  
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
 CC age-related disorders such as oxidative stress. These RAGE polypeptides  
 CC are also used, when immobilised, to purify AGE from a protein mixture and  
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
 CC interaction. They can also be used diagnostically to detect abnormal  
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
 CC interaction between AGE and RAGE or other receptors and for purification  
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
 CC used to express recombinant RAGE and as probes for isolating related  
 CC genes  
 XX  
 SQ Sequence 340 AA;

Query Match 99.8%; Score 1802; DB 2; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 2,7e-127;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGAQVGAQNTARIGBPLVLKCKGAPKPPQRLWKLTGRTEA 60  
 DB 1 MAAGTAVGAWLVLSLWGAQVGAQNTARIGBPLVLKCKGAPKPPQRLWKLTGRTEA 60  
 QY 61 WKVLSFQGGPPWDSVARVLPNGSLFLPAVGIQDEGIFRCQNNRNGKETKSNRYRVVQI 120  
 DB 61 WKVLSFQGGPPWDSVARVLPNGSLFLPAVGIQDEGIFRCQNNRNGKETKSNRYRVVQI 120  
 QY 121 PKGPEIVDSASELTAGVPNKVGTCSGSPYAGTILSWHLDGKPLVNEKGVSKQTRRH 180  
 DB 121 PKGPEIVDSASELTAGVPNKVGTCSGSPYAGTILSWHLDGKPLVNEKGVSKQTRRH 180  
 QY 181 PETGLFTLQSELMTVPARGGDPRTTFCFSFGLPRHRLRTAPIQPRVWEPVPLEEVQL 240  
 DB 181 PETGLFTLQSELMTVPARGGDPRTTFCFSFGLPRHRLRTAPIQPRVWEPVPLEEVQL 240  
 QY 241 VVEPEGGAVAPGCTVTLTCEVPAQSPQIHWKMDGVPPLPSPVLLPEIGPQDGTYIS 300  
 DB 241 VVEPEGGAVAPGCTVTLTCEVPAQSPQIHWKMDGVPPLPSPVLLPEIGPQDGTYIS 300  
 QY 301 CVATHSSHGPQBSRAVSIISIBPREGPTAGSVGGSL 338  
 DB 301 CVATHSSHGPQBSRAVSIISIBPREGPTAGSVGGSL 338

RESULT 4  
 ADP19666  
 ID ADP19666 standard; protein; 391 AA.  
 XX  
 AC ADP19666;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human LP2005 protein SEQ ID NO:12.  
 XX  
 KW human; LP2005; antidiabetic; neuroprotective; nootropic;

KW antinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;  
 KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;  
 KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
 KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
 KW systemic lupus erythematosus.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..23  
 FT Protein /label= signal  
 FT 24..391  
 FT /label= LP2005  
 XX  
 PN WO2004044126-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 PF 05-NOV-2003; 2003WO-US032734.  
 XX  
 PR 14-NOV-2002; 2002US-0426253P.  
 XX  
 PA (ELIL) LILLY & CO ELI.  
 XX  
 PI Na S, Perkins DR;  
 XX  
 DR WPI; 2004-411705/38.  
 DR N-PSDB; ADP19665.  
 XX  
 PT New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or  
 PT LP2003) for diagnosing or treating disorders associated with aberrant  
 PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome  
 PT identification.  
 XX  
 PS Claim 9; SEQ ID NO 12; 111pp; English.  
 XX  
 CC The present sequence represents human LP2005, which is used in the  
 CC exemplification of the present invention. The present invention  
 CC describes: (1) an isolated nucleic acid (I) comprising DNA having at  
 CC least 95% sequence identity to a polynucleotide selected from the group  
 CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown  
 CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a  
 CC polypeptide or mature form of a polypeptide having the amino acid  
 CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide  
 CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide  
 CC having a nucleotide sequence which is complementary to the nucleotide  
 CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector  
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an  
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method  
 CC and comprising an amino acid sequence comprising about 95% sequence  
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,  
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric  
 CC molecule comprising an LP polypeptide fused to a heterologous amino acid  
 CC sequence; (7) an antibody which specifically binds to an LP polypeptide  
 CC described above; (8) a composition (C) comprising a therapeutic amount of  
 CC an active agent selected from an LP polypeptide, an agonist to an LP  
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide  
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a  
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)  
 CC diagnosing or treating a mammal suffering from a disease, condition or  
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has  
 CC antidiabetic, neuroprotective, nootropic, antiinflammatory,  
 CC antirheumatic, antiarthritic, vulnery, cytostatic, immunosuppressive,  
 CC nephrotropic and dermatological activities, and can be used in gene  
 CC therapy. The compositions (C) and methods are useful for diagnosing or  
 CC treating disorders associated with aberrant levels of an LP polypeptide,  
 CC such as diabetes and its complications, Alzheimer's disease,  
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple  
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
 CC may also be used for chromosome identification. The LP polypeptide can  
 CC also be used in manufacturing a medicament for the treatment of the above  
 CC mentioned diseases, conditions or disorders associated with aberrant  
 CC levels of the LP polypeptide.

```

XX SQ Sequence 391 AA;
Query Match          99.8%; Score 1802; DB 8; Length 391;
Best Local Similarity 100.0%; Pred. No. 3.2e-127;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGVAGWVLVLSLWGA VVGAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTGA 60
Dd 1 MAAGTAGVAGWVLVLSLWGA VVGAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTGA 60

QY 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120
Dd 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120

QY 121 PKKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRH 180
Dd 121 PKKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRH 180

QY 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWPEVPLEEVOL 240
Dd 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWPEVPLEEVOL 240

QY 301 CVATHSHGPOESRAVSISIIPEGEGPTAGSVGGSL 338
Dd 301 CVATHSHGPOESRAVSISIIPEGEGPTAGSVGGSL 338

RESULT 5
ADE95564
ID ADE95564 standard; protein; 402 AA.
XX AC ADE95564;
XX DT 12-FEB-2004 (first entry)
XX DE Human NOVX16c protein.
XX KW NOVX protein; biochemical stimulation; physiological stimulation;
KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;
KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
KW notropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;
KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
KW depression; allergy; fertility disorder; NOVX16c.
XX OS Homo sapiens.
XX PN WO2003050245-A2.
XX PD 19-JUN-2003.
XX PF 03-DEC-2002; 2002WO-US038594.
XX PR 05-DEC-2001; 2001US-0336600P.
PR 07-DEC-2001; 2001US-0338285P.
PR 12-DEC-2001; 2001US-0341346P.
PR 17-DEC-2001; 2001US-0341477P.
PR 17-DEC-2001; 2001US-0341540P.
PR 20-DEC-2001; 2001US-0342592P.
PR 27-DEC-2001; 2001US-034297P.
PR 31-DEC-2001; 2001US-0344903P.
PR 17-APR-2002; 2002US-0373288P.
PR 15-MAY-2002; 2002US-0380981P.
PR 17-MAY-2002; 2002US-0381495P.

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PR 28-MAY-2002; 2002US-0383534P.
PR 28-MAY-2002; 2002US-0383744P.
PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-0384024P.
PR 07-AUG-2002; 2002US-0401788P.
PR 26-AUG-2002; 2002US-040353P.
PR 31-OCT-2002; 2002US-04041788.
PR 02-DEC-2002; 2002US-04046353.
XX (CURA-) CURAGEN CORP.
XX PA
XX PI Alsbrook JP, Anderson DW, Boldog FH, Burgess CE, Chillakuru RA;
PI Bainger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
PI Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphy R;
PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;
PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
XX WPI; 2003-513974/48.
XX DR N-PSDB; ADE95563.
XX PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX PS Claim 2; SEQ ID NO 96; 211pp; English.
XX CC This invention relates to novel NOVX proteins, and the DNA sequence which
CC encode them, having properties related to stimulation of biochemical or
CC physiological responses in a cell, a tissue, an organ or an organism.
CC Compounds which modulate the proteins of the invention may have cardiant,
CC antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,
CC antiarthritic, antidiabetic, nephrotropic, dermatological,
CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
CC notropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
CC antidepressant, antiallergic or gynaecological activities. The DNA
CC sequences of the invention may be useful for gene therapy whilst the
CC protein sequences may allow the development of a vaccine. The protein is
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease. The invention may be useful in
CC diagnosing, treating or preventing NOVX-associated disorders, for example
CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
CC fertility disorders. The nucleic acids may further be used as
CC hybridisation probes, in chromosome mapping, tissue typing, preventive
CC medicine, and pharmacogenomics. The present sequence is the amino acid
CC sequence of the human NOVX16c protein of the invention.
XX SQ Sequence 402 AA;
Query Match          99.8%; Score 1802; DB 7; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.3e-127;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGVAGWVLVLSLWGA VVGAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTGA 60
Dd 1 MAAGTAGVAGWVLVLSLWGA VVGAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTGA 60

QY 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120
Dd 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120

QY 121 PKKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRH 180
Dd 121 PKKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRH 180

QY 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWPEVPLEEVOL 240
Dd 181 PETGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWPEVPLEEVOL 240

QY 241 VVEPEGGA VAGGTVTLTCEVPAQPSQIHWMDGVLPLPFPSPVLILPEIGPDQGTYS 300

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Db 241 VVEPEGAVAPGVTTLTCEVPAQSPQIHHMKDGVPLPLPSPVLILPEIGPDQGTYS 300  
 QY 301 CVATHSSHGPQBSRAVSISIIIPGEGPTAGSVGGSGL 338  
 Db 301 CVATHSSHGPQBSRAVSISIIIPGEGPTAGSVGGSGL 338  
 RESULT 6  
 AAB81925  
 ID AAB81925 standard; protein; 404 AA.  
 XX AAB81925;  
 DT 15-JUN-2001 (first entry)  
 XX Extracorporeal circulation material receptor protein.  
 DE Extracorporeal circulation; carbonyl stress product; receptor; diabetes;  
 KW vascular lesion; excretory dysfunction.  
 XX Unidentified.  
 OS  
 XX  
 PN WO200118060-A1.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 08-SEP-2000; 2000WO-JP006172.  
 XX  
 PR 08-SEP-1999; 99JP-00254463.  
 XX  
 PA (TORA ) TORAY IND INC.  
 PI Shimizu S, Kubota M, Akiyama H, Usui M;  
 XX WPI; 2001-290314/30.  
 DR  
 XX Material for extracorporeal circulation, applicable in selective  
 PT elimination of diabetic complication factors such as carbonyl stress  
 PT products caused by abnormally promoted carbonyl stress from excretory  
 PT dysfunction in vascular lesions.  
 XX  
 PS Claim 1; Page 31-32; 36pp; Japanese.  
 XX  
 CC The present invention describes a material for extracorporeal circulation  
 CC which is made from a water-insoluble carrier immobilized with a protein  
 CC having the sequence shown here. The materials of the invention, including  
 CC adsorbents, are for extracorporeal circulation, which are applicable in  
 CC the selective elimination of diabetic complication factors from a body  
 CC fluid, and are therefore useful in treating vascular lesions like  
 CC arteriosclerosis due to carbonyl stress products caused by abnormally  
 CC promoted carbonyl stress from excretory dysfunction  
 CC  
 SQ Sequence 404 AA;  
 Query Match 99.8%; Score 1802; DB 4; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-127;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60  
 Db 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60  
 QY 61 WKVLSPQGGPNDVSVARVLPNGSLFLPVGIODEGIFRCQAMNRNGKTSNRYRVYQI 120  
 Db 61 WKVLSPQGGPNDVSVARVLPNGSLFLPVGIODEGIFRCQAMNRNGKTSNRYRVYQI 120  
 QY 121 PGKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTILSHWLDGKPLVNEKGVSKQETRRH 180  
 Db 121 PGKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTILSHWLDGKPLVNEKGVSKQETRRH 180  
 QY 181 PETGLFTLQSELMVTPARGDPRPTSCFSGLPRHRLRTAPIQPRVWVEPVLEEVQL 240

Db 181 PETGLFTLQSELMVTPARGDPRPTSCFSGLPRHRLRTAPIQPRVWVEPVLEEVQL 240  
 QY 241 VVEPEGAVAPGVTTLTCEVPAQSPQIHHMKDGVPLPLPSPVLILPEIGPDQGTYS 300  
 Db 241 VVEPEGAVAPGVTTLTCEVPAQSPQIHHMKDGVPLPLPSPVLILPEIGPDQGTYS 300  
 QY 301 CVATHSSHGPQBSRAVSISIIIPGEGPTAGSVGGSGL 338  
 Db 301 CVATHSSHGPQBSRAVSISIIIPGEGPTAGSVGGSGL 338  
 RESULT 7  
 AAB65011  
 ID AAB65011 standard; protein; 404 AA.  
 XX AAB65011;  
 DT 25-FEB-2003. (first entry)  
 XX Human protein SEQ ID 671.  
 DE  
 XX Human; expressed sequence tag; EST; haematopoietic disorder;  
 KW central nervous system disease; viral infection;  
 KW peripheral nervous system disease; non-healing wound; infectious disease;  
 KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;  
 KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;  
 KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;  
 KW cytostatic; haemostatic; virucide; antibacterial; fungicide;  
 KW immunostimulant; cerebroprotective.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200259260-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 16-NOV-2001; 2001WO-US042950.  
 XX  
 PR 17-NOV-2000; 2000US-00714936.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;  
 PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
 XX WPI; 2002-590824/63.  
 DR N-PSDB; ABQ99597.  
 XX  
 PT New isolated polynucleotide, useful in research, diagnostic or  
 PT therapeutic methods, e.g. preventing or treating disorders involving  
 PT aberrant protein expression or biological activity.  
 XX  
 PS Claim 20; SEQ ID NO 671; 394pp; English.  
 XX  
 CC The present invention relates to novel human coding sequences (ABQ99268-  
 CC ABQ99608) and proteins (AAB64682-ABP65022). The sequences are useful in  
 CC therapeutic, diagnostic and research methods. The polynucleotides may be  
 CC used in the field of molecular biology as hybridisation probes, primers  
 CC for PCR, for chromosome and gene mapping, for the recombinant production  
 CC of protein, or in generation of anti-sense DNA or RNA. The  
 CC polynucleotides are useful in diagnostics as expressed sequence tags  
 CC (ESTs) for identifying expressed genes or for physical mapping of the  
 CC human genome. The proteins may be used as molecular weight markers, or as  
 CC nutritional sources or supplements. The proteins may be used to maintain  
 CC and expand cell population in a totipotent or pluripotent state  
 CC useful for re-engineering damaged or diseased tissues, transplantation,  
 CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The  
 CC polynucleotides and proteins are useful for preventing, treating or  
 CC ameliorating disorders involving aberrant protein expression or  
 CC neurological activity, e.g. haematopoietic disorders, central/peripheral  
 CC nervous system diseases, mechanical and traumatic disorders, non-healing  
 CC wounds, immune deficiencies and disorders, infectious diseases caused by  
 CC viral, bacterial or fungal infection, autoimmune disorders, allergic

CC reactions and conditions, coagulation disorders, or cancer. The  
 CC polynucleotide sequences of the invention were assembled from ESTs  
 CC isolated mainly by sequencing by hybridisation, and in some cases,  
 CC sequences obtained from one or more public databases. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
 XX  
 SQ Sequence 404 AA;

Query Match 99.8%; Score 1802; DB 5; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-127;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVLCCKGAPKPPORLEWKLNTGRTEA 60  
 DB 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVLCCKGAPKPPORLEWKLNTGRTEA 60  
 QY 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120  
 DB 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120  
 QY 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180  
 DB 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180  
 QY 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFSGLPFRHRLRTAPIQPRVWEPVPLEVQL 240  
 DB 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFSGLPFRHRLRTAPIQPRVWEPVPLEVQL 240  
 QY 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHWMDGVPPLPSPVLILPEIGPDQGTYS 300  
 DB 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHWMDGVPPLPSPVLILPEIGPDQGTYS 300  
 QY 301 CVATHSHGPOESRAVSIISIEPGEETAGSVGGSL 338  
 DB 301 CVATHSHGPOESRAVSIISIEPGEETAGSVGGSL 338

RESULT 8  
 ADF31292  
 ID ADF31292 standard; protein; 404 AA.  
 XX  
 AC ADF31292;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human receptor of advanced glycation end products (RAGE).  
 XX  
 KW human; receptor; advanced glycation end product; RAGE;  
 KW receptor of advanced glycation end product; high yield; high purity.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP2003306500-A.  
 XX  
 PD 28-OCT-2003.  
 XX  
 PF 05-FEB-2003; 2003JP-00027992.  
 XX  
 PR 15-FEB-2002; 2002JP-00038380.  
 XX  
 PA (TORA ) TORAY IND INC.  
 XX  
 DR WPI; 2004-015267/02.  
 XX  
 PT Purifying receptor of advanced glycation end products derivative  
 PT containing IGV domain of receptor of advanced glycation end product using  
 PT one or more affinity columns.  
 XX  
 PS Disclosure; SEQ ID NO 1; 13pp; Japanese.  
 XX  
 CC The invention relates to a method of purifying a receptor of advanced

CC glycation end products (RAGE) derivative. The method is useful for  
 CC purifying receptor of advanced glycation end product derivative. The  
 CC method enables simple, rapid with high yield and high purity manufacture  
 CC of RAGE derivative. The present sequence represents the amino acid  
 CC sequence of human receptor of advanced glycation end products (RAGE).  
 XX  
 SQ Sequence 404 AA;

Query Match 99.8%; Score 1802; DB 8; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-127;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVLCCKGAPKPPORLEWKLNTGRTEA 60  
 DB 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVLCCKGAPKPPORLEWKLNTGRTEA 60  
 QY 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120  
 DB 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120  
 QY 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180  
 DB 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRH 180  
 QY 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFSGLPFRHRLRTAPIQPRVWEPVPLEVQL 240  
 DB 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFSGLPFRHRLRTAPIQPRVWEPVPLEVQL 240  
 QY 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHWMDGVPPLPSPVLILPEIGPDQGTYS 300  
 DB 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHWMDGVPPLPSPVLILPEIGPDQGTYS 300  
 QY 301 CVATHSHGPOESRAVSIISIEPGEETAGSVGGSL 338  
 DB 301 CVATHSHGPOESRAVSIISIEPGEETAGSVGGSL 338

RESULT 9  
 ADF42983  
 ID ADF42983 standard; protein; 404 AA.  
 XX  
 AC ADF42983;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human receptor of advanced glycation (RAGE) protein.  
 XX  
 KW diabetic complication factor; receptor of advanced glycation end product;  
 KW RAGE binding substance adsorption ligand; water-insoluble carrier;  
 KW biological evaluation; diabetic complication; renal-disease; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP2003306499-A.  
 XX  
 PD 28-OCT-2003.  
 XX  
 PF 05-FEB-2003; 2003JP-00027991.  
 XX  
 PR 15-FEB-2002; 2002JP-00038378.  
 XX  
 PA (TORA ) TORAY IND INC.  
 XX  
 DR WPI; 2004-015266/02.  
 XX  
 PT Obtaining diabetic complication factor comprises contacting biological  
 PT fluid with adsorbent, and immobilizing receptor of advanced glycation end  
 PT products binding substance ligand on carrier.  
 XX  
 PS Disclosure; SEQ ID NO 1; 18pp; Japanese.  
 XX  
 CC This invention relates to a novel method of obtaining a diabetic  
 CC complication factor which comprises contacting liquid from a biological

CC fluid with an adsorbent which immobilises a receptor of advanced  
 CC glycation end products (RAGE) binding substance adsorption ligand on a  
 CC water-insoluble carrier, cleaning the adsorbent in an aqueous solution,  
 CC separating and recovering the diabetically complicated factor by contacting  
 CC the adsorbent with the aqueous solution. The method is useful for  
 CC carrying out biological evaluation which involves determining advanced  
 CC degree of diabetically complicated or degree of a renal-disease.  
 XX  
 SQ Sequence 404 AA;

Query Match 99.8%; Score 1802; DB 8; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-127; Indels 0; Gaps 0;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60  
 DB 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60  
 QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNYRVRYQI 120  
 DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNYRVRYQI 120  
 QY 121 PGKPEIVDSASELTAGVPKNKVGTCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQETRRH 180  
 DB 121 PGKPEIVDSASELTAGVPKNKVGTCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQETRRH 180  
 QY 181 PETGLFTLQSELMTVPARGGDRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240  
 DB 181 PETGLFTLQSELMTVPARGGDRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240  
 QY 241 VVEPEGGAAPGCTVTLTCEVPAQSPQIHWMKDGVPPLPSPVLILPEIGPDQGTYS 300  
 DB 241 VVEPEGGAAPGCTVTLTCEVPAQSPQIHWMKDGVPPLPSPVLILPEIGPDQGTYS 300  
 QY 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338  
 DB 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338

RESULT 10  
 ADK00129  
 ID ADK00129 standard; protein; 404 AA.  
 AC ADK00129;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human RAGE protein.  
 XX  
 KW Advanced Glycation End Product Ligand Binding Element; RAGE-LBE;  
 KW Cystostatic; Antidiabetic; Nootropic; Antiarthritic; Osteopathic;  
 KW Neuroprotective; Antiinflammatory; Dermatological; Immunosuppressive;  
 KW Vasotropic; Antipruritic; Antibacterial; Antiartherosclerotic;  
 KW amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;  
 KW Chronic inflammatory disease; osteoarthritis; irritable bowel disease;  
 KW multiple sclerosis; psoriasis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO2004016229-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PP 18-AUG-2003; 2003WO-US025996.  
 XX  
 PR 16-AUG-2002; 2002US-0404205P.  
 XX  
 PA (AMHP ) WYETH.  
 XX  
 PI Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FM;  
 PI Feldmann M, Foxwell BJM, Feldman JL;  
 XX

DR WPI; 2004-192067/18.  
 XX N-PSDB; ADK00130.  
 XX  
 PT New fusion protein comprising a Receptor for Advanced Glycation End  
 PT Product Ligand Binding Element (RAGE-LBE) and an immunoglobulin element,  
 PT useful for preparing a composition for treating e.g., Alzheimer's  
 PT disease.  
 XX  
 PS Disclosure; SEQ ID NO 43; 100pp; English.  
 XX  
 CC The present invention relates to a new fusion protein comprising a  
 CC Receptor for Advanced Glycation End Product Ligand Binding Element (RAGE-  
 CC LBE) and an immunoglobulin element. The fusion protein is useful for  
 CC preparing a composition for treating RAGE-associated disorders such as  
 CC amyloidosis, cancer, Crohn's disease, diabetes, complications of  
 CC diabetes, prion-related disorders, vasculitis, nephropathies,  
 CC retinopathies and/or neuropathies; Alzheimer's disease, chronic  
 CC inflammatory disease e.g., rheumatoid arthritis, osteoarthritis,  
 CC irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute  
 CC inflammatory disease e.g., sepsis, or cardiovascular disease, e.g.,  
 CC atherosclerosis or restenosis. The present sequence represents human RAGE  
 CC protein.  
 XX  
 SQ Sequence 404 AA;

Query Match 99.8%; Score 1802; DB 8; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-127;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60  
 DB 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60  
 QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNYRVRYQI 120  
 DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNYRVRYQI 120  
 QY 121 PGKPEIVDSASELTAGVPKNKVGTCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQETRRH 180  
 DB 121 PGKPEIVDSASELTAGVPKNKVGTCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQETRRH 180  
 QY 181 PETGLFTLQSELMTVPARGGDRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240  
 DB 181 PETGLFTLQSELMTVPARGGDRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240  
 QY 241 VVEPEGGAAPGCTVTLTCEVPAQSPQIHWMKDGVPPLPSPVLILPEIGPDQGTYS 300  
 DB 241 VVEPEGGAAPGCTVTLTCEVPAQSPQIHWMKDGVPPLPSPVLILPEIGPDQGTYS 300  
 QY 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338  
 DB 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338

RESULT 11  
 AAM48746  
 ID AAM48746 standard; protein; 339 AA.  
 XX  
 AC AAM48746;  
 XX  
 DT 02-APR-2002 (first entry)  
 XX  
 DE Human eRAGE protein SEQ ID NO 2.  
 XX  
 KW Human; RAGE; receptor for advanced glyated endproduct; receptor;  
 KW antidiabetic; neuroprotective; cystostatic; antiinflammatory; vasotropic;  
 KW nephrotropic; dermatological; antiatherosclerotic; nootropic; diabetes;  
 KW Alzheimer's disease; cancer; inflammation; kidney failure;  
 KW systemic lupus; nephritis; erectile dysfunction; atherosclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192892-A2.

XX 06-DEC-2001.  
XX 30-MAY-2001; 2001WO-US017447.  
XX 30-MAY-2000; 2000US-0207342P.  
XX 05-MAR-2001; 2001US-00799152.  
XX (TRAN-) TRANS TECH PHARMA.  
XX Shahbaz M;  
XX WPI; 2002-114372/15.  
XX  
XX Detecting a receptor for advanced glycosylated endproducts (RAGE) modulators,  
XX for treating e.g., cancer, diabetes or inflammation, comprises measuring  
XX the amount of bound anti-RAGE antibody.  
XX  
XX Claim 2; Fig 2; 49pp; English.  
XX  
XX The invention relates to detecting receptor for advanced glycosylated  
XX endproducts (RAGE) modulators comprising determining the amount of RAGE  
XX protein or its fragment bound to the pre-adsorbed ligand by measuring the  
XX amount of anti-RAGE antibody bound to the solid surface. The method is  
XX useful for rapid, high-throughput identification of compounds that  
XX modulate RAGE. The compounds are useful for treating symptoms of diabetes  
XX and symptoms of diabetic late complications, amyloidosis, Alzheimer's  
XX disease, cancer, inflammation, kidney failure, systemic lupus nephritis  
XX or inflammatory lupus nephritis, erectile dysfunction and atherosclerosis  
XX  
XX Sequence 339 AA;

Query Match 99.5%; Score 1797; DB 5; Length 339;  
Best Local Similarity 100.0%; Pred. No. 6.3e-127;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AAGTAVGAWLVLSLWGAAGVGAQNTARIGEPVLKCKGAPKPPORLEWKLNTGRTEAW 61  
DB 2 AAGTAVGAWLVLSLWGAAGVGAQNTARIGEPVLKCKGAPKPPORLEWKLNTGRTEAW 61  
QY 62 KVLSPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETSRYRVYQIP 121  
DB 62 KVLSPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETSRYRVYQIP 121  
QY 122 GKPEIVDSASELTAGVKNKVTGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSKQTRRHP 181  
DB 122 GKPEIVDSASELTAGVKNKVTGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSKQTRRHP 181  
QY 182 ETGLFTLQSELMTVPARGGDPRTFSCSFGLPRHRLTAPIQPRVWEPVPLEEVQLV 241  
DB 182 ETGLFTLQSELMTVPARGGDPRTFSCSFGLPRHRLTAPIQPRVWEPVPLEEVQLV 241  
QY 242 VEPEGGAVAPGGTITLTCEVPAQPSQIHWMDGVLPLPPSPVLLILPEIGPDQGTYS 301  
DB 242 VEPEGGAVAPGGTITLTCEVPAQPSQIHWMDGVLPLPPSPVLLILPEIGPDQGTYS 301  
QY 302 VATHSHGPOESRAVSISIIIEPEGEGTAGSVGGSL 338  
DB 302 VATHSHGPOESRAVSISIIIEPEGEGTAGSVGGSL 338

RESULT 12  
AAM48745  
ID AAM48745 standard; protein; 404 AA.  
XX AAM48745;  
XX  
XX 02-APR-2002 (first entry)  
XX Human RAGE protein SEQ ID NO 1.  
XX  
XX Human; RAGE; receptor for advanced glycosylated endproduct; receptor;  
XX antidiabetic; neuroprotective; cytosolic; antiinflammatory; vasotropic;

KW nephrotropic; dermatological; antiarteriosclerotic; nootropic; diabetes;  
KW Alzheimer's disease; cancer; inflammation; kidney failure;  
KW systemic lupus; nephritis; erectile dysfunction; atherosclerosis.  
XX Homo sapiens.  
OS  
XX  
PN WO200192892-A2.  
XX  
PD 06-DEC-2001.  
XX  
XX 30-MAY-2001; 2001WO-US017447.  
XX  
XX 30-MAY-2000; 2000US-0207342P.  
XX 05-MAR-2001; 2001US-00799152.  
XX  
XX (TRAN-) TRANS TECH PHARMA.  
PA  
XX  
PI Shahbaz M;  
XX  
XX WPI; 2002-114372/15.  
XX  
XX Detecting a receptor for advanced glycosylated endproducts (RAGE) modulators,  
XX for treating e.g., cancer, diabetes or inflammation, comprises measuring  
XX the amount of bound anti-RAGE antibody.  
XX  
XX Claim 1; Fig 2; 49pp; English.  
XX  
XX The invention relates to detecting receptor for advanced glycosylated  
XX endproducts (RAGE) modulators comprising determining the amount of RAGE  
XX protein or its fragment bound to the pre-adsorbed ligand by measuring the  
XX amount of anti-RAGE antibody bound to the solid surface. The method is  
XX useful for rapid, high-throughput identification of compounds that  
XX modulate RAGE. The compounds are useful for treating symptoms of diabetes  
XX and symptoms of diabetic late complications, amyloidosis, Alzheimer's  
XX disease, cancer, inflammation, kidney failure, systemic lupus nephritis  
XX or inflammatory lupus nephritis, erectile dysfunction and atherosclerosis  
XX  
XX Sequence 404 AA;

Query Match 99.5%; Score 1797; DB 5; Length 404;  
Best Local Similarity 100.0%; Pred. No. 7.8e-127;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AAGTAVGAWLVLSLWGAAGVGAQNTARIGEPVLKCKGAPKPPORLEWKLNTGRTEAW 61  
DB 2 AAGTAVGAWLVLSLWGAAGVGAQNTARIGEPVLKCKGAPKPPORLEWKLNTGRTEAW 61  
QY 62 KVLSPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETSRYRVYQIP 121  
DB 62 KVLSPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETSRYRVYQIP 121  
QY 122 GKPEIVDSASELTAGVKNKVTGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSKQTRRHP 181  
DB 122 GKPEIVDSASELTAGVKNKVTGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSKQTRRHP 181  
QY 182 ETGLFTLQSELMTVPARGGDPRTFSCSFGLPRHRLTAPIQPRVWEPVPLEEVQLV 241  
DB 182 ETGLFTLQSELMTVPARGGDPRTFSCSFGLPRHRLTAPIQPRVWEPVPLEEVQLV 241  
QY 242 VEPEGGAVAPGGTITLTCEVPAQPSQIHWMDGVLPLPPSPVLLILPEIGPDQGTYS 301  
DB 242 VEPEGGAVAPGGTITLTCEVPAQPSQIHWMDGVLPLPPSPVLLILPEIGPDQGTYS 301  
QY 302 VATHSHGPOESRAVSISIIIEPEGEGTAGSVGGSL 338  
DB 302 VATHSHGPOESRAVSISIIIEPEGEGTAGSVGGSL 338

RESULT 13  
ADS10986  
ID ADS10986 standard; protein; 381 AA.  
XX  
XX ADS10986;

XX 16-DEC-2004 (first entry)  
XX Human therapeutic protein - SEQ ID 1223.  
XX  
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;  
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
KW aplastic anaemia; cancer; wound healing; gene therapy.  
XX  
XX Homo sapiens.  
XX WO2004080148-A2.  
XX  
XX 23-SEP-2004.  
XX  
XX 30-SEP-2003; 2003WO-US030720.  
XX  
XX 02-OCT-2002; 2002US-0416186P.  
XX  
XX (NUVE-) NUVELO INC.  
XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;  
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;  
XX  
XX WPI; 2004-668857/65.  
XX N-PSDB; ADS10302.  
XX  
XX New polynucleotide, useful in preparing a composition for diagnosing or  
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
PT aplastic anemia or cancer for promoting wound healing.  
XX  
XX Claim 20; SEQ ID NO 1223; 718pp; English.  
XX  
XX The invention relates to a novel isolated polynucleotide and the encoded  
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,  
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may  
CC be useful in preparing a composition for diagnosing or treating  
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
CC disorders, such as aplastic anaemia or cancer, as well as for promoting  
CC wound healing. The molecules may also be utilised during gene therapy  
CC procedures. The current sequence is that of a human therapeutic protein  
CC of the invention. The current sequence is not shown explicitly within the  
CC specification but can be accessed from the WIPO web-site.  
XX  
XX Sequence 381 AA;  
XX  
XX Query Match 99.4%; Score 1796; DB 8; Length 381;  
XX Best Local Similarity 99.7%; Pred. No. 8.7e-127; Indels 0; Gaps 0;  
XX Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAAGTAVGAWVLVLSLWGVAVGAGQNTARIGBPLVLCCKGAPKPPQRLWKLNTGRTEA 60  
DB 1 MAAGTAVGAWVLVLSLWGVAVGAGQNTARIGBPLVLCCKGAPKPPQRLWKLNTGRTEA 60  
QY 61 WKVLSPPQGGPNDVSARVLPNGSLFLPVGIODEGIFRCQAMNRNGKETKSNYRVRYQI 120  
DB 61 WKVLSPPQGGPNDVSARVLPNGSLFLPVGIODEGIFRCQAMNRNGKETKSNYRVRYQI 120  
QY 121 PKGPETVDSASELTAGVPKNKCTCYSEGSYPAGTILSWHLDDGKPLVPNEKGVSKQTRRH 180  
DB 121 PKGPETVDSASELTAGVPKNKCTCYSEGSYPAGTILSWHLDDGKPLVPNEKGVSKQTRRH 180  
QY 181 PETGLFTLQSELMVTVPARGDPRPTSCFSFGLPHRALRTAPQPRVWEPVPLEEVOL 240  
DB 181 PETGLFTLQSELMVTVPARGDPRPTSCFSFGLPHRALRTAPQPRVWEPVPLEEVOL 240  
QY 241 VVEPEGAVAPGTVTLTCEVPAQSPQIHMKDGVPLPLPPSPVLIILPEIGPQGGTYS 300  
DB 241 VVEPEGAVAPGTVTLTCEVPAQSPQIHMKDGVPLPLPPSPVLIILPEIGPQGGTYS 300  
QY 301 CVATHSSHGPQBSRAVSIISIIIPGEGPTAGSVGGSL 338  
DB 301 CVATHSSHGPQBSRAVSIISIIIPGEGPTAGSVGGSL 338

RESULT 14  
AAU77543  
ID AAU77543 standard; protein; 404 AA.  
XX  
XX AC AAU77543;  
XX  
XX 05-JUN-2002 (first entry)  
XX  
XX Human receptor for advanced glycosylation end product (RAGE).  
XX  
XX Receptor for advanced glycation end product; RAGE; receptor;  
KW amyloid beta peptide; blood-brain barrier; neurovascular stress;  
KW cerebral vasoconstriction suppressor; cerebral blood flow enhancer;  
KW cerebral amyloid angiopathy; transgenic animal; amyloid beta precursor;  
KW Alzheimer's disease; Down's syndrome; head trauma; stroke; human.  
XX  
XX Homo sapiens.  
XX WO200214519-A1.  
XX  
XX 21-FEB-2002.  
XX  
XX 14-AUG-2001; 2001WO-US025416.  
XX  
XX 14-AUG-2000; 2000US-00638648.  
XX  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX Stern DM, Schmidt AM; Yan SD, Zlokovic B;  
XX WPI; 2002-257610/30.  
XX N-PSDB; ABK10856.  
XX  
XX Ameliorating neurovascular stress and decreasing cerebral  
PT vasoconstriction in subject suffering from chronic/acute cerebral amyloid  
PT angiopathy, by administering inhibitor of receptor for advanced glycation  
PT endproduct.  
XX  
XX Disclosure; Page 16; 68pp; English.  
XX  
XX The invention describes a method of ameliorating neurovascular stress,  
CC and decreasing cerebral vasoconstriction in subject suffering from  
CC chronic or acute cerebral amyloid angiopathy, comprising administering an  
CC inhibitor (I) of receptor for advanced glycation end product (RAGE). (I)  
CC inhibits transcytosis of amyloid beta peptides across blood-brain  
CC barrier, thus decreasing cerebral vasoconstriction and increasing  
CC cerebral blood flow. (I) is useful for treating amyloid angiopathy in a  
CC subject, decreasing cerebral vasoconstriction in a transgenic non-human  
CC animal (preferably, transgenic mouse overexpressing mutant human amyloid  
CC beta precursor protein) or a human, suffering from chronic or acute  
CC cerebral amyloid angiopathy, preferably, Alzheimer's disease, and for  
CC ameliorating neurovascular stress comprising cerebral amyloid angiopathy  
CC in a subject, where the neurovascular stress is caused by Alzheimer's  
CC disease, aging, Down's syndrome, head trauma or stroke. This is the amino  
CC acid sequence of human receptor for advanced glycation end product (RAGE)  
CC described in the invention  
XX  
XX Sequence 404 AA;  
XX  
XX Query Match 99.3%; Score 1793; DB 5; Length 404;  
XX Best Local Similarity 99.7%; Pred. No. 1.6e-126;  
XX Matches 336; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 AAGTAVGAWVLVLSLWGVAVGAGQNTARIGBPLVLCCKGAPKPPQRLWKLNTGRTEAM 61  
DB 2 AAGTAVGAWVLVLSLWGVAVGAGQNTARIGBPLVLCCKGAPKPPQRLWKLNTGRTEAM 61  
QY 62 KVLSPQGGPNDVSARVLPNGSLFLPVGIODEGIFRCQAMNRNGKETKSNYRVRYQIP 121  
DB 62 KVLSPQGGPNDVSARVLPNGSLFLPVGIODEGIFRCQAMNRNGKETKSNYRVRYQIP 121

QY 122 GKPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHP 181  
 Db 122 GKPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHP 181  
 QY 182 ETGLFTLOSELMTVPARGGDRPTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVQLV 241  
 Db 182 ETGLFTLOSELMTVPARGGDRPTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVQLV 241  
 QY 242 VEPEGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPSPVLIILPEIGPQDQGTYS 301  
 Db 242 VEPEGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPSPVLIILPEIGPQDQGTYS 301  
 QY 302 VATHSSHGPOESRAVSISIIIEPGEGPTAGSVGSGSL 338  
 Db 302 VATHSSHGPOESRAVSISIIIEPGEGPTAGSVGSGSL 338

## RESULT 15

AAE23219  
 ID AAE23219 standard; protein; 404 AA.  
 XX  
 AC AAE23219;

XX 27-AUG-2002 (first entry)  
 XX

XX Human receptor for advanced glycosylation end product (RAGE) protein.  
 XX

XX Human; Receptor for advanced glycosylation end product; RAGE; cardiant;  
 KW tissue growth; neointimal formation; blood vessel; restenosis; diabetes;  
 KW myocardial infarction; angioplasty; peripheral vascular surgery; angina;  
 KW transgenic animal; acute thrombotic stroke; venous thrombosis.  
 XX

OS Homo sapiens.  
 XX

XX WO200230889-A2.  
 XX

XX 18-APR-2002.  
 XX

XX 12-OCT-2001; 2001WO-US032036.  
 XX

XX 13-OCT-2000; 2000US-00687528.  
 XX

XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX

XX Stern DM, Schmidt A, Marso S, Topol E, Lincoff AM;  
 XX

XX WPI; 2002-426260/45.  
 XX

XX N-PSDB; AAD36952.  
 XX

XX Inhibiting new tissue growth or neointimal formation in blood vessels of  
 PT subject suffering from diabetes, stroke and preventing restenosis,  
 PT comprises administering inhibitor of receptor for advance glycation end  
 PT product.  
 XX

XX Disclosure; Page 16; 43pp; English.  
 XX

XX The invention relates to a method for inhibiting new tissue growth or  
 CC neointimal formation in blood vessels in a subject that has experienced  
 CC blood vessel injury and preventing exaggerated restenosis in a diabetic  
 CC subject. The method comprises administering an inhibitor of receptor for  
 CC advanced glycation/glycosylation end product (RAGE), so as to inhibit new  
 CC tissue growth or neointimal formation in subject's blood vessels and  
 CC preventing restenosis in the subject. The method is useful for inhibiting  
 CC new tissue growth or neointimal formation in blood vessels in a subject  
 CC like non-human animal, a transgenic non-human animal or a human suffering  
 CC from diabetes, acute thrombotic stroke, venous thrombosis, unstable  
 CC angina, myocardial infarction, abrupt closure following angioplasty or  
 CC stent placement, or thrombosis as a result of peripheral vascular surgery  
 CC The method is also useful for preventing restenosis and for determining  
 CC whether a compound inhibits new tissue growth in a blood vessel in a  
 CC subject. The present sequence is human receptor for advanced  
 CC glycosylation end product (RAGE) protein  
 XX

SQ Sequence 404 AA;

Query Match 99.3%; Score 1793; DB 5; Length 404;  
 Best Local Similarity 99.7%; Pred. No. 1.6e-126;  
 Matches 336; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGTAVGAWVLVLSLWGA VVGAQNTARIGEPVLVKCKGAPKKPPORLEWKINTGRTAW 61

Db 2 AAGTAVGAWVLVLSLWGA VVGAQNTARIGEPVLVKCKGAPKKPPORLEWKINTGRTAW 61

QY 62 KVLSPQGGGPWDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNVRRVYQIP 121

Db 62 KVLSPQGGGPWDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNVRRVYQIP 121

QY 122 GKPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHP 181

Db 122 GKPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHP 181

QY 182 ETGLFTLOSELMTVPARGGDRPTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVQLV 241

Db 182 ETGLFTLOSELMTVPARGGDRPTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVQLV 241

QY 242 VEPEGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPSPVLIILPEIGPQDQGTYS 301

Db 242 VEPEGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPSPVLIILPEIGPQDQGTYS 301

QY 302 VATHSSHGPOESRAVSISIIIEPGEGPTAGSVGSGSL 338

Db 302 VATHSSHGPOESRAVSISIIIEPGEGPTAGSVGSGSL 338

Search completed: March 15, 2005, 11:27:10

Job time : 81 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 15, 2005, 10:43:33 ; Search time 27 Seconds  
(without alignments)  
937.260 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 1806

Sequence: 1 MAAGTAVGAWVLVSLMGAV.....IIEPGEETAGSVGGSLV 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/prodata/1/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/6C COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1802	99.8	340	2	US-08-633-148-2
2	1802	99.8	404	4	US-09-949-016-11025
3	1793	99.3	404	4	US-09-638-649-3
4	1793	99.3	404	4	US-09-638-648-3
5	1782.5	98.7	405	4	US-08-755-235-4
6	1690	93.6	318	2	US-08-633-148-4
7	1690	93.6	332	4	US-09-062-365-1
8	1495	82.8	278	2	US-08-432-016-5
9	1495	82.8	278	2	US-08-684-594-5
10	1480	81.9	416	4	US-09-638-649-1
11	1480	81.9	416	4	US-08-755-235-2
12	1480	81.9	416	4	US-09-638-648-1
13	1404.5	77.8	403	4	US-09-638-649-5
14	1404.5	77.8	403	4	US-09-638-648-5
15	223.5	12.4	582	4	US-09-702-705-334
16	223.5	12.4	582	4	US-09-736-457-334
17	223.5	12.4	582	4	US-09-614-124B-334
18	223.5	12.4	582	4	US-09-671-325-334
19	223.5	12.4	582	4	US-09-589-184-334
20	223.5	12.4	582	4	US-09-658-824-334
21	223.5	12.4	604	4	US-09-949-016-9548
22	221.5	12.3	583	2	US-08-432-016-2
23	221.5	12.3	583	2	US-08-684-594-2
24	218.5	12.1	623	4	US-09-949-016-11206
25	218.5	12.1	646	4	US-09-653-961-2
26	217.5	12.0	646	4	US-09-949-016-6728
27	217.5	12.0	646	4	US-09-653-961-4

28	212.5	11.8	466	2	US-08-432-016-4	Sequence 4, Appli
29	212.5	11.8	466	2	US-08-684-594-4	Sequence 4, Appli
30	209	11.6	1651	3	US-09-540-245A-18	Sequence 18, Appli
31	205	11.4	477	2	US-08-432-016-3	Sequence 3, Appli
32	205	11.4	477	2	US-08-684-594-3	Sequence 3, Appli
33	198	11.0	4391	4	US-10-006-011A-2	Sequence 2, Appli
34	197	10.9	486	2	US-08-432-016-6	Sequence 6, Appli
35	197	10.9	486	2	US-08-684-594-6	Sequence 6, Appli
36	190.5	10.3	1953	4	US-09-917-254-92	Sequence 92, Appli
37	186.5	10.3	924	1	US-08-481-130-28	Sequence 28, Appli
38	186.5	10.3	924	1	US-08-656-984A-28	Sequence 28, Appli
39	186.5	10.3	924	1	US-08-485-604-28	Sequence 28, Appli
40	186.5	10.3	924	2	US-08-487-595-28	Sequence 28, Appli
41	185.5	10.3	313	4	US-09-700-397-4	Sequence 3, Appli
42	185.5	10.3	344	4	US-09-700-397-3	Sequence 3, Appli
43	183.5	10.2	1297	3	US-09-540-245A-17	Sequence 17, Appli
44	182.5	10.1	698	2	US-08-602-725-36	Sequence 36, Appli
45	182.5	10.1	702	4	US-09-949-016-6484	Sequence 6484, Ap

ALIGNMENTS

RESULT 1  
US-08-633-148-2  
; Sequence 2, Application US/08633148  
; Patent No. 5864018  
; GENERAL INFORMATION:  
; APPLICANT: MORSE, MICHAEL J.  
; APPLICANT: NAGASHIMA, MARIKO  
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,148  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY ESQ., MATTHEW B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 014618-00560005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 340 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-633-148-2

Query Match 99.8%; Score 1802; DB 2; Length 340;  
Best Local Similarity 100.0%; Pred. No. 1.2e-145;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWVLVSLMGAVGAQNITARIIGPLVLKCKGAPKPPQRLWKLNTGRTEA 60  
DB 1 MAAGTAVGAWVLVSLMGAVGAQNITARIIGPLVLKCKGAPKPPQRLWKLNTGRTEA 60

[illegible]

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RESULT 2
US-09-949-016-11025
; Sequence 11025, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11025
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11025

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Db 301 CVATHSHGPQESRAVSIISIEFGEETAGSVGGSL 338

RESULT 3  
US-09-638-649-3  
; Sequence 3, Application US/09638649  
; Patent No. 6563015  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED  
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 0575/62175  
; CURRENT APPLICATION NUMBER: US/09/638,649  
; CURRENT FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ. ID. NO 3  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Human  
US-09-638-649-3

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RESULT 4
US-09-638-648-3
/ Sequence 3, Application US/09638648
/ Patent No. 6825164
/ GENERAL INFORMATION:
/ APPLICANT: Stern, David M.
/ APPLICANT: Schmidt, Ann Marie
/ APPLICANT: Yan, Shi Du
/ APPLICANT: Zlokovici, Berislav
/ TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
/ TITLE OF INVENTION: ANGIOPATHY
/ FILE REFERENCE: 0575/62097
/ CURRENT APPLICATION NUMBER: US/09/638,648
/ CURRENT FILING DATE: 2000-08-14
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 404
/ TYPE: PRT
/

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; ORGANISM: Human		; Sequence 4, Application US/08633148	
US-09-638-648-3		; Patent No. 5864018	
Query Match		; GENERAL INFORMATION:	
Best Local Similarity 99.3%; Score 1793; DB 4; Length 404;		; APPLICANT: MORSE, MICHAEL J.	
Matches 336; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		; APPLICANT: NAGASHIMA, MARIO	
		; APPLICANT: HOLLANDER, DORIS A.	
		; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION	
		; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR	
		; NUMBER OF SEQUENCES: 23	
		; CORRESPONDENCE ADDRESS:	
		; ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP	
		; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR	
		; CITY: SAN FRANCISCO	
		; STATE: CALIFORNIA	
		; COUNTRY: U.S.A.	
		; ZIP: 94111	
		; COMPUTER READABLE FORM:	
		; MEDIUM TYPE: Floppy disk	
		; COMPUTER: IBM PC compatible	
		; OPERATING SYSTEM: PC-DOS/MS-DOS	
		; SOFTWARE: PatentIn Release #1.0, Version #1.30	
		; CURRENT APPLICATION DATA:	
		; APPLICATION NUMBER: US/08/633,148	
		; FILING DATE: 16-APR-1996	
		; CLASSIFICATION: 435	
		; ATTORNEY/AGENT INFORMATION:	
		; NAME: MURPHY ESQ., MATTHEW B.	
		; REGISTRATION NUMBER: 39,787	
		; REFERENCE/DOCKET NUMBER: 014618-00560005	
		; TELECOMMUNICATION INFORMATION:	
		; TELEPHONE: (415) 326-2400	
		; TELEFAX: (415) 326-2422	
		; INFORMATION FOR SEQ ID NO: 4:	
		; SEQUENCE CHARACTERISTICS:	
		; LENGTH: 318 amino acids	
		; TYPE: amino acid	
		; STRANDEDNESS: single	
		; TOPOLOGY: linear	
		; MOLECULE TYPE: peptide	
		US-08-633-148-4	
		Query Match 93.6%; Score 1690; DB 2; Length 318;	
		Best Local Similarity 100.0%; Pred. No. 3.9e-136;	
		Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	242	VEPEGGAVAPGGT	VTLTCEVPAQSPQIHMMKDGVPPLPPSPVLILPEIGPDQGTYS
Qy	302	VATHSHGPOESRA-VSISIIIEPGEPTAGSVGGSL	338
Db	302	VATHSHGPOESRAVVSIIIEPGEPTAGSVGGSL	339
RESULT 6			
US-08-633-148-4			
; Sequence 4, Application US/08633148			
; Patent No. 5864018			
; GENERAL INFORMATION:			
; APPLICANT: MORSE, MICHAEL J.			
; APPLICANT: NAGASHIMA, MARIO			
; APPLICANT: HOLLANDER, DORIS A.			
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION			
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR			
; NUMBER OF SEQUENCES: 23			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP			
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR			
; CITY: SAN FRANCISCO			
; STATE: CALIFORNIA			
; COUNTRY: U.S.A.			
; ZIP: 94111			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/633,148			
; FILING DATE: 16-APR-1996			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: MURPHY ESQ., MATTHEW B.			
; REGISTRATION NUMBER: 39,787			
; REFERENCE/DOCKET NUMBER: 014618-00560005			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 326-2400			
; TELEFAX: (415) 326-2422			
; INFORMATION FOR SEQ ID NO: 4:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 318 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: peptide			
US-08-633-148-4			
Query Match 93.6%; Score 1690; DB 2; Length 318;			
Best Local Similarity 100.0%; Pred. No. 3.9e-136;			
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	23	AQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTTEAMKVLSPQGGPWSVARVLPNG	82
Db	1	AQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTTEAMKVLSPQGGPWSVARVLPNG	60
Qy	83	SLFLPAVGIQDEGIFRCQAMNNGKETSNNYRVYQIPGKPEIVDSASELTAGVPNKVG	142
Db	61	SLFLPAVGIQDEGIFRCQAMNNGKETSNNYRVYQIPGKPEIVDSASELTAGVPNKVG	120
Qy	143	TCVSGSPGAGTSLWHLGKPLVPNEKGVSKVKEQTRRHPTGLFTLQSELMTVPARGGDP	202
Db	121	TCVSGSPGAGTSLWHLGKPLVPNEKGVSKVKEQTRRHPTGLFTLQSELMTVPARGGDP	180
Qy	203	RPTFSCSPGLPRHRLRTAPIQPRVMEPVEEVQLVVEPEGGAVAPGGTTLTCEVP	262
Db	181	RPTFSCSPGLPRHRLRTAPIQPRVMEPVEEVQLVVEPEGGAVAPGGTTLTCEVP	240
Qy	263	AQPSQIHMMKDGVPPLPPSPVLILPEIGPDQGTYSVATHSHSGPOESRAVSIIE	322

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Db 241 AQPSPQIHWKMDGVLPPLPPSPVLILPEIGPDQGTSCVATHSHGQESRAVSIIE 300
QY 323 PGEAGTAGSVGGSL 338
Db 301 PGEAGTAGSVGGSL 316

RESULT 7
US-09-062-365-1
; Sequence 1, Application US/09062365
; Patent No. 6465422
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
; FILE REFERENCE: 55424
; CURRENT APPLICATION NUMBER: US/09/062.365
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-062-365-1

Query Match 93.6%; Score 1690; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 4.2e-136; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0;

QY 23 AONITARIIGPLVKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGPMDSVARVLPNG 82
Db 1 AONITARIIGPLVKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGPMDSVARVLPNG 60
QY 83 SLFLPAVGIQDEGIFRCQAMNRNGKTKSNYRVVYQIPGKPEIVDSASELTAGVFNKVG 142
Db 61 SLFLPAVGIQDEGIFRCQAMNRNGKTKSNYRVVYQIPGKPEIVDSASELTAGVFNKVG 120
QY 143 TCVSEGSYPAGTLSWHLGDKPLVNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGGDP 202
Db 121 TCVSEGSYPAGTLSWHLGDKPLVNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGGDP 180
QY 203 RPTFSCSFSGLPRLRALRTAPIQPRVWEPVPLEVQVVEPEGGAAPGGTTLTCEVP 262
Db 181 RPTFSCSFSGLPRLRALRTAPIQPRVWEPVPLEVQVVEPEGGAAPGGTTLTCEVP 240
QY 263 AQPSPQIHWKMDGVLPPLPPSPVLILPEIGPDQGTSCVATHSHGQESRAVSIIE 322
Db 241 AQPSPQIHWKMDGVLPPLPPSPVLILPEIGPDQGTSCVATHSHGQESRAVSIIE 300
QY 323 PGEAGTAGSVGGSL 338
Db 301 PGEAGTAGSVGGSL 316

RESULT 8
US-08-432-016-5
; Sequence 5, Application US/08432016
; Patent No. 5968768
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: PATEL, DHAVALKUMAR
; APPLICANT: BOWEN, MICHAEL A.
; APPLICANT: MARQUARDT, HANS
; TITLE OF INVENTION: CD6 LIGAND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA

```

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; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,016
; FILING DATE: 01-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,350
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,903
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-432-016-5

Query Match 82.8%; Score 1495; DB 2; Length 278;
Best Local Similarity 99.6%; Pred. No. 1.4e-119;
Matches 277; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 30 IGEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGPMDSVARVLPNGSLFLPAV 89
Db 1 IGEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGPMDSVARVLPNGSLFLPAV 60
QY 90 GIQDEGIFRCQAMNRNGKTKSNYRVVYQIPGKPEIVDSASELTAGVFNKVGTCVSEGS 149
Db 61 GIQDEGIFRCQAMNRNGKTKSNYRVVYQIPGKPEIVDSASELTAGVFNKVGTCVSEGS 120
QY 150 YPAGTLSWHLGDKPLVNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGGDPRTFSCS 209
Db 121 YPAGTLSWHLGDKPLVNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGGDPRTFSCS 180
QY 210 FSPGLPRHRLRTAPIQPRVWEPVPLEVQVVEPEGGAAPGGTTLTCEVPAQSPQI 269
Db 181 FSPGLPRHRLRTAPIQPRVWEPVPLEVQVVEPEGGAAPGGTTLTCEVPAQSPQI 240
QY 270 HWMKDGVPPLPSPVLILPEIGPDQGTSCVATHSS 307
Db 241 HWMKDGVPPLPSPVLILPEIGPDQGTSCVATHSS 278

RESULT 9
US-08-684-594-5
; Sequence 5, Application US/08684594
; Patent No. 5998172
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: PATEL, DHAVALKUMAR
; APPLICANT: BOWEN, MICHAEL A.
; APPLICANT: MARQUARDT, HANS
; TITLE OF INVENTION: CD6 LIGAND
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD

```

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; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,594
; FILING DATE: 18-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/432,016
; FILING DATE: 01-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,350
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,903
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-684-594-5

Query Match      82.8%; Score 1495; DB 2; Length 278;
Best Local Similarity 99.6%; Pred. No. 1.4e-119;
Matches 277; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 30 IGEPVLVKCKGAPKPPQRLWKLTGRTAEAWKLSPPQGGPMDSDVARVLPNGSLFLPAV 89
DB 1 IGEPVLVKCKGAPKPPQRLWKLTGRTAEAWKLSPPQGGPMDSDVARVLPNGSLFLPAV 60

QY 90 GIQDEGIFRCQAMNRNGKTKSNRYRVYQIPGKPEIVDSASELTAGVKNKVGTCVSEGS 149
DB 61 GIQDEGIFRCQAMNRNGKTKSNRYRVYQIPGKPEIVDSASELTAGVKNKVGTCVSEGS 120

QY 150 YPAGTLSWHLDDGKPLVPNEKGVSKQTRRHPTGLFTLQSELMTVPARGGDPRTFSCS 209
DB 121 YPAGTLSWHLDDGKPLVPNEKGVSKQTRRHPTGLFTLQSELMTVPARGGDPRTFSCS 180

QY 210 FSPGLPRHRLRTPAQTPRWEPVPLEEVOLVVEPEGGAAPGCTVTLTCEVPAQSPQI 269
DB 181 FSPGLPRHRLRTPAQTPRWEPVPLEEVOLVVEPEGGAAPGCTVTLTCEVPAQSPQI 240

QY 270 HWMKDGVPPLPSPVLILPEIGPQDQGYSCVATHSS 307
DB 241 HWMKDGVPPLPSPVLILPEIGPQDQGYSCVATHSS 278

RESULT 10
US-09-638-649-1
; Sequence 1, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND

; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,594
; FILING DATE: 18-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/432,016
; FILING DATE: 01-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,350
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,903
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-684-594-5

Query Match      81.9%; Score 1480; DB 4; Length 416;
Best Local Similarity 80.5%; Pred. No. 4.6e-118;
Matches 281; Conservative 22; Mismatches 34; Indels 12; Gaps 2;

QY 1 MAAGTAVGAWLVLSLWGAIVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTAE 60
DB 1 MAAGTAVGAWLVLSLWGAIVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTAE 60

QY 61 WKVLSPPQGGPMDSDVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTKSNRYRVYQI 120
DB 61 WKVLSPPQGGPMDSDVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTKSNRYRVYQI 119

QY 121 PGKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTLSWHLDDGKPLVPNEKGVSKQTRRH 180
DB 120 PGKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTLSWHLDDGKPLVPNEKGVSKQTRRH 179

QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTPAQTPRWEPVPLEEVOLV 230
DB 180 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTPAQTPRWEPVPLEEVOLV 239

QY 231 -EPVPLEEVOLVVEPEGGAAPGCTVTLTCEVPAQSPQIHWMKDGVPPLPSPVLILP 289
DB 240 VDAVPLKEVQLVVEPEGGAAPGCTVTLTCEVPAQSPQIHWMKDGVPPLPSPVLILP 299

QY 290 EIGPQDQGYSCVATHSSHGPOESSRAVSIIEPGEGTAGSVGGSL 338
DB 300 EVGPEDQGYSCVATHSSHGPOESSRAVSIIEPGEGTAGSVGGSL 348

RESULT 11
US-08-755-235-2
; Sequence 2, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Bovine
; US-08-755-235-2

Query Match      81.9%; Score 1480; DB 4; Length 416;
Best Local Similarity 80.5%; Pred. No. 4.6e-118;
Matches 281; Conservative 22; Mismatches 34; Indels 12; Gaps 2;

QY 1 MAAGTAVGAWLVLSLWGAIVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTAE 60
DB 1 MAAGTAVGAWLVLSLWGAIVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTAE 60

QY 61 WKVLSPPQGGPMDSDVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTKSNRYRVYQI 120
DB 61 WKVLSPPQGGPMDSDVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTKSNRYRVYQI 119
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QY 121 PGKPEIVDSASELTAGVKNKGTCTVSEGSYPAGTSLSHWLDGKPLVNEKGVSKQTRRH 180
Db 120 PGKPEIVDPASELMAGVKNKGTCTVSEGGYPAGTSLNWLDDGKTLIPDGGKGVSKETKRH 179
QY 181 PETGLFTLQSELMTVPARGDPRPTSCFSFGLPRHRLRTAPIQPRVW----- 230
Db 180 PKTGLFTLHSELMTVPARGGALHPTSCSFTPLPRRALHTAPQLRVWSEHRGEGEPN 239
QY 231 -EVPLEEVQVVEPPGGAVAGGTGTTLTCEVPAQSPQIHKMDGVPPLPPSPVLILP 289
Db 240 VDAVPLKEVQVVEPPGGAVAGGTGTTLTCEAPAQPPIQIHWIKDGRPLPLPPGMLLLP 299
QY 290 EIGPQDQGYTSCVATHSHSGPQESRAVSIIIEPGEETAGSVGGSL 338
Db 300 EVGPEDQGYTSCVATHPSHGQESRAVSIIIEETGEGTTAGSVEGPGL 348

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## RESULT 12

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US-09-638-648-1
; Sequence 1, Application US/09638648
; Patent No. 6825164
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; APPLICANT: Zlokovic, Berislav
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
; FILE REFERENCE: 0575/62097
; CURRENT APPLICATION NUMBER: US/09/638,648
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Bos Taurus
US-09-638-648-1

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Query Match 81.9%; Score 1480; DB 4; Length 416;
Best Local Similarity 80.5%; Pred. No. 4.6e-118;
Matches 281; Conservative 22; Mismatches 34; Indels 12; Gaps 2;

QY 1 MAAGTAVGAWVLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60
Db 1 MAAGTAVGAWVLVLSLGTGTGQNTITARIGKPLVNLCKGAPKPPQQLWKLTGRTEA 60
QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKTSNRYRVYQI 120
Db 61 WKVLSPO-GDPWDSVARVLPNGSLLLPAVGIODEGTFRCATSRSGKTSNRYRVYQI 119
QY 121 PGKPEIVDSASELTAGVKNKGTCTVSEGSYPAGTSLSHWLDGKPLVNEKGVSKQTRRH 180
Db 120 PGKPEIVDPASELMAGVKNKGTCTVSEGGYPAGTSLNWLDDGKTLIPDGGKGVSKETKRH 179
QY 181 PETGLFTLQSELMTVPARGDPRPTSCFSFGLPRHRLRTAPIQPRVW----- 230
Db 180 PKTGLFTLHSELMTVPARGGALHPTSCSFTPLPRRALHTAPQLRVWSEHRGEGEPN 239
QY 231 -EVPLEEVQVVEPPGGAVAGGTGTTLTCEVPAQSPQIHKMDGVPPLPPSPVLILP 289
Db 240 VDAVPLKEVQVVEPPGGAVAGGTGTTLTCEAPAQPPIQIHWIKDGRPLPLPPGMLLLP 299
QY 290 EIGPQDQGYTSCVATHSHSGPQESRAVSIIIEPGEETAGSVGGSL 338
Db 300 EVGPEDQGYTSCVATHPSHGQESRAVSIIIEETGEGTTAGSVEGPGL 348

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## RESULT 13

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US-09-638-649-5
; Sequence 5, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:

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; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Murine
US-09-638-649-5

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Query Match 77.8%; Score 1404.5; DB 4; Length 403;
Best Local Similarity 78.4%; Pred. No. 1.2e-111;
Matches 265; Conservative 20; Mismatches 52; Indels 1; Gaps 1;

QY 1 MAAGTAVGAWVLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60
Db 1 MPAGTAARAWVLVLAAGVAGGQNTARIGEPVLVSCGAPKPPQQLWKLTGRTEA 60
QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKTSNRYRVYQI 120
Db 61 WKVLSPO-GGPWDSVAQILPNSLLPATGIVDEGTFRCATNRGKTSNRYRVYQI 119
QY 121 PGKPEIVDSASELTAGVKNKGTCTVSEGSYPAGTSLSHWLDGKPLVNEKGVSKQTRRH 180
Db 120 PGKPEIVDPASELTASVPNKVGTCTVSEGSYPAGTSLSHWLDGKPLVNEKGVSKQTRRH 179
QY 181 PETGLFTLQSELMTVPARGDPRPTSCFSFGLPRHRLRTAPIQPRVWPEVPLEBVOL 240
Db 180 PETGLFTLRLSELTVIPTQGGTHTFTSCFSGLGIPRRPLNTAPIQLRVREPPEGIQL 239
QY 241 VVEPEGGAVAPGTVTLTCEVPAQSPQIHKMDGVPPLPPSPVLILPPIGPDQGTYS 300
Db 240 LVEPEGGIVAPGTVTLTCAISAPPPQVHWIKDGAFLPLAPSPVLLLPVGHADGTYS 299
QY 301 CVATHSHSGPQESRAVSIIIEPGEETAGSVGGSL 338
Db 300 CVATHSHSGPQESPPVSIRVTETGDEGPAESVGSGL 337

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## RESULT 14

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US-09-638-648-5
; Sequence 5, Application US/09638648
; Patent No. 6825164
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; APPLICANT: Zlokovic, Berislav
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
; FILE REFERENCE: 0575/62097
; CURRENT APPLICATION NUMBER: US/09/638,648
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mouse
US-09-638-648-5

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Query Match 77.8%; Score 1404.5; DB 4; Length 403;
Best Local Similarity 78.4%; Pred. No. 1.2e-111;
Matches 265; Conservative 20; Mismatches 52; Indels 1; Gaps 1;

QY 1 MAAGTAVGAWVLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60

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61	WKVLSPO- GGPWDSVAQILPNGSLLLPAT	GIVDEGTFRCRATNRGKEVKSNYRVVQI	119
121	PGKPEI VDSASELTAGVKNKVGTCVSEGS	YPAGTILSWHLDGKPLVPNEKGVSVKQTRR	180
120	PGKPEI VDPASELTASVKNKVGTCVSEGS	YPAGTILSWHLDGKLLIPDGKETLVKQETRR	179
181	PETGLFTLQSELMVTPARGGDPDRPTFSC	SFSGPLPRHRLRTAPIQPRWVEVPLEEQVL	240
180	PETGLFTLRSELVTPIQGGTTHPTFSCSF	SGLPRRLPLNTAPIQLRVRESGPPEGIQL	239
241	VVEPEGGAVASPGVTTLTCEVPAOPSPQI	HWKDGVPILPSPSVLILPEIQPQQGYS	300
240	LVEPEGGIVAFGGVTTLTCAISAQPPQVH	MIKDGAPLPLAPSPLLPEVGHADGTVS	299
301	CVATHSHGPOESRAVSIISIEPGEEGPTAG	SVGGSL	338
300	CVATHSHGPOESPVSIRVTETDGGPAESV	GESGL	337

**RESULT 15**

US-09-702-705-334  
; Sequence 334, Application US/09702705

; Patent No. 6504010

: GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Bangor, Chaitanya

APPLICANT: Lodes, Michael A.

: AFFILIANT: Fanger, Gary

APPLICANT: Ranger, Gary  
APPLICANT: Vedvick, Tom

APPLICANT: VEDUVICK, TOM

;	APPLICANT:	Carter, Darrin
:	APPLICANT:	Potter, Marc

; APPLICANT: Ketter, Ma:

APPLICANT: Mannion, Jane  
APPLICANT: For Licensing

APPLICANT: Fan, Liqun

TITLE OF INVENTION: COMPOSITIONS AND METHODS

# COMPOSITION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:

FILE REFERENCE	310121	478G14
TITLE OF INVENTION:	DIAGNOSIS OF	

FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705

;  
CURRENT FILING

; NUMBER OF SEQ

; SOFTWARE: F8

; SEQ ID NO 334

; LENGTH: 582

Query Match	12.4%;	Score	223.5;	DB	4;	Length	582;
Best Local Similarity	25.8%;	Pred. No.	1.1e-10;				
Matches	80;	Conservative	46;	Mismatches	133;	Indels	51;
Gaps	12;						
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DB	25	LGHYTVNSAGVDTHIIIFCR	---LDVPQNLMF---	GK---	WKYEKPGSPVFIARFSSTK	74	
QY	71	---PWDSV-----	ARVLPNGSLFLP	AVGIQDEGIFRCQAMNRNGKETSNY	-----	RVR	116
DB	75	KSQYDDVPEYKDRLNLSENVTLIS	SNARISDEKRFVCLV	-----	TEDNVPEAPTIVK	128	
QY	117	VYQIPGKPEIVDSASELTAGVPNKVCHTCEGSPAGTLS	SHWLDCKPLVPNEKCVSVKEQ	176			
DB	129	VFKQSPKEIVSKALFLETEQLKGLGDCIS	EDSYPDGNITWYRNGKVLHLEGAWVIFIK	188			
QY	177	TRRHPTGLFTLQSELWVT	PARGDPRPTSCS---	FSPGLPRHRLARTAPIQRPVWE	-P	232	
DB	189	KEMDPVQLYTMWTSLEYKTTK	-ADIQMPFTCSVYYGPS	-----	GQKTHSEQAVFDIY	242	
QY	233	VPLEEVQLVVEPEGGAVAGPGT	VTLTCEVPAQPS	-QIHWKMGQGVLPPLPPSPVLI	LP	291	

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: March 15, 2005, 11:27:19 ; Search time 333 Seconds  
(without alignments)  
335.788 Million cell updates/sec

Title: US-10-091-019-3  
Perfect score: 1806  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Query		Description	
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1	1806	100.0	339	14	US-10-091-019-3	Sequence 3, Appli	
2	1802	99.8	404	15	US-10-309-290-96	Sequence 96, Appl	
3	1782.5	98.7	405	8	US-08-755-235-4	Sequence 4, Appli	
4	1768	97.9	347	17	US-10-472-507A-2	Sequence 2, Appli	
5	1709	94.6	390	15	US-10-309-290-100	Sequence 100, App	
6	1705	94.4	390	15	US-10-309-290-98	Sequence 98, Appl	
7	1690	93.6	332	9	US-09-872-185B-2	Sequence 2, Appli	
8	1690	93.6	332	9	US-09-851-071-1	Sequence 1, Appli	
9	1480	81.9	416	8	US-08-755-235-2	Sequence 2, Appli	
10	1379.5	76.4	342	16	US-10-408-765A-641	Sequence 641, App	
11	595	32.9	112	9	US-09-872-185B-1	Sequence 1, Appli	
12	229.5	12.7	3931	15	US-10-120-801-18	Sequence 18, Appl	
13	224.5	12.4	1034	15	US-10-094-749-2631	Sequence 2631, Ap	

14	223.5	12.4	570	17	US-10-741-600-1431	Sequence 1431, Ap
15	223.5	12.4	582	9	US-09-736-457-334	Sequence 334, App
16	223.5	12.4	582	9	US-09-902-941-334	Sequence 334, App
17	223.5	12.4	582	9	US-09-849-626-334	Sequence 334, App
18	223.5	12.4	582	10	US-09-476-300-334	Sequence 334, App
19	223.5	12.4	582	14	US-10-017-754-334	Sequence 334, App
20	223.5	12.4	582	14	US-10-113-872-334	Sequence 334, App
21	223.5	12.4	582	15	US-10-283-017-334	Sequence 334, App
22	223.5	12.4	583	17	US-10-741-600-1430	Sequence 1430, Ap
23	223.5	12.3	583	14	US-10-176-847-64	Sequence 64, Appl
24	222.5	12.3	583	14	US-10-205-823-12	Sequence 12, Appl
25	222.5	12.3	583	15	US-10-170-385-277	Sequence 277, App
26	222.5	12.3	583	15	US-10-058-270A-136	Sequence 136, App
27	222.5	12.3	583	17	US-10-741-600-1433	Sequence 1433, Ap
28	217.5	12.0	645	15	US-10-295-027-352	Sequence 352, App
29	217.5	12.0	646	14	US-10-021-660-75	Sequence 75, Appl
30	217.5	12.0	646	14	US-10-021-660-106	Sequence 106, App
31	217.5	12.0	646	15	US-10-211-482-20	Sequence 20, Appl
32	217.5	12.0	646	15	US-10-211-482-125	Sequence 125, App
33	215.5	11.9	3409	16	US-10-367-094-165	Sequence 165, App
34	214	11.8	1479	15	US-10-021-956A-325	Sequence 325, App
35	214	11.8	1496	14	US-10-021-660-125	Sequence 125, App
36	214	11.8	1496	15	US-10-331-496A-28	Sequence 28, Appl
37	214	11.8	1496	15	US-10-211-482-87	Sequence 87, Appl
38	214	11.8	1498	15	US-10-243-552-899	Sequence 899, App
39	214	11.8	1498	15	US-10-276-774-1957	Sequence 1957, Ap
40	212.5	11.8	753	13	US-10-105-934-5	Sequence 5, Appli
41	212.5	11.8	753	17	US-10-895-676-5	Sequence 5, Appli
42	211.5	11.7	532	17	US-10-741-600-1432	Sequence 1432, Ap
43	209	11.6	1477	14	US-10-274-583-20	Sequence 20, Appl
44	209	11.6	1651	14	US-10-289-776-18	Sequence 18, Appl
45	205	11.4	961	15	US-10-162-335-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1  
US-10-091-019-3  
; Sequence 3, Application US/10091019  
; Publication No. US20030166063A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Robert B.  
; APPLICANT: Shen, Jane M.  
; APPLICANT: Shabbaz, Manouchehr M.  
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins  
; FILE REFERENCE: 41305-270555  
; CURRENT APPLICATION NUMBER: US/10/091, 019  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/273,418  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-091-019-3

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Best Local Similarity	100.0%	Pred. No.	3.9e-116				
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Db	1	MAAGTAGAGWLVLSLWGA	VGAQNTARIGBPLVKCKGAPKPPORLEWKLNTGRTA	60			
QY	61	WKVLSFQGGPWSVARVLP	NGSLFPAVIGIODEGIFRCQAMNRNGKETSRYRVYQI	120			
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Db 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLMDGKPLVPNEKGVSKQTRRH 180  
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QY 241 VVEPEGAVAPGGTGTTLTCEVPAQSPQIHMKDGVPLPLPPSPVLILPEIGPDQGTYS 300  
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QY 301 CVATHSHGPOESRAVSISIIIEPEGPTAGSVGGSLV 339  
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## RESULT 2

US-10-309-290-96  
; Sequence 96, Application US/10309290  
; Publication No. US20040023241A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsbrook II, John P.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Chilikuru, Rajeev A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Gould-Rothberg, Bonnie E.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Jeffers, Michael E.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Li, Li  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Murphey, Ryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Peyman, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Starling, Gary  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Voss, Edward Z.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS, ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-502A  
; CURRENT APPLICATION NUMBER: US/10/309,290  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/336,600  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,285  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/341,346  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/341,477  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/341,540  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/342,592  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/344,297  
; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/344,903  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/373,288  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 60/380,981  
; PRIOR FILING DATE: 2002-05-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 274

; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 96  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-290-96

Query Match 99.8%; Score 1802; DB 15; Length 404;  
Best Local Similarity 100.0%; Pred. No. 9e-116;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIIGBPLVKCKGAPKPPQRLWKLTGRTEA 60  
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Db 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIDDEGIFRCQAMNRNGKETKSNYRVVQI 120  
QY 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLMDGKPLVPNEKGVSKQTRRH 180  
Db 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLMDGKPLVPNEKGVSKQTRRH 180  
QY 181 PETGLFTLQSELMVTPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 240  
Db 181 PETGLFTLQSELMVTPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 240  
QY 241 VVEPEGAVAPGGTGTTLTCEVPAQSPQIHMKDGVPLPLPPSPVLILPEIGPDQGTYS 300  
Db 241 VVEPEGAVAPGGTGTTLTCEVPAQSPQIHMKDGVPLPLPPSPVLILPEIGPDQGTYS 300  
QY 301 CVATHSHGPOESRAVSISIIIEPEGPTAGSVGGSL 338  
Db 301 CVATHSHGPOESRAVSISIIIEPEGPTAGSVGGSL 338

## RESULT 3

US-08-755-235-4  
; Sequence 4, Application US/08755235  
; Publication No. US20030059423A1  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Wu, Jun  
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES  
; FILE REFERENCE: 0575/50159  
; CURRENT APPLICATION NUMBER: US/08/755,235  
; CURRENT FILING DATE: 1996-11-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 405  
; TYPE: PRT  
; ORGANISM: Human  
US-08-755-235-4

Query Match 98.7%; Score 1782.5; DB 8; Length 405;  
Best Local Similarity 99.4%; Pred. No. 2e-114;  
Matches 336; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 AAGTAVGAWLVLSLWGAVVGAQNITARIIGBPLVKCKGAPKPPQRLWKLTGRTEA 61  
Db 2 AAGTAVGAWLVLSLWGAVVGAQNITARIIGBPLVKCKGAPKPPQRLWKLTGRTEA 61  
QY 62 KVLSPQGGGPDWSVARVLPNGSLFLPAVGIDDEGIFRCQAMNRNGKETKSNYRVVQI 121  
Db 62 KVLSPQGGGPDWSVARVLPNGSLFLPAVGIDDEGIFRCQAMNRNGKETKSNYRVVQI 121  
QY 122 GKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLMDGKPLVPNEKGVSKQTRRH 181  
Db 122 GKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLMDGKPLVPNEKGVSKQTRRH 181  
QY 182 ETGLFTLQSELMVTPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 241



Db 182 ETGLFTLQSELMVTPARGDPRPTFCSPSGLPRHRLRTAPIQVRWVEPVPLEEVQLV 241  
Qy 242 VEPEGAVAPGGTVTITCEVPAQPSQIHWMKDGVPPLPPSPVLITLPRIGPDQGTYS 301  
Db 242 VEPEGAVAPGGTVTITCEVPAQPSQIHWMKDGVPPLPPSPVLITLPRIGPDQGTYS 301  
Qy 302 VATSHSHGPOESRA-VSIISIIBPGBEGPTAGSVGGSL 338  
Db 302 VATSHSHGPOESRAVSIISIIBPGBEGPTAGSVGGSL 339

RESULT 4

US-10-472-507A-2  
; Sequence 2, Application US/10472507A  
; Publication No. US2005033017A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamamoto, Hiroshi  
; APPLICANT: Yonekura, Hideto  
; APPLICANT: Yamamoto, Yasuhiko  
; APPLICANT: Sakurai, Shigeru  
; APPLICANT: Watanabe, Takuo  
; TITLE OF INVENTION: Soluble Rage Protein  
; FILE REFERENCE: 026350-089  
; CURRENT APPLICATION NUMBER: US/10/472,507A  
; PRIOR FILING DATE: 2003-09-22  
; PRIOR APPLICATION NUMBER: PCT/JP02,02623  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: JP 2001-78409  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: JP 2001-243114  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: JP 2002-48182  
; PRIOR FILING DATE: 2002-02-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 347  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-472-507A-2

Query Match 97.9%; Score 1768; DB 17; Length 347;  
Best Local Similarity 100.0%; Pred. No. 1.6e-113;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGPLVLKCKGAPKPKPQRLWKLTGRTGA 60  
Db 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGPLVLKCKGAPKPKPQRLWKLTGRTGA 60  
Qy 61 WKVLSPPQGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120  
Db 61 WKVLSPPQGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120  
Qy 121 PKPEIVDSASELTAGVPKNKGTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSVKQGTTRH 180  
Db 121 PKPEIVDSASELTAGVPKNKGTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSVKQGTTRH 180  
Qy 181 PETGLFTLQSELMVTPARGDPRPTFCSPSGLPRHRLRTAPIQVRWVEPVPLEEVQL 240  
Db 181 PETGLFTLQSELMVTPARGDPRPTFCSPSGLPRHRLRTAPIQVRWVEPVPLEEVQL 240  
Qy 241 VVEPEGAVAPGGTVTITCEVPAQPSQIHWMKDGVPPLPPSPVLITLPRIGPDQGTYS 300  
Db 241 VVEPEGAVAPGGTVTITCEVPAQPSQIHWMKDGVPPLPPSPVLITLPRIGPDQGTYS 300  
Qy 301 CVATHSHGPOESRAVSIISIIBPGBEGPTAG 331  
Db 301 CVATHSHGPOESRAVSIISIIBPGBEGPTAG 331

RESULT 5

US-10-309-290-100

; Sequence 100, Application US/10309290  
; Publication No. US20040023241A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsobrook II, John P.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Chillakuru, Rajeev A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Gould-Rothberg, Bonnie E.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Jeffers, Michael E.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Li, Li  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Murphey, Ryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Peyman, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Starling, Gary  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Voss, Edward Z.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
; FILE REFERENCE: 21402-502A  
; CURRENT APPLICATION NUMBER: US/10/309,290  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/336,600  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,285  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/341,346  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/341,477  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/341,540  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/342,592  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/344,297  
; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/344,903  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/373,288  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 60/380,981  
; PRIOR FILING DATE: 2002-05-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 100  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-290-100

Query Match 94.6%; Score 1709; DB 15; Length 390;  
Best Local Similarity 95.9%; Pred. No. 2.1e-109;  
Matches 324; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
Qy 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGPLVLKCKGAPKPKPQRLWKLTGRTGA 60  
Db 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGPLVLKCKGAPKPKPQRLWKLTGRTGA 60  
Qy 61 WKVLSPPQGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120

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Db 54 -----GGGPWDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQI 106
Qy 121 PKPEIVDSASELTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 180
Db 107 PKPEIVDSASELTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 166
Qy 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
Db 167 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 226
Qy 241 VVEPEGAVAPGGTIVTLTCEVPAQSPQIHWMDGVPLPLPPSPVLILPIGPDQGTYS 300
Db 227 VVEPEGAVAPGGTIVTLTCEVPAQSPQIHWMDGVPLPLPPSPVLILPIGPDQGTYS 286
Qy 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 338
Db 287 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 324

RESULT 6
US-10-309-290-98
; Sequence 98, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
```

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; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 98
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-98

Query Match 94.4%; Score 1705; DB 15; Length 390;
Best Local Similarity 95.6%; Pred. No. 4e-109;
Matches 323; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

Qy 1 MAAGTAVGAWLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPQRLWK LNTGRTEA 60
Db 1 MAAGTAVGTWVLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPQRLWK L----- 53

Qy 61 WKVLS PQGGP WDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQI 120
Db 54 -----GGGPWDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQI 106

Qy 121 PKPEIVDSASELTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 180
Db 107 PKPEIVDSASELTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 166

Qy 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
Db 167 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 226

Qy 241 VVEPEGAVAPGGTIVTLTCEVPAQSPQIHWMDGVPLPLPPSPVLILPIGPDQGTYS 300
Db 227 VVEPEGAVAPGGTIVTLTCEVPAQSPQIHWMDGVPLPLPPSPVLILPIGPDQGTYS 286

Qy 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 338
Db 287 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 324

RESULT 7
US-09-872-185B-2
; Sequence 2, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-872-185B-2

Query Match 93.6%; Score 1690; DB 9; Length 332;
Best Local Similarity 100.0%; Pred. No. 3.6e-108;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AQNITARI GEPLV LKCKGAPKPPQRLWK LNTGRTEA WKLSPQGGP WDSVARVLPNG 82
Db 1 AQNITARI GEPLV LKCKGAPKPPQRLWK LNTGRTEA WKLSPQGGP WDSVARVLPNG 60

Qy 83 SLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQI PGKPEIVDSASELTAGVFNKVG 142
Db 61 SLFLPAVGIODEGIFRCQAMNRNGKETKSNRYRVYQI PGKPEIVDSASELTAGVFNKVG 120
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QY 143 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHBPETGLFTLQSELMTVPARGGDP 202  
DB 121 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHBPETGLFTLQSELMTVPARGGDP 180  
QY 203 RPTFSCSFSGPLPRHRLATAPIQPRVWPVPLEEVQVVEGGAVAPGGTTLTCEVP 262  
DB 181 RPTFSCSFSGPLPRHRLATAPIQPRVWPVPLEEVQVVEGGAVAPGGTTLTCEVP 240  
QY 263 AQPSPQIHWKMDGVPPLPPLPPSVLLILPEIGPQDQGTYSVATHSSHGPOESRAVSISIIIE 322  
DB 241 AQPSPQIHWKMDGVPPLPPLPPSVLLILPEIGPQDQGTYSVATHSSHGPOESRAVSISIIIE 300  
QY 323 PGEEGTAGSVGSGGL 338  
DB 301 PGEEGTAGSVGSGGL 316

RESULT 8  
US-09-851-071-1  
; Sequence 1, Application US/09851071  
; Patent No. US20020177550A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Anne Marie  
; APPLICANT: Stern, David  
; TITLE OF INVENTION: A METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A SUBJECT  
; FILE REFERENCE: 0575/55424-Z/JPW/SHS/MVM  
; CURRENT APPLICATION NUMBER: US/09/851,071  
; CURRENT FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Human  
US-09-851-071-1

Query Match 93.6%; Score 1690; DB 9; Length 332;  
Best Local Similarity 100.0%; Pred. No. 3.6e-108;  
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIIGEPLVLCCKGAPKPPQRLWKLNTGRTEANKVLSPOGGGPDWSVARVLPNG 82  
DB 1 AQNITARIIGEPLVLCCKGAPKPPQRLWKLNTGRTEANKVLSPOGGGPDWSVARVLPNG 60  
QY 83 SLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQIPCKPEIVDSASELTAGVPNKVG 142  
DB 61 SLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQIPCKPEIVDSASELTAGVPNKVG 120  
QY 143 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHBPETGLFTLQSELMTVPARGGDP 202  
DB 121 TCVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRHBPETGLFTLQSELMTVPARGGDP 180  
QY 203 RPTFSCSFSGPLPRHRLATAPIQPRVWPVPLEEVQVVEGGAVAPGGTTLTCEVP 262  
DB 181 RPTFSCSFSGPLPRHRLATAPIQPRVWPVPLEEVQVVEGGAVAPGGTTLTCEVP 240  
QY 263 AQPSPQIHWKMDGVPPLPPLPPSVLLILPEIGPQDQGTYSVATHSSHGPOESRAVSISIIIE 322  
DB 241 AQPSPQIHWKMDGVPPLPPLPPSVLLILPEIGPQDQGTYSVATHSSHGPOESRAVSISIIIE 300  
QY 323 PGEEGTAGSVGSGGL 338  
DB 301 PGEEGTAGSVGSGGL 316

RESULT 9  
US-08-755-235-2  
; Sequence 2, Application US/08755235  
; Publication No. US20030059423A1  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Wu, Jun  
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES  
; FILE REFERENCE: 0575/50159  
; CURRENT APPLICATION NUMBER: US/08/755,235  
; CURRENT FILING DATE: 1996-11-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 416  
; TYPE: PRT  
; ORGANISM: Bovine  
US-08-755-235-2

Query Match 81.9%; Score 1480; DB 8; Length 416;  
Best Local Similarity 80.5%; Pred. No. 1.2e-93;  
Matches 281; Conservative 22; Mismatches 34; Indels 12; Gaps 2;

QY 1 MAAGTAVGAWVLVLSLWGAIVGAQNTARIGEPVLVLCCKGAPKPPQRLWKLNTGRTEA 60  
DB 1 MAAGAVVGAWMLVLSLGGTGTVDQNTARIGKVLNCKGAPKPPQRLWKLNTGRTEA 60  
QY 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120  
DB 61 WKVLSPOGDPWDVARVLPNGSLFLPAVGIQDEGIFRCATRSRSGKETKSNYRVVYQI 119  
QY 121 PKPPIVDSASELTAGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRH 180  
DB 120 PKPPIVDPASSELMAVGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRH 179  
QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSFSGPLPRHRLATAPIQPRVW----- 230  
DB 180 PKTGLFTLHSELMTVPARGGALHPTFSCSFTPLPRRRALHTAPIQLRVMSBHRGSGGN 239  
QY 231 -BPVPLEEVQVVEGGAVAPGGTTLTCEVPAQSPQIHWKMDGVPPLPPLPPSVLILP 289  
DB 240 VDAVPLEVQVVEGGAVAPGGTTLTCEVPAQPPQIHWIKDGRPLPLPPGMLLLP 299  
QY 290 ETGPDQGTYSVATHSSHGPOESRAVSISIIIEPGEEGTAGSVGSGGL 338  
DB 300 EVGPEDQGTYSVATHSSHGPOESRAVSIIETGEGTAGSVGSGGL 348

RESULT 10  
US-10-408-765A-641  
; Sequence 641, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Roin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 641  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-641

Query Match 76.4%; Score 1379.5; DB 16; Length 342;  
Best Local Similarity 78.4%; Pred. No. 7.9e-87;  
Matches 279; Conservative 6; Mismatches 28; Indels 43; Gaps 6;  
QY 1 MAAGTAVGAWVLVLSLWGAIVGAQNTARIGEPVLVLCCKGAPKPPQRLWKLNTGRTEA 60

Db 1 MAAGTAVGAVVLVLSLWAGVVAQNTARIGEPLVLKCKGAPKPPORLEWL----- 53  
 QY 61 WKVLSPOGGGWDVSVARVLPNGSLFLPAVGQDEGIFRCQAMNRNGKETKSNRYRVYQI 120  
 Db 54 -----GGGPDVSVARVLPNGSLFLPAVGQDEGIFRCQAMNRNGKETKSNRYRVYQI 106  
 QY 121 FGPKEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLWHLDGKPLVPNEKGVSVKEQTRRH 180  
 Db 107 FGPKEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLWHLDGKPLVPNEKGVSVKEQTRRH 166  
 QY 181 PETGLTLOSBLMTVPARGDPRTFSCSPGLPRHRLRTAPIQPRVWPEVPLEVQL 240  
 Db 167 PETGLTLOSBLMTVPARGDPRTFSCSPGLPRHRLRTAPIQPRVWPEVPLEVQL 226  
 QY 241 VVEPEGAVAPGGTWTLTCEVPAQSPQIHWMDGVPLPLPPSVLLIPGPDQGTYS 300  
 Db 227 VVEPEGAVAPGGTWTLTCEVPAQSPQIHWMDGVPLPLPPSVLLIPGPDQGTYS 277  
 QY 301 C-----VATHSHG-----PQSR-----AVSIIIEPGEEGP-TAGSVGGS 336  
 Db 278 CRLCGIRAGNSPSPGDPGRPGDSRPAHWGHLVAKAATPRRGEGRKPGGRGA 333

## RESULT 11

US-09-872-185B-1  
 ; Sequence 1, Application US/09872185B  
 ; Patent No. US2002012799A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stern, David M.  
 ; APPLICANT: Herold, Kevan  
 ; APPLICANT: Yan, Shi Du  
 ; APPLICANT: Schmidt, Ann Marie  
 ; APPLICANT: Lamster, Ira  
 ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION  
 ; FILE REFERENCE: 0575/64080  
 ; CURRENT APPLICATION NUMBER: US/09/872,185B  
 ; CURRENT FILING DATE: 2001-06-01  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 112  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-872-185B-1

Query Match 32.9%; Score 595; DB 9; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIIGEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGPWDVSVARVLPNG 82  
 Db 1 AQNITARIIGEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGPWDVSVARVLPNG 60  
 QY 83 SFLPAPVQDEGIFRCQAMNRNGKETKSNRYRVYQIPKPEIVDSASELT 134  
 Db 61 SFLPAPVQDEGIFRCQAMNRNGKETKSNRYRVYQIPKPEIVDSASELT 112

## RESULT 12

US-10-120-801-18  
 ; Sequence 18, Application US/10120801  
 ; Publication No. US20030203843A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pena, Carol  
 ; APPLICANT: Guo, Xiaojia  
 ; APPLICANT: Shimkets, Richard  
 ; APPLICANT: Padigar, Muralidhara  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Spytek, Kimberly  
 ; APPLICANT: Mehraban, Fuad  
 ; APPLICANT: Topper, James N.  
 ; APPLICANT: Malvankar, Uriel  
 ; APPLICANT: Wasserman, Scott

; APPLICANT: Edinger, Shlomit  
 ; APPLICANT: Smithson, Glennda  
 ; APPLICANT: Gunther, Erik  
 ; APPLICANT: Komuves, Laszlo  
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 21402-340  
 ; CURRENT APPLICATION NUMBER: US/10/120,801  
 ; CURRENT FILING DATE: 2002-04-11  
 ; PRIOR APPLICATION NUMBER: 60/285748  
 ; PRIOR FILING DATE: 2001-04-23  
 ; PRIOR APPLICATION NUMBER: 60/286068  
 ; PRIOR FILING DATE: 2001-04-24  
 ; PRIOR APPLICATION NUMBER: 60/286292  
 ; PRIOR FILING DATE: 2001-04-25  
 ; PRIOR APPLICATION NUMBER: 60/288334  
 ; PRIOR FILING DATE: 2001-05-03  
 ; PRIOR APPLICATION NUMBER: 60/291241  
 ; PRIOR FILING DATE: 2001-05-16  
 ; PRIOR APPLICATION NUMBER: 60/322284  
 ; PRIOR FILING DATE: 2001-09-14  
 ; PRIOR APPLICATION NUMBER: 60/285609  
 ; PRIOR FILING DATE: 2001-04-20  
 ; NUMBER OF SEQ ID NOS: 155  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 18  
 ; LENGTH: 3931  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-120-801-18

Query Match 12.7%; Score 229.5; DB 15; Length 3931;  
 Best Local Similarity 28.3%; Pred. No. 1.3e-06;  
 Matches 86; Conservative 38; Mismatches 127; Indels 53; Gaps 13;  
 QY 31 GEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGPWDVSVARVLPNGSLFLPAVG 90  
 Db 1934 GQEVRLDCE-ADGQPPDPVAV-LKDG-----SPLQDMGPHLRFYLDGSLVLKGLR 1983  
 QY 91 IQDEGIFRCQAMNRNGKETKSNRYRVYQIPKPEIVDSASELTAGVFNKVT--CVSEG 148  
 Db 1984 ASDAGAYTCVAHNPADEARL-HTVNVLPPTIKQADGSGTLVSR-PGELVTWVCPVRG 2041  
 QY 149 SYPAGTSLWHLDGKPLVPNEK-----GVSVKETRRHPETGLTLOSELMTVPARGDP 202  
 Db 2042 SPPI-HVSWLKDGLPLPLSQRTLAHSGHTLRISKVQLADAGIETC---VAASAPGVADR 2097  
 QY 203 RPTSCSFSPGLPRHRLRTAPIQPRVWPEVPLEEVLVVEPEGAVAPGGTWTLTCEVP 262  
 Db 2098 NFTLQVQVPP-----VLEPVEFQNDVVVVR-----GSLVELPCEAR 2133  
 QY 263 AQPSPQIHWMDGVPL---PLPPSPVLLIPGPDQGTYSVATHSHGHPQESRAVVIS 319  
 Db 2134 GVPLPLVSWMDKGFLLSQLEQPSLOLEAVGAGDSGTYSVAV--SEAGEARRHFOLT 2191  
 QY 320 IIEP 323  
 Db 2192 VMEP 2195

## RESULT 13

US-10-094-749-2631  
 ; Sequence 2631, Application US/10094749  
 ; Publication No. US20030219741A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ISOGAI, TAKAO  
 ; APPLICANT: SUGIYAMA, TOMOYASU  
 ; APPLICANT: OTSUKI, TETSUJI  
 ; APPLICANT: WAKAMATSU, AI  
 ; APPLICANT: SATO, HIROYUKI  
 ; APPLICANT: ISHII, SHIZUKO  
 ; APPLICANT: YAMAMOTO, JUN-ICHI  
 ; APPLICANT: ISONO, YUUKO  
 ; APPLICANT: HIO, YURI

```

; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2631
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2631

Query Match 12.4%; Score 224.5; DB 15; Length 1034;
Best Local Similarity 24.6%; Pred. No. 6.3e-07;
Matches 84; Conservative 44; Mismatches 132; Indels 81; Gaps 13;

QY 15 SLWGAVGQNTARI-----GELVLKCKGAPKPPQRLWKLNTGRT----- 58
DB 51 SLNGSRVGPEDAMPRIVEQPPDLLVSRGSPATLPCR-ABGRPRPNITKNGARVATVRE 109
QY 59 --EAWKVLSPQGGPWSVARVLNGLSLFLPAV-----GIQDEGIFRCOAMNRNGKETKS 111
DB 110 DPAHKL-----LPSGALFPRLVHGRRARPDEGVTCVARVNLGAABR 155
QY 112 NYRVRY-----YQIPGRPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPL 164
DB 156 NASLEAVLRLDDFRQSPGNVW-----AVGEP-AVLECVPRGHPSPVSMRKDGARL 207
QY 165 VNEKGVSVKEQTRRRPETGLFTLOSELMTVPARGGDPRTTSCSPGLPHRALRTAP 224
DB 208 KEEGRITIR-----GGLMMSHTLXSD-AGMYVCVAS-NNAGERESAAA- 250
QY 225 IQPRVWEVPLEEVQLVVEPEGAVAPGTVTLTCEVPAQPSQ-PIHMMKDGVPPLP 279
DB 251 -----EVMVLERPSPLRPPVNVQVVLADAPVTLCEVKGDPPLRLWRKEDGELPTGRYE 304
QY 280 LPPSPVLLIPEIQPOQGTCTVSYVATHSSRHGQESRAVSISI 320
DB 305 IRSDSLWIGHVSAEDEGTYTCAENSVGRAESGSLSVHV 345

RESULT 14
US-10-741-600-1431
; Sequence 1431, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1431
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1431
```

```

Query Match 12.4%; Score 223.5; DB 17; Length 570;
Best Local Similarity 25.8%; Pred. No. 3.7e-07;
Matches 80; Conservative 46; Mismatches 133; Indels 51; Gaps 12;

QY 21 VQAQNTARIGPEPLVLKCKGAPKPPQRLWKLNTGRTAWEKVLSPQGG----- 70
DB 26 LGWYTVNSAYGDTIIIPCR---LDVPQNLMP-----GK---WKYKPDGSPVFIAPRSSTK 75
QY 71 ----PWDSV-----ARVLNGLSLFLPAVGIQDEGIFRCOAMNRNGKETKSNY-----RVR 116
DB 76 KSVQYDDVPEYKDRNLNLSNYTSLISNARISDEKRFVCLV-----TEDNVFEAPTIVK 129
QY 117 VYQIPGKPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVNEKGVSVKEQ 176
DB 130 VFQPSKPEIVSKALFLETEQKLKGLDCISESDSPDGNITWYRNGKVLHPLLEGAVVIFK 189
QY 177 TRRHPEETGLTLOSELMTVPARGGDPRTTSCS---FSPGLPHRALRTAPQPRVWE-P 232
DB 190 KEMDPVTQLYTWTSTLEYKTK-ADIQMPTTCSVTYYGPS-----GQKTIHSEQAVFDIY 243
QY 233 VPLEEVQLVVEPEGAVAPGTVTLTCEVPAQPS-PIHMMKDGVPPLPPLPPSPVLILPEI 291
DB 244 YPTEQVTIQLVPPKNAIKEGDNITLKCLNGNPPPEEFLFYLPGQPEGIRSSNTYTLTDV 303
QY 292 GPQDOGTYSK 301
DB 304 RNNATGDYKC 313

RESULT 15
US-09-736-457-334
; Sequence 334, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-334

Query Match 12.4%; Score 223.5; DB 9; Length 582;
Best Local Similarity 25.8%; Pred. No. 3.8e-07;
Matches 80; Conservative 46; Mismatches 133; Indels 51; Gaps 12;

QY 21 VQAQNTARIGPEPLVLKCKGAPKPPQRLWKLNTGRTAWEKVLSPQGG----- 70
DB 25 LGWYTVNSAYGDTIIIPCR---LDVPQNLMP-----GK---WKYKPDGSPVFIAPRSSTK 74
QY 71 ----PWDSV-----ARVLNGLSLFLPAVGIQDEGIFRCOAMNRNGKETKSNY-----RVR 116
DB 75 KSVQYDDVPEYKDRNLNLSNYTSLISNARISDEKRFVCLV-----TEDNVFEAPTIVK 128
QY 117 VYQIPGKPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVNEKGVSVKEQ 176
DB 129 VFQPSKPEIVSKALFLETEQKLKGLDCISESDSPDGNITWYRNGKVLHPLLEGAVVIFK 188
```



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OM protein - protein search, using sw model

Run on: March 15, 2005, 09:06:31 ; Search time 24 Seconds  
(without alignments)  
1359.062 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 1806

Sequence: 1 MAAGTAVGAWVLVLSLWGA.....IIEPGEGETAGSVGGSLV 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1802	99.8	404	1	I61596
2	1480	81.9	416	1	A42879
3	1402	77.6	402	2	T03062
4	223.5	12.4	1344	2	T14316
5	222.5	12.3	583	2	I39428
6	217.5	12.0	646	2	I38049
7	212.5	11.8	523	2	I50478
8	212.5	11.8	588	2	A45254
9	210.5	11.7	588	2	JH0506
10	209	11.6	1612	2	T30805
11	204.5	11.3	587	2	JH0464
12	203	11.2	1651	2	T14160
13	198	11.0	4391	2	A38096
14	196	10.9	1033	2	S19247
15	195.5	10.8	584	2	I50419
16	187	10.4	3707	2	S18252
17	185.5	10.3	521	2	S34338
18	183.5	10.2	423	2	T29549
19	183.5	10.2	1273	2	T42405
20	182.5	10.1	702	2	A36319
21	182	10.1	5175	2	T20992
22	182	10.1	5198	2	T43290
23	180.5	10.0	1265	1	A37967
24	180	10.0	6642	2	T29757
25	179.5	9.9	458	2	JC1509
26	175.5	9.7	344	2	I56551
27	174	9.6	739	2	JS0675
28	169.5	9.4	458	1	WNMSR1
29	169.5	9.4	521	2	JC1508

Query Match 99.8% Score 1802; DB 1; Length 404;

#### ALIGNMENTS

##### RESULT 1

I61596

advanced glycosylation end-products receptor precursor - human

N:Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence revision 07-Feb-1997 #text\_change 09-Jul-2004

C:Accession: I61596; B42879; S27968

R:Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, H.; Genomics 23, 408-419, 1994

A>Title: Three genes in the human MHC class III region near the junction with the class I

nterpart of mouse mammary tumor gene int-3.

A:Reference number: A55562; MUID:95137587; PMID:7835890

A:Accession: I61596

A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL

A:Molecule type: DNA

A:Residues: 1-404 <RES>

A:Cross-references: UNIPROT:Q15109; GB:D28769; NID:9561657; PIDN:BA005958.1; PID:G561659

R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St

J. Biol. Chem. 267, 14998-15004, 1992

A>Title: Cloning and expression of a cell surface receptor for advanced glycosylation en

A:Reference number: A42879; MUID:92340547; PMID:1378843

A:Accession: B42879

A:Molecule type: mRNA

A:Residues: 'G',2-99,'R',101-404 <NEE>

A:Cross-references: EMBL:M91211; NID:G190845; PIDN:AAA03574.1; PID:G190846

A:Experimental source: lung

A>Note: sequence extracted from NCBI backbone (NCBIP:109438)

C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosyl

cellular function, thus contributing to tissue lesions in diabetes.

C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on r

ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.

C:Genetics:

A:Gene: GDB:AGER

A:Cross-references: GDB:306354; OMIM:600214

A:Map position: 6p21.3-6p21.3

A:Introns: 18/1, 53/3, 119/1, 140/3, 170/1, 231/1, 274/3, 322/1, 331/1, 373/2

C:Function:

A>Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neurit

C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology

C:Keywords: Alzheimer's disease; Glycoprotein; receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-404/Product: advanced glycosylation end products receptor #status predicted <MAT>

F:23-344/Domain: extracellular #status predicted <EXT>

F:31-101/Domain: immunoglobulin homology <IM1>

F:137-210/Domain: immunoglobulin homology <IM2>

F:252-303/Domain: immunoglobulin homology <IM3>

F:345-362/Domain: transmembrane #status predicted <TM>

F:363-404/Domain: intracellular #status predicted <INT>

F:25.81/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:38-99,144-208,255-301/disulfide bonds: #status predicted

Best Local Similarity 100.0%; Pred. No. 3.4e-113;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWVLVLSLWGAUVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEA 60  
Db 1 MAAGTAVGAWVLVLSLWGAUVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEA 60

QY 61 WKVLSPOGGPWBDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120  
Db 61 WKVLSPOGGPWBDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120

QY 121 PKRPEIVDSASELTAGVNPKNVGTCSSEGSYPAGTLSWHLDDGKPLVNEKGVSKVKEQTRRH 180  
Db 121 PKRPEIVDSASELTAGVNPKNVGTCSSEGSYPAGTLSWHLDDGKPLVNEKGVSKVKEQTRRH 180

QY 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWPEVLEEVOL 240  
Db 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWPEVLEEVOL 240

QY 241 VVEPEGAVAGGTGVTLTCEVPAQPSQIHHMKDGVPLPLPSPVLLILPEIGPDQGTYS 300  
Db 241 VVEPEGAVAGGTGVTLTCEVPAQPSQIHHMKDGVPLPLPSPVLLILPEIGPDQGTYS 300

QY 301 CVATHSHGPOESRAVSIISIIIEPGEGRGTAGSVGGSL 338  
Db 301 CVATHSHGPOESRAVSIISIIIEPGEGRGTAGSVGGSL 338

RESULT 2  
A42879  
Advanced glycosylation end-products receptor precursor - bovine  
N;Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 04-Mar-1993 #sequence revision 07-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: A42879; A42878; S27949  
R;Neuper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St  
J. Biol. Chem. 267, 14998-15004, 1992  
A;Title: Cloning and expression of a cell surface receptor for advanced glycosylation en  
A;Reference number: A42879; MUID:92340547; PMID:1378843  
A;Accession: A42879  
A;Molecule type: mRNA  
A;Residues: 1-416 <NEE>  
A;Cross-references: UNIPROT:Q28173; GB:M91212; NID:G163650; PIDN:AAA03575.1; PID:G163651  
A;Experimental source: lung  
A;Note: sequence extracted from NCBI backbone (NCBIP:109436)  
R;Schmidt, A.M.; Vianna, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He  
J. Biol. Chem. 267, 14987-14997, 1992  
A;Title: Isolation and characterization of two binding proteins for advanced glycosylati  
A;Reference number: A42878; MUID:92340546; PMID:1321822  
A;Accession: A42878  
A;Molecule type: protein  
A;Residues: 23-24,'X',26-37,'X',39-49,'XX',52-54 <SCH>  
A;Experimental source: endothelial cells  
A;Note: sequence extracted from NCBI backbone (NCBIP:109434)  
C;Comment: advanced glycosylation end products are heterogeneous nonenzymatically glycos  
cellular function, thus contributing to tissue lesions in diabetes.  
C;Comment: this receptor appears also to mediate the effects of amyloid beta peptide on  
aces in the neurotoxic pathway that produces dementia in Alzheimer's disease.  
C;Function:  
A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neuro  
C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology  
C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted <M  
F;23-354/Domain: extracellular #status predicted <EXT>  
F;31-100/Domain: immunoglobulin homology <IM1>  
F;136-209/Domain: immunoglobulin homology <IM2>  
F;262-313/Domain: immunoglobulin homology <IM3>  
F;355-372/Domain: transmembrane #status predicted <TM>  
F;373-416/Domain: intracellular #status predicted <INT>  
F;25.80/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;38-98,143-207,269-311/disulfide bonds: #status predicted

Query Match 81.9%; Score 1480; DB 1; Length 416;  
Best Local Similarity 80.5%; Pred. No. 1.1e-91;  
Matches 281; Conservative 22; Mismatches 34; Indels 12; Gaps 2;

QY 1 MAAGTAVGAWVLVLSLWGAUVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEA 60  
Db 1 MAAGTAVGAWVLVLSLWGAUVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEA 60

QY 61 WKVLSPOGGPWBDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120  
Db 61 WKVLSPOGGPWBDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 119

QY 121 PKRPEIVDSASELTAGVNPKNVGTCSSEGSYPAGTLSWHLDDGKPLVNEKGVSKVKEQTRRH 180  
Db 121 PKRPEIVDSASELTAGVNPKNVGTCSSEGSYPAGTLSWHLDDGKPLVNEKGVSKVKEQTRRH 179

QY 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWPEVLEEVOL 240  
Db 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWPEVLEEVOL 239

QY 231 -EPVPLEEVOLVWPEEGGAVAGGTGVTLTCEVPAQPSQIHHMKDGVPLPLPSPVLLILP 289  
Db 240 VDAVPLKEVQLVWPEEGGAVAGGTGVTLTCEVPAQPSQIHHMKDGVPLPLPSPVLLILP 299

QY 290 RIGPDQGTYSQVATHSHGPOESRAVSIISIIIEPGEGRGTAGSVGGSL 338  
Db 300 EVGPDQGTYSQVATHSHGPOESRAVSIISIIIEPGEGRGTAGSVGGSL 348

RESULT 3  
T09062  
Probable advanced glycosylation end-products receptor precursor - mouse  
N;Alternate names: RAGE  
C;Species: Mus musculus (house mouse)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T09062  
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sch  
submitted to the EMBL Data Library, October 1997  
A;Description: Sequence of the mouse major histocompatibility locus class III region.  
A;Reference number: Z16543  
A;Accession: T09062  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-402 <ROW>  
C;Cross-references: UNIPROT:O35444; EMBL:AF030001; NID:G2564945; PID:G2564950  
C;Genetics:  
A;Gene: RAGE  
A;Map position: 17  
A;Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2  
C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology  
C;Keywords: receptor; transmembrane protein  
F;31-100/Domain: immunoglobulin homology <IMW>

Query Match 77.6%; Score 1402; DB 2; Length 402;  
Best Local Similarity 78.7%; Pred. No. 1.8e-86;  
Matches 266; Conservative 20; Mismatches 50; Indels 2; Gaps 2;

QY 1 MAAGTAVGAWVLVLSLWGAUVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEA 60  
Db 1 MPAGTAAWVLVLLMGAVAGQNTARIGEPVLVLSCKGAPKPPQRLWKLNTGRTEA 60

QY 61 WKVLSPOGGPWBDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120  
Db 61 WKVLSPOGGPWBDSVARVLPNGSLFLPATGIVDEGIFRCATNRNKGKSNYRVVYQI 119

QY 121 PKRPEIVDSASELTAGVNPKNVGTCSSEGSYPAGTLSWHLDDGKPLVNEKGVSKVKEQTRRH 180  
Db 121 PKRPEIVDSASELTAGVNPKNVGTCSSEGSYPAGTLSWHLDDGKPLVNEKGVSKVKEQTRRH 179

QY 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWPEVLEEVOL 240  
Db 181 PETGLFTLQSELMTVPARGGDPRTFTSCSPGLPRHRLARTAPIQPRVWPEVLEEVOL 238



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OM protein - protein search, using sw model

Run on: March 15, 2005, 11:25:56 ; Search time 82 Seconds  
(without alignments)  
2117.010 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 1806

Sequence: 1 MAAGTAVGAWVLVLSMGAV.....IIEPGEGETAGSVGGSLV 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1802	99.8	404	1	RAGE_HUMAN	Q15109 homo sapien
2	1768	97.9	347	2	Q86SN1	Q86sn1 homo sapien
3	1480	81.9	416	1	RAGE_BOVIN	Q28173 bos taurus
4	1409	78.0	402	2	Q6MG86	Q6mg86 rattus norv
5	1404.5	77.8	403	1	RAGE_MOUSE	Q62151 mus musculu
6	1402	77.6	402	2	Q35444	Q35444 mus musculu
7	1401	77.6	402	1	RAGE_RAT	Q63495 rattus norv
8	1057	58.5	330	2	Q6QP58	Q6qp58 canis famil
9	754.5	41.8	161	2	Q6UFY5	Q6ufy5 sus scrofa
10	709	39.3	147	2	Q71BG7	Q71bg7 homo sapien
11	553.5	30.6	119	2	Q6TYZ6	Q6tyz6 canis famil
12	227.5	12.6	583	1	C166_MOUSE	Q61490 mus musculu
13	227.5	12.6	1366	1	ROB3_MOUSE	Q92214 mus musculu
14	225	12.5	573	2	Q6GN50	Q6gn50 xenopus lae
15	224.5	12.4	1386	1	ROB3_HUMAN	Q96ms0 homo sapien
16	223.5	12.4	564	2	Q61OX4	Q6icx4 brachydanio
17	222.5	12.3	564	1	C166_BRARE	Q90460 brachydanio
18	222.5	12.3	583	1	C166_HUMAN	Q13740 homo sapien
19	221.5	12.3	564	2	Q7ZU00	Q7zu00 brachydanio
20	220	12.2	521	1	C166_RABIT	Q46651 oryctolagus
21	219.5	12.2	646	2	C95812	Q95812 homo sapien
22	219	12.1	555	1	C166_CARAU	Q90304 carassius a
23	218.5	12.1	646	2	Q6PHR3	Q6phr3 homo sapien
24	217.5	12.0	646	1	MU18_HUMAN	P43121 homo sapien
25	217	12.0	570	2	Q6GLY1	Q6gly1 xenopus lae
26	216	12.0	583	1	C166_RAT	Q35112 rattus norv
27	215	11.9	1134	2	Q71B05	Q71b05 brachydanio
28	214	11.8	544	2	Q7Z285	Q7z285 brachydanio
29	214	11.8	1340	2	Q8NDA2	Q8nda2 homo sapien
30	214	11.8	1496	2	Q92626	Q92626 homo sapien
31	210.5	11.7	330	2	Q90242	Q90242 gallus gall

32	210.5	11.7	588	1	C166_CHICK	P42292 gallus gall
33	209	11.6	1612	1	ROB1_MOUSE	Q89026 mus musculu
34	209	11.6	1651	1	ROB1_HUMAN	Q9y6n7 homo sapien
35	208	11.5	583	1	C166_BOVIN	Q9b613 bos taurus
36	205.5	11.4	606	2	Q6IRH8	Q6icrh8 rattus norv
37	204	11.3	521	1	C166_CANFA	Q46634 canis famil
38	204	11.3	814	2	Q8IVU1	Q8ivul1 homo sapien
39	204	11.3	5636	2	Q96RW7	Q96rw7 homo sapien
40	203	11.2	1651	1	ROB1_RAT	O55005 rattus norv
41	201	11.1	793	2	O70246	O70246 mus musculu
42	201	11.1	813	2	Q8BQC3	Q8bcq3 mus musculu
43	201	11.1	1389	2	Q90Z69	Q90z69 brachydanio
44	201	11.1	1419	2	Q98SW3	Q98sw3 brachydanio
45	200.5	11.1	485	2	Q801WS	Q801ws brachydanio

#### ALIGNMENTS

##### RESULT 1

ID RAGE\_HUMAN STANDARD; PRT; 404 AA.  
AC Q15109; Q15279; Q9H2X7; Q9V3R3;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Advanced glycosylation end product-specific receptor precursor  
DE (Receptor for advanced glycosylation end products).  
GN Name=AGER; Synonyms=RAGE;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Lung;  
RX MEDLINE=92340547; PubMed=1378843;  
RA Nepper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,  
RA Elliston K., Stern D., Shaw A.;  
RT "Cloning and expression of a cell surface receptor for advanced  
RT glycosylation end products of proteins.";  
RL J. Biol. Chem. 267:14998-15004(1992).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=95137587; PubMed=7835890;  
RA Sugaya K., Fukagawa T., Matsuoto K., Mita K., Takahashi E., Ando A.,  
RA Inoko H., Ikemura T.;  
RT "Three genes in the human MHC class III region near the junction with  
RT the class II: gene for receptor of advanced glycosylation end  
RT products, PBX2 homeobox gene and a notch homolog, human counterpart of  
RT mouse mammary tumor gene int-3.";  
RL Genomics 23:408-419(1994).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,  
RA Banta A., Spies T., Hood L.;  
RT "Sequence determination of 300 kilobases of the human class III MHC  
RT locus.";  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.  
RA Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,  
RA Yamamoto H.;  
RT "Molecular heterogeneity of the receptor for advanced glycation  
RT endproducts.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RA Malherbe P., Richards J., Gaillard H., Thompson A., Diener C.,  
RA Schuler A., Huber G.;  
RT "cDNA cloning of a novel secreted isoform of the human receptor for  
RT advanced glycation end products (RAGE) and characterization of cells  
RT co-expressing cell-surface scavenger receptors and Swedish mutant

RT amyloid precursor protein.";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [7]  
 RP SEQUENCE OF 1-12 FROM N.A.  
 RA Hudson B.I., Futers T.S.;  
 RT "Novel polymorphisms in the receptor for advanced glycation end-  
 products (RAGE) gene";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Mediates interactions of advanced glycosylation end  
 products (AGE). These are nonenzymatically glycosylated proteins  
 which accumulate in vascular tissue in aging and at an accelerated  
 rate in diabetes. Receptor for amyloid beta peptide.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).  
 CC Secreted. (isoform 2).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q15109-1; Sequence=Displayed;  
 CC Name=2; Synonyms=RAGSEC;  
 CC IsoId=Q15109-2; Sequence=VSP\_002551, VSP\_002552;  
 CC -1- TISSUE SPECIFICITY: Endothelial cells.  
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M91211; AAA03574.1; -;  
 DR EMBL; D28769; BAA05958.1; -;  
 DR EMBL; U93336; AAB47491.1; -;  
 DR EMBL; AB036432; BAA89369.1; -;  
 DR EMBL; AJ133822; CAB43108.1; -;  
 DR EMBL; BC020669; AAB20669.1; -;  
 DR EMBL; AF208289; AAG35728.1; -;  
 DR PIR; I61596; I61596.  
 DR Genew; HGNC:320; AGER.  
 DR H-InvDB; HIX0005749; -;  
 DR MIM; 600214; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004888; F:transmembrane receptor activity; TAS.  
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; ig; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 KW Alternative splicing; Glycoprotein; Immunoglobulin domain;  
 KW Polymorphism; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 22 Potential.  
 FT CHAIN 23 404 Advanced glycosylation end product-  
 specific receptor.  
 FT DOMAIN 23 342 Extracellular (Potential).  
 FT TRANSMEM 343 363 Potential.  
 FT DOMAIN 364 404 Cytoplasmic (Potential).  
 FT DOMAIN 23 116 Ig-like V-type.  
 FT DOMAIN 124 221 Ig-like C2-type 1.  
 FT DOMAIN 227 317 Ig-like C2-type 2.  
 FT DISULFID 38 99 Potential.  
 FT DISULFID 144 208 Potential.  
 FT DISULFID 259 301 Potential.  
 FT CARBOHYD 25 25 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 81 81 N-linked (GLCNAC. .) (Potential).  
 FT VARSPPLIC 380 384 Poly-Glu.  
 FT VARSPPLIC 54 67 Missing (in isoform 2).  
 FT VARSPPLIC 275 404 /FTID=VSP\_002551.  
 FT GVPLEPPSPFVLLILPEIGPDQGTVCVATHSSHGPOESRA  
 FT VSIILIERGEGPTAGSGGLGTLALALGILGLGTAAL  
 FT LGVILWRRQRKREKAPENQBEERAEELNQSSEEPAG  
 FT ESSTGGP -> VSDLERGAGTRRGANCLRCIRAGNS  
 FT PCGDPGRPGDSRPAHGHVAKAATPRRGEGPRKPGGRG  
 FT GACRTESVGGT (in isoform 2).  
 FT /FTID=VSP\_002552.  
 FT Q -> R.  
 FT /FTID=VAR\_011338.  
 FT M -> G (in Ref. 1).  
 FT CONFLICT 1 1  
 FT SEQUENCE 404 AA; 42802 MW; 0D584C436C30CCE7 CRC64;  
 SQ  
 Query Match 99.8%; Score 1802; DB 1; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-106;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAAGTAVGAWVLVLSLWGAVVGAQNIITARIGEPIVLKCKGAPKPPORLEWKLNTGRTA 60  
 DB 1 MAAGTAVGAWVLVLSLWGAVVGAQNIITARIGEPIVLKCKGAPKPPORLEWKLNTGRTA 60  
 QY 61 WKVLSPOGGPQSDVSVARVLPNGSLFLPAVGIQDGIIFRCAMNNGKETSNRVRYQI 120  
 DB 61 WKVLSPOGGPQSDVSVARVLPNGSLFLPAVGIQDGIIFRCAMNNGKETSNRVRYQI 120  
 QY 121 PGKPEIVDSASELTAGVNVKVTGTCVSEGSYPAGTSLWHLDGKPLVPNEKGVSKVKEQTRRH 180  
 DB 121 PGKPEIVDSASELTAGVNVKVTGTCVSEGSYPAGTSLWHLDGKPLVPNEKGVSKVKEQTRRH 180  
 QY 181 PETGLFTLQSELMTVPARGDPRPTSCSPSGLPFRHRLTAPIQPRVWEPVLEEVQL 240  
 DB 181 PETGLFTLQSELMTVPARGDPRPTSCSPSGLPFRHRLTAPIQPRVWEPVLEEVQL 240  
 QY 241 VVEPEGGAAPGGTTLTCEVPAQPSQIHWMDKGVPLPLPPSPFVLLILPEIGPDQGTYS 300  
 DB 241 VVEPEGGAAPGGTTLTCEVPAQPSQIHWMDKGVPLPLPPSPFVLLILPEIGPDQGTYS 300  
 QY 301 CVATHSSHGPOESRAVSIILIERGEGPTAGSGGL 338  
 DB 301 CVATHSSHGPOESRAVSIILIERGEGPTAGSGGL 338  
 RESULT 2  
 Q86SN1 PRELIMINARY; PRT; 347 AA.  
 ID Q86SN1  
 AC Q86SN1; 01-JUN-2003 (T-EMBLrel. 24, Created)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Soluble form of receptor for advanced glycation endproducts  
 DE precursor.  
 GN Name=RAGE;

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22510265; PubMed=12495433; DOI=10.1042/BJ20021371;
RA Yonekura H., Yamamoto Y., Sakurai S., Petrova R.G., Abedin Md.J.,
RA Li H., Yasui K., Takeuchi M., Makita Z., Takasawa S., Okamoto H.,
RA Watanabe T., Yamamoto H.;
RT "Novel splice variants of the receptor for advanced glycation end-
RT products expressed in human vascular endothelial cells and pericytes,
RT and their putative roles in diabetes-induced vascular injury.";
RL Biochem. J. 370:1107-1109(2003).
DR EMBL; AB061668; BAC65465.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor; Signal.
FT SIGNAL 1 22
SQ SEQUENCE 347 AA; 37050 MW; 519E377C4D6AC62C CRC64;

Query Match 97.9%; Score 1768; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 4,4e-104; Indels 0; Gaps 0;
Matches 331; Conservative 0; Mismatches 0;

QY 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
DB 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60

QY 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTSNRYRVYQI 120
DB 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTSNRYRVYQI 120

QY 121 PKGPEIVDSASELTAGVPKNKGVTCVSEGSYPAGTLSLWHDGKPLVNEKGVSKETRHH 180
DB 121 PKGPEIVDSASELTAGVPKNKGVTCVSEGSYPAGTLSLWHDGKPLVNEKGVSKETRHH 180

QY 181 PETGLFTLQSELMTVPARGDPRPTSCFSFSGPLPRHRLRTAPIQRYWEPVPLEEVOL 240
DB 181 PETGLFTLQSELMTVPARGDPRPTSCFSFSGPLPRHRLRTAPIQRYWEPVPLEEVOL 240

QY 241 VVEPEGAVAPGTTVLTCEVPAQSPQIHMMKDGVLPLPSPVLILPEIGPDQGTYS 300
DB 241 VVEPEGAVAPGTTVLTCEVPAQSPQIHMMKDGVLPLPSPVLILPEIGPDQGTYS 300

QY 301 CVATHSHGQPQSRVAVSISITIEPGEAGTAG 331
DB 301 CVATHSHGQPQSRVAVSISITIEPGEAGTAG 331

RESULT 3
RAGE_BOVIN STANDARD; PRT; 416 AA.
AC Q28173;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN Name=AGER; Synonyms=RAGE;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=92340547; PubMed=1378843;
RA Neepser M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
RA Elliston K., Stern D., Shaw A.;
RT "Cloning and expression of a cell surface receptor for advanced
RT glycosylation end products of proteins.";
RL J. Biol. Chem. 267:14998-15004(1992).
CC FUNCTION: Mediates interactions of advanced glycosylation end
CC products (AGE). These are nonenzymatically glycosylated proteins
CC which accumulate in vascular tissue in aging and at an accelerated
CC rate in diabetes.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Endothelial cells.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M91212; AAA03575.1; -.
DR PIR; A42879; A42879.
DR HSSP; PI3590; 1IB5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 22
FT CHAIN 23 416
FT DOMAIN 23 352 Advanced glycosylation end product-
FT TRANSMEM 353 373 specific receptor.
FT DOMAIN 374 416 Extracellular (Potential).
FT DOMAIN 23 115 Potential.
FT DOMAIN 123 220 Cytoplasmic (Potential).
FT DOMAIN 238 327 Ig-like V-type.
FT DISULFID 38 98 Ig-like C2-type 1.
FT DISULFID 143 207 Ig-like C2-type 2.
FT DISULFID 269 311 Potential.
FT CARBOHYD 25 25 Potential.
FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
FT DOMAIN 391 396 Poly-Glu.
SQ SEQUENCE 416 AA; 44182 MW; B703815573E767AE CRC64;

Query Match 81.9%; Score 1480; DB 1; Length 416;
Best Local Similarity 80.5%; Pred. No. 8,8e-86;
Matches 281; Conservative 22; Mismatches 34; Indels 12; Gaps 2;

QY 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
DB 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60

QY 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTSNRYRVYQI 120
DB 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTSNRYRVYQI 119

QY 121 PKGPEIVDSASELTAGVPKNKGVTCVSEGSYPAGTLSLWHDGKPLVNEKGVSKETRHH 180
DB 121 PKGPEIVDSASELTAGVPKNKGVTCVSEGSYPAGTLSLWHDGKPLVNEKGVSKETRHH 179

QY 181 PETGLFTLQSELMTVPARGDPRPTSCFSFSGPLPRHRLRTAPIQRYWEPVPLEEVOL 230
DB 181 PETGLFTLQSELMTVPARGDPRPTSCFSFSGPLPRHRLRTAPIQRYWEPVPLEEVOL 239

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QY 231 -EPVPLEVQLVVEPEGAVAPGGTTLTCEVPAQSPQIHMWKGVLPLPSPVLILP 289
Db 240 VDAVPLKEVQLVVEPEGAVAPGGTTLTCEVPAQSPQIHMWKGVLPLPSPVLLP 299
QY 290 EIGPDQGTYSVATHSHGQPSRAVSIIEPGEAGTAGSVGGSL 338
Db 300 EVGPEDQGTYSVATHSHGQPSRAVSIIEPGEAGTAGSVGGSL 348

RESULT 4
Q6MG86
ID Q6MG86 PRELIMINARY; PRT; 402 AA.
AC Q6MG86;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Advanced glycosylation end product-specific receptor.
GN Name=Ager;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Brown Norway;
RX PubMed=15060004; DOI=10.1101/gr.1987704;
RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;
RT "The genomic sequence and comparative analysis of the rat major
RT histocompatibility complex.";
RL Genome Res. 14:631-639(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Brown Norway;
RA Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosiura A.,
RA Lang N., Lehrach S., Thiel J., Sontag M., Hurt P., Himmelbauer H.,
RA Sudbrak R., Reinhardt R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX883044; CAE83960.1;
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IgC2; 2.
DR SMART; SM00408; IgC2; 2.
DR PROSITE; PS08335; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Receptor.
SQ SEQUENCE 402 AA; 42644 MW; CEA49453C05E1CA1 CRC64;

Query Match 78.0%; Score 1409; DB 2; Length 402;
Best Local Similarity 78.1%; Pred. No. 2.6e-81;
Matches 264; Conservative 25; Mismatches 47; Indels 2; Gaps 2;

QY 1 MAAGTAVGAWLVLSLWGAVGAQNTARIGEPVLKCKGAPKPPQRLWKLTGRTEA 60
Db 1 MPTGTVARAWLVLSLWGAVGAQNTARIGEPVLKCKGAPKPPQRLWKLTGRTEA 60
QY 61 WKVLSPOGGPNDVSVARVLPNGSLFPAVCIODEGIFRCQANVRNGKTSNYRVVQI 120
Db 61 WKVLSFQ-GDPNDVSVARVLPNGSLFPAVCIODEGIFRCQANVRNGKTSNYRVVQI 119
QY 121 PKGPEIVDSASLTAGVPNKNVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180
Db 120 PKGPEIVNPASELTANVPNKNVGTCTVSEGSYPAGTLSWHLDGKPLPDGKGTWKETRRH 179
QY 181 PETGLFTLOSELMTVPARGDPRPTSCFSGLPRHRLRTAPIQPRVWEPVLEEVOL 240
Db 180 PETGLFTLRSELMTVPARGDPRPTSCFSGLPRHRLRTAPIQPRVWEPVLEEVOL 238

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QY 241 VVEPEGAVAPGGTTLTCEVPAQSPQIHMWKGVLPLPSPVLILPEIGPDQGTYS 300
Db 239 LVEPEGVAPGGTTLTCEVPAQSPQIHMWKGVLPLPSPVLILPEVGHDEGIYS 298
QY 301 CVATHSHGQPSRAVSIIEPGEAGTAGSVGGSL 338
Db 299 CVATHSHGQPSRAVSIIEPGEAGTAGSVGGSL 336

RESULT 5
RAGE MOUSE
ID RAGE MOUSE STANDARD; PRT; 403 AA.
AC Q62151;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN Name=Ager; Synonym=V-type;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Lung;
RX MEDLINE=97368045; PubMed=9224812;
RA Renard C., Chappoy O., Wautier M.P., Nagashima M., Lundh E.,
RA Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautier J.L.;
RT "Recombinant advanced glycation end product receptor pharmacokinetics
RT in normal and diabetic rats.";
RL Mol. Pharmacol. 52:54-62(1997).
CC -!- FUNCTION: Mediates interactions of advanced glycosylation end
CC products (AGE). These are nonenzymatically glycosylated proteins
CC which accumulate in vascular tissue in aging and at an accelerated
CC rate in diabetes.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Endothelial cells.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
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CC
CC EMBL; L33412; AAA40040.1; -.
CC MGD; MGI:893592; Ager.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0006810; P:transport; IDA.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00408; IgC2; 1.
CC PROSITE; PS08335; IG_LIKE; 3.
CC PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Immunoglobulin domain; Repeat; Signal; Transmembrane.
FT SIGNAL 1 22
FT CHAIN 23 403
FT DOMAIN 23 341
FT TRANSMEM 342 362
FT DOMAIN 363 403
FT DOMAIN 23 109
FT DOMAIN 123 220
FT DOMAIN 234 316
FT DISULFID 38 98
FT DISULFID 143 207
FT DISULFID 258 300

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FT CARBOHYD 25 25 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 80 80 N-linked (GlcNAc... ) (Potential).  
 SQ SEQUENCE 403 AA; 42668 MW; 1279796FD1579357 CRC64;

Query Match 77.8%; Score 1404.5; DB 1; Length 403;  
 Best Local Similarity 78.4%; Pred. No. 5.1e-81;  
 Matches 265; Conservative 20; Mismatches 52; Indels 1; Gaps 1;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60  
 Db 1 MPAGTAARAWLVLLWGA VAGGQNTARIGEPVLVLSCKGAPKPPQQLWKLTGRTEA 60

QY 61 WKVLSPOGGPMDSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120  
 Db 61 WKVLSPO-GGPMDSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 119

QY 121 PGKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTILSHWLDGKPLVNEKGVSKVKEOTRRH 180  
 Db 120 PGKPEIVDPASELTASVPNKVGTCSSEGSYPAGTILSHWLDGKLLIPDGKETLVKEOTRRH 179

QY 181 PETGLFTLQSELMTVPARGGDRPTFSCFSGLPRHRLARTAPIQRYVWEPVPLEEVOL 240  
 Db 180 PETGLFTLASELTAVITQGGTHPTFSCFSGLPRRRPLNTAPIQLRVREPCPPGGIQL 239

QY 241 VVEPEGGAVAPGGTTLTCEVPAQSPQIHMKDGVPLPLPPSPVLILPEIGPDQGTYS 300  
 Db 240 LVEPEGGIVAPGGTTLTCAISAQPPQVHWIKDGLPLFLAPSPVLLPEVGHDEGTYS 299

QY 301 CVATHSSHGQPSRVSISIIIEGEGGTAGSVGGSL 338  
 Db 300 CVATHPSHGQPSPPVSVIRVTETGDEGPAEGSVGESGL 337

RESULT 6  
 ID O35444 PRELIMINARY; PRT; 402 AA.

AC O35444;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE RAGE (Advanced glycosylation end product-specific receptor).  
 GN Name=RAGE; Synonyms=Ager;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14656967; DOI=10.1101/gr.1736803;  
 RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,  
 RA Campbell R.D., Hood L.;  
 RT "Analysis of the gene-dense major histocompatibility complex class III  
 region and its comparison to mouse."  
 RL Genome Res. 13:2621-2636(2003).  
 RN [2]

RP TISSUE=Lung and heart;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Rickard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung and heart;  
 RA Strausberg R.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF030001; AAB82007.1; -;  
 DR EMBL; BC061182; AAH61182.1; -;  
 DR FIR; T09062; T09062.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; ig; 2; 1.  
 DR SMART; SM00408; IGC2; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Receptor.  
 SQ SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8CB902 CRC64;

Query Match 77.6%; Score 1402; DB 2; Length 402;  
 Best Local Similarity 78.7%; Pred. No. 7.3e-81;  
 Matches 266; Conservative 20; Mismatches 50; Indels 2; Gaps 2;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60  
 Db 1 MPAGTAARAWLVLLWGA VAGGQNTARIGEPVLVLSCKGAPKPPQQLWKLTGRTEA 60

QY 61 WKVLSPOGGPMDSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120  
 Db 61 WKVLSPO-GGPMDSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 119

QY 121 PGKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTILSHWLDGKPLVNEKGVSKVKEOTRRH 180  
 Db 120 PGKPEIVDPASELTASVPNKVGTCSSEGSYPAGTILSHWLDGKLLIPDGKETLVKEOTRRH 179

QY 181 PETGLFTLQSELMTVPARGGDRPTFSCFSGLPRHRLARTAPIQRYVWEPVPLEEVOL 240  
 Db 180 PETGLFTLASELTAVITQGGTHPTFSCFSGLPRRRPLNTAPIQLRVREPCPPGGIQL 238

QY 241 VVEPEGGAVAPGGTTLTCEVPAQSPQIHMKDGVPLPLPPSPVLILPEIGPDQGTYS 300  
 Db 239 LVEPEGGIVAPGGTTLTCAISAQPPQVHWIKDGLPLFLAPSPVLLPEVGHDEGTYS 298

QY 301 CVATHSSHGQPSRVSISIIIEGEGGTAGSVGGSL 338  
 Db 299 CVATHPSHGQPSPPVSVIRVTETGDEGPAEGSVGESGL 336

RESULT 7  
 ID RAGE RAT STANDARD; PRT; 402 AA.

AC O63495;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Advanced glycosylation end product-specific receptor precursor  
 DE (Receptor for advanced glycosylation end products).  
 GN Name=Ager; Synonyms=Rage;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Lung;  
 RX MEDLINE=97368045; PubMed=9224812;  
 RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lundh B.,  
 RA Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautier J.L.;

RT "Recombinant advanced glycation end product receptor pharmacokinetics  
 RL in normal and diabetic rats.";  
 CC Mol. Pharmacol. 52:54-62(1997).  
 CC -1- FUNCTION: Mediates interactions of advanced glycosylation end  
 CC products (AGE). These are nonenzymatically glycosylated proteins  
 CC which accumulate in vascular tissue in aging and at an accelerated  
 CC rate in diabetes.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Endothelial cells.  
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -----  
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 CC -----  
 CC EMBL; L33413; AAA42027.1; -;  
 CC RGD; 69258; Ager.  
 CC InterPro; IPR007110; Ig-like.  
 CC InterPro; IPR003598; Ig\_C2.  
 CC InterPro; IPR003006; Ig\_MHC.  
 CC Pfam; PF00047; Ig; 3.  
 CC SMART; SM00408; IGC2; 1.  
 CC PROSITE; PS00835; IG\_LIKE; 3.  
 CC PROSITE; PS00290; IG\_MHC; 1.  
 CC Glycoprotein; Immunoglobulin domain; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 22  
 FT CHAIN 23 402  
 FT DOMAIN 23 341  
 FT TRANSMEM 342 362  
 FT DOMAIN 363 402  
 FT DOMAIN 23 109  
 FT DOMAIN 123 219  
 FT DOMAIN 233 315  
 FT DISULFID 38 98  
 FT DISULFID 143 206  
 FT DISULFID 257 299  
 FT CARBOHYD 25 25  
 FT CARBOHYD 80 80  
 FT SEQUENCE 402 AA; 42663 MW; 594481BC3A51E394E CRC64;  
 Query Match 77.6%; Score 1401; DB 1; Length 402;  
 Best Local Similarity 77.8%; Pred. No. 8 4e-81;  
 Matches 263; Conservative 25; Mismatches 48; Indels 2; Gaps 2;  
 QY 1 MAAAGTAVGAWLVLSLWGVAVGQNTARIGBPLVLCCKGAPKPPQRLKLTGRTEA 60  
 DB 1 MPTGTVARAWLVLSLWGVAVGQNTARIGBPLVLCCKGAPKPPQRLKLTGRTEA 60  
 QY 61 WKVLSFQGGPNDVARVLPNGSLFPAVGIODEGIFRCQAMNRNGKETKSNRYRVQI 120  
 DB 61 WKVLSFQ-GDPNDVARVLPNGSLLPALGIVDEGIFRCATNRNGKETKSNRYRVQI 119  
 QY 121 PGKPEIVDSASELTAGVPNKVGTCSGSGYPAGTSLSHWLDGKPLVPNEKGVSGQTRRH 180  
 DB 120 PGKPEIVNPASELTANVPNKVGTCSGSGYPAGTSLSHWLDGKPLVPNEKGVSGQTRRH 179  
 QY 181 PETGLTLOSELMTVPARGDPRPTSCFSFGLPRLHRLTAPIQPRVWEPVLEEVL 240  
 DB 180 PETGLTFLSELVTPAQGG-TTPTVSCSFLGLPRLHRLTAPIQPRVWEPVLEEVL 238  
 QY 241 VVEPEGGAVAGTGTTLTCEVPAQSPQIHHMKDGVLPPLPSPVLILPEIGPOQGY 300  
 DB 239 LVEPEGGTVAPGGTTLTCAISAPPPQIHHMKDGVLPPLPSPVLILPEIGPOQGY 298  
 QY 301 CVATHSHGQPSRAVSISIIIEPGEETAGSVGGSL 338  
 DB 299 CVATHSHGQPSPPVNIIVTETDEGAAGSVGGSL 336

## RESULT 8

Q6QP58  
 ID Q6QP58 PRELIMINARY; PRT; 330 AA.  
 AC Q6QP58;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RAGE (Fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Murua Escobar H., Soller J.T., Sterenczak K.A., Richter A., Meyer B.,  
 RA Winkler S., Nolte I., Bullerdiek J.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY530943; AAS21266.1; -;  
 DR InterPro; IPR003599; Ig-like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00409; IG; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 FT NON\_TER 1  
 FT NON\_TER 330  
 FT SEQUENCE 330 AA; 35418 MW; 16B15C31E78D99A2 CRC64;  
 Query Match 58.5%; Score 1057; DB 2; Length 330;  
 Best Local Similarity 73.0%; Pred. No. 3 9e-59;  
 Matches 208; Conservative 20; Mismatches 35; Indels 22; Gaps 5;  
 QY 54 NTRGRTEAMKVLSPQGGPMDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNV 113  
 DB 1 NTRGRTEAMKVLSPQ-GGPMDSVARVLPNGSLFLPAVGIDEGIFRCATNRNGKETRSTY 59  
 QY 114 RVVVQIIPKPEIVDSASELTAGVPNKVGTCSGSGYPAGTSLSHWLDGKPLVPNEKGVSV 173  
 DB 60 QRVVQIIPKPEIINPTSELNAGVPSKVGTCVSEGGVPARTLSWHWDGKPLIPDGKGVSV 119  
 QY 174 KEOTRRHPETGLTLOSELMTVPARGDPRPTSCFSFGLPRLHRLTAPIQPRVWEPV 233  
 DB 120 QETRRHPETGLTLOSELMTVPAGGAPHPFTSCFSFGLPRLHRLHAAPIQLNVWESV 179  
 QY 234 PLEEVQVVEPEGGAVAGTGTTLTCEVPAQSPQIHHMKDGVLPPLPSPVLILPEIGP 293  
 DB 180 PL-EVQVWVEP-GGMLAPGGTTLTCTETPAQSSVQ-----ILSEVKP 219  
 QY 294 ODQGYTSCVATHSHGQPSRAVSISIIIEPGEETAGSVGGSL 338  
 DB 220 EDQGYTSCVAMHPSHGQPSRAVSISIIIEPGEETAGSVGGSL 263

## RESULT 9

Q6UPY5  
 ID Q6UPY5 PRELIMINARY; PRT; 161 AA.  
 AC Q6UPY5;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Receptor for advanced glycosylation end products (Fragment).  
 GN Name=RAGE;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schupp N., Stopper H., Heidland A.;  
 RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 RL

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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 18:50:14 ; Search time 1561.84 Seconds  
(without alignments)  
10424.190 Million cell updates/sec

Title: US-10-091-019-4  
Perfect score: 336  
Sequence: 1 gctcaaaacatcacagcccg.....attctgctctgaactcacg 336

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	336	100.0	1218	6	CQ730900 Sequence
2	336	100.0	1223	6	BD176670 Soluble R
3	336	100.0	1223	9	AB061668 Homo sapi
4	336	100.0	1268	9	AB036432 Homo sapi
5	336	100.0	1436	9	BC020669 Homo sapi
6	336	100.0	1451	9	AB061669 Homo sapi
7	332.8	99.0	1391	6	AR321600 Sequence
8	332.8	99.0	1391	9	HUMRAGE
9	270.6	80.5	1426	4	BOVRAGE
10	270.6	80.5	1426	6	AR321599 Sequence
11	248.4	73.9	358	4	AY382178 Canis fam
12	242.2	72.1	1399	10	BC061182 Mus muscu
13	242.2	72.1	1420	10	RAYTRECEP
14	242	72.0	1250	9	HSAL13822
15	239	71.1	1348	6	AR321601
16	239	71.1	1348	10	MUSRECEP
17	206.6	61.5	483	4	AY370908
18	197	58.6	5062	9	HSM808526
19	197	58.6	10108	9	HUMHOXRAGE

C	20	197	58.6	56747	9	AL845464	AL845464 Human DNA
	21	197	58.6	62944	6	AX334775	AX334775 Sequence
	22	197	58.6	62944	6	AX336090	AX336090 Sequence
	23	197	58.6	62944	9	BSMHC3W5A	U89336 Homo sapien
	24	197	58.6	80063	9	AX284686	AX284686 Human DNA
	25	197	58.6	102588	9	AX2927239	AX2927239 Human DNA
	26	197	58.6	103327	9	AL662830	AL662830 Human DNA
	27	197	58.6	137935	9	AL662884	AL662884 Human DNA
	28	197	58.6	197811	2	AC009833	AC009833 Homo sapi
	29	197	58.6	200685	2	AP001455	AP001455 Homo sapi
	30	195.4	58.2	87610	2	CR812478	CR812478 Homo sapi
	31	176.2	52.4	159822	9	AC148714	AC148714 Macaca mu
	32	175.8	52.3	590	4	AY530943	AY530943 Canis fam
	33	152.6	45.4	127266	4	AL773562	AL773562 Pig DNA s
	34	133.8	39.8	106278	2	RLN520N23	AL732653 Rattus no
	35	133.4	39.7	266517	2	AC107094	AC107094 Rattus no
	36	133.4	39.7	340493	10	BM883044	BM883044 Rattus no
	37	128	38.1	201964	10	MMHC29N7	AF030001 Mus muscu
	38	128	38.1	201986	10	AC006289	AC006289 Mus muscu
	39	128	38.1	239339	2	AC091703	AC091703 Mus muscu
	40	122.2	36.4	364	11	BV105988	BV105988 MARC 1043
	41	120.2	35.8	349980	6	AX344566	AX344566 Sequence
	42	120.2	35.8	349980	6	AX344567	AX344567 Sequence
	43	112.8	33.6	349980	6	AX344557	AX344557 Sequence
	44	112.8	33.6	349980	6	AX344558	AX344558 Sequence
	45	81	24.1	255	9	HSA012753	AJ012753 Homo sapi

ALIGNMENTS

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ACCESSION	CQ730900.1	GI:42306010			
VERSION					
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.				
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof				
JOURNAL	Patent: WO 02068579-A 16834 06-SEP-2002;				
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Db	127	AGAAACACACCCAGCGGCTGGAATGGAACACTGACACAGCGCGGACAGAGCTTGGAG	186		
Qy	121	GTCTCTGTCTCCCGAGGAGGCGCCCTGGGACAGTGGCTCGTCTCTTCCCAACGGC	180		
Db	187	GTCTCTGTCTCCCGAGGAGGCGCCCTGGGACAGTGGCTCGTCTCTTCCCAACGGC	246		
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Db      307  |||||TTCCTTCCGCGTCCGAGTCCAGGATGGGATTTTCGCGTGCCAGCAATG 366
QY      301  AAGCCAGAAATTTAGATTCTGCCTCTGAACATCAG 336
Db      367  AAGCCAGAAATTTAGATTCTGCCTCTGAACATCAG 402

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LOCUS      Soluble RAGE protein. 1223 bp DNA linear PAT 18-MAR-2003
DEFINITION
ACCESSION BD176670
VERSION   BD176670.1 GI:29122380
KEYWORDS  WO 02074805-A/1.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 1223)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLES    Yamamoto, H., Yonekura, H., Yamamoto, Y., Sakurai, S. and Watanabe, T.
          Soluble RAGE protein
          Patent: WO 02074805-A 1 26-SEP-2002;
          JAPAN AS REPRESENTED BY PRESIDENT OF KANAZAWA UNIVERSITY, HIROSHI
          YAMAMOTO, HIDETO YONEKURA, YASUHIKO YAMAMOTO, SHIGERU SAKURAI, TAKUO
          WATANABE
JOURNAL   OS Homo sapiens (human)
          PN WO 02074805-A/1
          PD 26-SEP-2002
          PF 19-MAR-2002 WO 2002JP002623
          PR 19-MAR-2001 JP 01P 078409, 10-AUG-2001 JP 01P 243114 PR
          25-FEB-2002 JP 02P 048182
          PI HIROSHI YAMAMOTO, HIDETO YONEKURA, YASUHIKO YAMAMOTO, SHIGERU PI
          SAKURAI,
          PI TAKUO WATANABE
          PC C07K14/47, C12N15/12, C12N1/21, C12N5/10, C12N1/19, A61K39/395, PC
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          PC G01N33/15, G01N33/50, G01N33/53, G01N33/577
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Db      211 GTCTGTCTCTCCAGGAGAGAGCCCTCGGACAGTGTGCTGTCTCTCTCCCAACGCG 270
QY      181 TCCTCTCTCTCTCCGCGTGTCCGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 240
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QY      301  AAGCCAGAAATTTAGATTCTGCCTCTGAACATCAG 336
Db      391  AAGCCAGAAATTTAGATTCTGCCTCTGAACATCAG 426

RESULT 3
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LOCUS      Homo sapiens RAGE mRNA for soluble form of receptor for advanced
DEFINITION glycation endproducts, complete cds.
ACCESSION AB061668
VERSION   AB061668.1 GI:28971759
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLES    Yonekura, H., Yamamoto, Y., Sakurai, S., Petrova, R.G., Abedin, Md.J.,
          Li, H., Yasui, K., Takeuchi, M., Makita, Z., Takasawa, S., Okamoto, H.,
          Watanabe, T. and Yamamoto, H.
          Novel splice variants of the receptor for advanced glycation
          end-products expressed in human vascular endothelial cells and
          pericytes, and their putative roles in diabetes-induced vascular
          injury
JOURNAL   Biochem. J. 370 (Pt 3), 1097-1109 (2003)
MEDLINE   22510265
PUBMED    12495433
REFERENCE 2 (bases 1 to 1223)
AUTHORS   Yonekura, H., Yamamoto, Y., Sakurai, S. and Yamamoto, H.
TITLES    Direct Submission
          Submitted (11-MAY-2001) Hideto Yonekura, Kanazawa University,
          Graduate School of Medical Science; 13-1 Takara-machi, Kanazawa,
          Ishikawa 920-8640, Japan [E-mail:hyone@med.kanazawa-u.ac.jp,
          Tel:81-76-265-2182, Fax:81-76-234-4226]
JOURNAL   Location/Qualifiers
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinska, M.I., Skalska, U., Smalhus, D.E., Schnercher, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932  
2 (bases 1 to 1436)  
Direct Submission  
Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: CLONTECH  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (ILML)  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at: <http://image.llnl.gov>  
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## ORIGIN

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DEFINITION Homo sapiens RAGE mRNA for N-terminal truncated form of receptor for advanced glycation endproducts, complete cds.  
ACCESSION AB061669  
VERSION AB061669.1 GI:28971761  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Yonekura, H., Yamamoto, Y., Sakurai, S., Petrova, R.G., Abedin, Md.J., Li, H., Yasui, K., Takeuchi, M., Makita, Z., Takasawa, S., Okamoto, H., Watanabe, T., and Yamamoto, H.  
TITLE Novel splice variants of the receptor for advanced glycation end-products expressed in human vascular endothelial cells and pericytes, and their putative roles in diabetes-induced vascular injury  
JOURNAL Biochem. J. 370 (Pt 3), 1097-1109 (2003)  
MEDLINE 22510265  
PUBMED 12495433  
REFERENCE 2 (bases 1 to 1451)  
AUTHORS Yonekura, H., Yamamoto, Y., Sakurai, S. and Yamamoto, H.  
TITLE Direct Submission  
JOURNAL Submitted (11-MAY-2001) Hideto Yonekura, Kanazawa University, Graduate School of Medical Science; 13-1 Takara-machi, Kanazawa, Ishikawa 920-8640, Japan (E-mail: hyone@med.kanazawa-u.ac.jp, Tel:81-76-265-2182, Fax:81-76-234-4226)  
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DEFINITION Sequence 4 from patent US 6563015.  
ACCESSION AR321600  
VERSION AR321600.1 GI:33706829  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1391)  
AUTHORS Stern,D.M., Schmidt,A.M. and Yan,S.D.  
TITLE Transgenic mice over-expressing receptor for advanced glycation  
endproduct (RAGE) and mutant APP in brain and uses thereof  
JOURNAL Patent: US 6563015-A 4 13-MAY-2003;  
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DB 367 AAGCCAGAATGTAGATTCTGCTCTGAATCAACG 402  
  
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DEFINITION Human receptor for advanced glycosylation end products (RAGE) mRNA,  
partial cds.  
ACCESSION M91211.1 GI:190845  
VERSION M91211.1  
KEYWORDS RAGE; cell surface receptor.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1391)  
AUTHORS Nepper,M., Schmidt,A.M., Brett,J., Yan,S.D., Wang,F., Pan,Y.C.,  
Elliston,K., Stern,D. and Shaw,A.  
TITLE Cloning and expression of a cell surface receptor for advanced  
glycosylation end products of proteins  
J. Biol. Chem. 267 (21), 14998-15004 (1992)  
JOURNAL 92340547  
MEDLINE 1378843  
PUBMED  
REFERENCE 2 (bases 1 to 1391)  
AUTHORS Shaw,A.  
TITLE Direct Submission  
JOURNAL Submitted (15-APR-1992) A. Shaw, Department of Cellular and  
Molecular Biology, Merck Sharp and Dohme Research Laboratories,  
West Point, PA 19486 USA  
COMMENT Original source text: Homo sapiens cDNA to mRNA.  
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RESULT 9
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DEFINITION
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ACCESSION
  M91212.1 GI:163650
VERSION
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KEYWORDS
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ORGANISM
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REFERENCE
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  Nepper, M., Schmidt, A.M., Brett, J., Yan, S.D., Wang, F., Pan, Y.C.,
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  Cloning and expression of a cell surface receptor for advanced
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  J Biol Chem. 267 (21), 14998-15004 (1992)
JOURNAL
  MEDLINE
  PUBMED
  1378843
REFERENCE
  2 (bases 1 to 1426)
  Shaw, A.
  Direct Submission
  Submitted (15-APR-1992) A. Shaw, Department of Cellular and
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  West Point, PA 19486 USA
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## FEATURES

source

## CDS

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Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

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Db 79 CAAAACATCACAGCCCGGATTGGGAGCCACTGGTGTGAAGTGAAGGGGCCCCCAAG 138
Qy 64 AAACACACCCAGCGCTGGAATGGAACACTGAACACAGCCCGGACAGAACTTGGAAAGTC 123
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Qy 124 CTGTCTCCCGAGGAGAGGCCCTCGGACAGTGTGGTGTGCTTCCCAAGCGGTCC 183
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Qy 184 CTCTCTCTCCCGTGTGGGATCCAGATGAGGGGATTTTCGGTGCAGGCAATCAAC 243
Db 256 CTCCTCTCCCGCTGTGGGATCCAGATGAGGGGATTTTCGGTGCAGGCAACGAGC 315

RESULT 10
AR321599
LOCUS
DEFINITION
  Sequence 2 from patent US 6563015.
ACCESSION
  AR321599
VERSION
  AR321599.1 GI:33706828
KEYWORDS
  Unknown.
ORGANISM
  Unclassified.
  1 (bases 1 to 1426)
  Stern, D.M., Schmidt, A.M. and Yan, S.D.
  Transgenic mice over-expressing receptor for advanced glycation
  endproduct (RAGE) and mutant APP in brain and uses thereof
  Patent: US 6563015-A 2 13-MAY-2003;
  Location/Qualifiers
  1. .1426
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ORIGIN
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Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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11: Geneseqn2003ds.\*  
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13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	336	100.0	957	2	AAV06518 Human RAG
3	336	100.0	1020	6	ABQ79956 Human sol
4	336	100.0	1023	2	AAV12394 Human sol
5	336	100.0	1023	2	AAV06517 Human RAG
6	336	100.0	1090	12	Adm80824 Human CAD
7	336	100.0	1194	12	ADP19657 Human LP2
8	336	100.0	1223	6	ABV73151 Human sol
9	336	100.0	1223	10	ADG37043 Receptor
10	336	100.0	1239	12	ADP19663 Human LP2
11	336	100.0	1268	10	ADG33024 Human DNA
12	336	100.0	1291	12	ADP19655 Human LP2
13	336	100.0	1329	12	ADP19665 Human LP2
14	336	100.0	1339	12	ADP19661 Human LP2
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16	336	100.0	1391	6	ABQ79955 Human RAG
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25	332.8	99.0	957	2	AAV12395	Aav12395 Human mat
26	332.8	99.0	1391	6	ABK10856	Abk10856 DNA encod
27	332.8	99.0	1391	6	ABK84114	Abk84114 Human cDN
28	332.8	99.0	1391	6	ABK36952	Abk36952 Human rec
29	332.8	99.0	1391	10	AAD59952	Aad59952 Human RAG
30	332.8	99.0	1391	10	ADG32021	Adg32021 Human DNA
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35	270.6	80.5	1426	10	AAD59951	Aad59951 Bovine RA
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37	242	72.0	1173	10	ADE95567	Ade95567 Human NOV
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39	242	72.0	1294	12	ADP19669	Adp19669 Human LP2
40	242	72.0	1678	9	ACC59907	Acc59907 Human REM
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ALIGNMENTS

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ID ABQ79957 standard; DNA; 336 BP.  
XX  
AC ABQ79957;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Human RAGE V-domain nucleotide sequence.  
XX  
KW Receptor for Advanced Glycated end product; RAGE; recombinant; nootropic;  
KW antiarteriosclerotic; antidiabetic; cytostatic; nephrotropic; vasotropic;  
KW neuroprotective; antiinflammatory; gene therapy; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200270667-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 05-MAR-2002; 2002WO-US006881.  
XX  
PR 05-MAR-2001; 2001US-0273418P.  
XX  
PA (TRAN-) TRANSTECH PHARMA INC.  
XX  
PI Harris R, Shen J, Shahbaz M;  
XX  
DR WPI; 2002-713443/77.  
XX  
PT High level expression of recombinant Receptors for Advanced Glycated end  
PT products (RAGE) proteins for treating increased levels of advanced  
PT glycosylation end products, comprises infecting cells with a high titer  
PT recombinant virus.  
XX  
PS Claim 14; Fig 2C; Sipp; English.  
XX  
CC The invention relates to a method for high level expression of  
CC recombinant forms of the Receptor for Advanced Glycated end products  
CC (RAGE) or its fragments. The method involves (i) subcloning a nucleotide  
CC sequence encoding RAGE or its fragment into a virus; (ii) preparing a  
CC high titer stock of recombinant virus; and (iii) infecting host cells  
CC with the high titer recombinant virus under conditions such that

CC predetermined levels of RAGE or its fragment is produced, where the  
 CC predetermined levels of RAGE comprises at least 25 mg recombinant protein  
 CC per liter of culture. The method is useful for high level expression of  
 CC recombinant RAGE polypeptide or its fragment which may be useful in  
 CC preventing, creating or ameliorating diseases associated with increased  
 CC levels of advanced glycosylation end products, such as atherosclerosis,  
 CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's  
 CC disease, inflammation, systemic lupus nephritis, inflammatory lupus  
 CC nephritis, cancer or erectile dysfunction. The present sequence  
 CC represents the nucleotide sequence of the V-domain of human RAGE  
 XX  
 XX Sequence 336 BP; 81 A; 95 C; 99 G; 61 T; 0 U; 0 Other;  
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 Best Local Similarity 100.0%; Pred. No. 9.5e-93;  
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 ID AAV06518 standard; DNA; 957 BP.  
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 AC AAV06518;  
 XX  
 DT 08-MAY-1998 (first entry)  
 XX  
 DE Human RAGE polypeptide (318 amino acid residues) encoding DNA.  
 XX  
 KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
 KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;  
 KW Alzheimer's disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1. .1023  
 FT /tag= a  
 FT /product= "RAGE polypeptide"  
 XX  
 PN WO9739121-A1.  
 XX  
 PD 23-OCT-1997.  
 XX  
 PF 11-APR-1997; 97WO-EP001832.  
 XX  
 PR 16-APR-1996; 96US-00633147.  
 XX  
 PA (SCHD ) SCHERING AG.  
 XX

PI Morser MJ, Nagashima M;  
 XX  
 DR WPI; 1997-526458/48.  
 DR P-PSDB; AAW33754.  
 XX  
 PT New soluble advanced glycosylation end-product receptor polypeptide -  
 PT used for reducing vascular permeability, complications of diabetes etc.,  
 PT also for purification and to screen for modulators.  
 XX  
 XX Claim 12; Fig 1B; 91pp; English.  
 PS  
 XX This genomic DNA encodes a human advanced glycosylation end-product  
 CC receptor (RAGE) polypeptide (318 amino acid residues). The RAGE  
 CC polypeptides and its active fragments or their mimetics, inhibit  
 CC interaction between advanced glycosylation end-products (AGE) and a  
 CC receptor (specifically RAGE). They are used to treat diseases associated  
 CC with AGE/RAGE interaction, such as increased vascular permeability,  
 CC diabetes mellitus (particularly complications such as micro- or macro-  
 CC vasculopathy or occlusive vascular disorders such as neuropathy,  
 CC nephropathy, retinopathy or atherosclerosis) or haemodialysis-associated  
 CC amyloidosis, also activation of microglial cells by beta-amyloid peptides  
 CC in Alzheimer's disease or age-related disorders such as oxidative stress.  
 CC These RAGE polypeptides are also used, when immobilised, to purify AGE  
 CC from a protein mixture and to screen for compounds that are agonists and  
 CC antagonists of AGE/RAGE interaction. They can also be used diagnostically  
 CC to detect abnormal levels of AGE. Antibodies against RAGE polypeptides  
 CC are useful as immunoassay reagents for measurement of RAGE levels, and as  
 CC inhibitors of interaction between AGE and RAGE or other receptors, and for  
 CC purification and quantification of RAGE polypeptides. The encoding  
 CC nucleic acids are used to express recombinant RAGE and as probes for  
 CC isolating related genes  
 XX  
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 Best Local Similarity 100.0%; Pred. No. 1.4e-92;  
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 QY 61 AAGAAACACCCAGCGGCTGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 120  
 DB |||||  
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 QY 121 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTCTCTCCCAACGGC 180  
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 QY 181 TCCCTCTTCTCCCGCTGTCCGGATCCAGGATGAGGGATTTTCGGTGCAGGCAATG 240  
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 QY 181 TCCCTCTTCTCCCGCTGTCCGGATCCAGGATGAGGGATTTTCGGTGCAGGCAATG 240  
 DB |||||  
 QY 241 AACAGGAATGGAAGAGAGCCAACTGCAACTACCGAGTCCGCTGTAACACTCAGC 300  
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 QY 241 AACAGGAATGGAAGAGAGCCAACTGCAACTACCGAGTCCGCTGTAACACTCAGC 300  
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 DB |||||  
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 ID ABQ79956 standard; DNA; 1020 BP.  
 XX  
 AC ABQ79956;  
 XX  
 DT 23-DEC-2002 (first entry)  
 XX  
 DE Human soluble RAGE (sRAGE) encoding DNA.  
 XX

KW Receptor for Advanced Glycated end product; RAGE; recombinant; nootropic;  
 KW antidiabetic; antidiabetic; cytosolic; nephrotropic; vasotropic;  
 KW neuroprotective; antiinflammatory; gene therapy; human; gene; ds.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH 1. .1020  
 FT /\*tag= a  
 FT /product= "sRAGE"  
 FT /note= "soluble, extracellular portion of RAGE"

XX WO200270667-A2.

XX 12-SEP-2002.

XX 05-MAR-2002; 2002WO-US006881.

XX 05-MAR-2001; 2001US-0273418P.

XX (TRAN-) TRANSTECH PHARMA INC.

XX Harris R, Shen J, Shahbaz M;

XX WPI; 2002-713443/77.

DR P-PSDB; ABB82164.

XX High level expression of recombinant Receptors for Advanced Glycated end  
 PT products (RAGE) proteins for treating increased levels of advanced  
 PT glycosylation end products, comprises infecting cells with a high titer  
 PT recombinant virus.

XX Claim 13; Fig 2B; 5lpp; English.

XX The invention relates to a method for high level expression of  
 CC recombinant forms of the Receptor for Advanced Glycated end products  
 CC (RAGE) or its fragments. The method involves (i) subcloning a nucleotide  
 CC sequence encoding RAGE or its fragment into a virus; (ii) preparing a  
 CC high titer stock of recombinant virus; and (iii) infecting host cells  
 CC with the high titer recombinant virus under conditions such that  
 CC predetermined levels of RAGE or its fragment is produced, where the  
 CC predetermined levels of RAGE comprises at least 25 mg recombinant protein  
 CC per liter of culture. The method is useful for high level expression of  
 CC recombinant RAGE polypeptide or its fragment which may be useful in  
 CC preventing, treating or ameliorating diseases associated with increased  
 CC levels of advanced glycosylation end products, such as atherosclerosis,  
 CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's  
 CC disease, inflammation, systemic lupus nephritis, inflammatory lupus  
 CC nephritis, cancer or erectile dysfunction. The present sequence  
 CC represents the nucleotide sequence of human sRAGE (soluble, extracellular  
 CC portion of RAGE)

XX Sequence 1020 BP; 216 A; 299 C; 316 G; 189 T; 0 U; 0 Other;

Query Match 100.0%; Score 336; DB 6; Length 1020;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-92;  
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGCCCC 126

QY 61 AAGAAACACCCAGCGGTGGAATGGAATCTGAACACAGCGCGGACAGAGCTTGGAG 120

DB 127 AAGAAACACCCAGCGGTGGAATGGAATCTGAACACAGCGCGGACAGAGCTTGGAG 186

QY 121 GTCCTGTCTCCAGGAGAGAGCCCTCGGACAGTGTGGTCTGTCTTCCCAACGGC 180

DB 187 GTCCTGTCTCCAGGAGAGAGCCCTCGGACAGTGTGGTCTGTCTTCCCAACGGC 246

QY 181 TCCCTCTTCTCCGCTGTCCGGATCCAGGATGAGGGATTTTCGGTGCAGGCAATG 240

DB 247 TCCCTCTTCTCCGCTGTCCGGATCCAGGATGAGGGATTTTCGGTGCAGGCAATG 306

QY 241 AACAGGAATGGAAGAGAGACCAAGTCCAATACCGAGTCCGTGCTTACCAGATTCTCTGG 300  
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RESULT 4

AAV12394  
 ID AAV12394 standard; DNA; 1023 BP.

XX AAV12394;

XX 14-MAY-1998 (first entry)

XX Human soluble receptor to an advanced glycosylation end product DNA.

XX Human; soluble receptor; advanced glycosylation end product; RAGE; AGE;  
 KW antibody; vascular permeability; diabetes mellitus; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 1. .1023  
 FT /\*tag= a  
 FT /product= "soluble RAGE"

XX WO9739125-A1.

XX 23-OCT-1997.

XX 11-APR-1997; 97WO-EP001834.

XX 16-APR-1996; 96US-00633148.

XX (SCHD ) SCHERING PATENTE AG.

XX Morser MJ, Nagaehima M, Hollander DA;

XX WPI; 1997-558580/51.

DR P-PSDB; AAW44199.

XX Anti-advanced glycosylation end product polypeptide antibody - prevents  
 PT receptor binding and therefore reduces vascular permeability, useful to  
 PT treat diabetes mellitus.

XX Disclosure; Page 39; 90pp; English.

XX The present sequence encodes a soluble human receptor to an advanced  
 CC glycosylation end product (RAGE) polypeptide. The present invention  
 CC describes an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are non-  
 CC enzymatically glycosylated proteins, which accumulate in vascular tissue  
 CC in aging, and at an accelerated rate in individuals with diabetes. The  
 CC Ab, which prevents the interaction between an AGE and it's receptor  
 CC (RAGE), reduces vascular permeability. The Ab can be used to treat  
 CC diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular  
 CC disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated  
 CC amyloidosis or atherosclerosis. The Ab can also be used for the isolation  
 CC and purification of human RAGE polypeptide

XX Sequence 1023 BP; 218 A; 299 C; 317 G; 189 T; 0 U; 0 Other;

Query Match 100.0%; Score 336; DB 2; Length 1023;

Best Local Similarity 100.0%; Pred. No. 1.4e-92;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGCCCC 126

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DB 127 AAGAAACACCCAGCGCTGGAAATGAACTGAACACAGCCGCGACAGAGCTTGAAG 186  
QY 121 GTCTGTCTCCAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCCAACGGC 180  
DB 187 GTCTGTCTCCAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCCAACGGC 246  
QY 181 TCCCTCTCTCCAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCCAACGGC 240  
DB 247 TCCCTCTCTCCAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCCAACGGC 306  
QY 241 AACAGGAATGCAAGAGAGCAAGTCCAACTACCGAGTCCGCTCTACAGATTCCTGGG 300  
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QY 301 AAGCAGAAATTTAGATTTCTGCTCTGAATCAACG 336  
DB 367 AAGCAGAAATTTAGATTTCTGCTCTGAATCAACG 402

RESULT 5  
AAV06517 standard; DNA; 1023 BP.  
XX AAV06517;  
AC AC  
XX 08-MAY-1998 (first entry)  
XX Human RAGE polypeptide (340 amino acid residues) encoding DNA.  
XX Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;  
KW Alzheimer's disease; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 1..1023  
FT /\*tag= a  
FT /product= "RAGE polypeptide"

XX WO9739121-A1.  
XX 23-OCT-1997.  
XX 11-APR-1997; 97WO-EP001832.  
XX 16-APR-1996; 96US-00633147.  
XX (SCHD ) SCHERING AG.  
XX Morser MJ, Nagashima M;  
XX WPI; 1997-526458/48.  
XX P-PSDB; AAW33753.  
XX New soluble advanced glycosylation end-product receptor polypeptide -  
PT used for reducing vascular permeability, complications of diabetes etc.,  
PT also for purification and to screen for modulators.  
XX Claim 12; Fig 1A; 91pp; English.  
XX This genomic DNA encodes a human advanced glycosylation end-product  
CC receptor (RAGE) polypeptide (340 amino acid residues). The RAGE  
CC polypeptides and its active fragments or their mimetics, inhibit  
CC interaction between advanced glycosylation end-products (AGE) and a  
CC receptor (specifically RAGE). They are used to treat diseases associated  
CC with AGE/RAGE interaction, such as increased vascular permeability,  
CC diabetes mellitus (particularly complications such as micro- or macro-  
CC vasculopathy or occlusive vascular disorders such as neuropathy, or  
CC nephropathy, retinopathy or atherosclerosis) or haemodialysis-associated

CC amyloidosis, also activation of microglial cells by beta-amyloid peptides  
CC in Alzheimer's disease or age-related disorders such as oxidative stress.  
CC These RAGE polypeptides are also used, when immobilised, to purify AGE  
CC from a protein mixture and to screen for compounds that are agonists and  
CC antagonists of AGE/RAGE interaction. They can also be used diagnostically  
CC to detect abnormal levels of AGE. Antibodies against RAGE polypeptides  
CC are useful as immunoassay reagents for measurement of RAGE levels, and as  
CC inhibitors of interaction between AGE and RAGE or other receptors, and for  
CC purification and quantification of RAGE polypeptides. The encoding  
CC nucleic acids are used to express recombinant RAGE and as probes for  
CC isolating related genes  
XX

QY Sequence 1023 BP; 218 A; 299 C; 317 G; 189 T; 0 U; 0 Other;  
Query Match 100.0%; Score 336; DB 2; Length 1023;  
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QY 1 GCTCAAAACATCACAGCCGCGATTCGGAGCCACCTGGTGAAGTGAAGGGGCCCCC 60  
DB 67 GCTCAAAACATCACAGCCGCGATTCGGAGCCACCTGGTGAAGTGAAGGGGCCCCC 126  
QY 61 AAGAAACACCCAGCGCTGGAATGGAATGGAACACAGAGCCGCGACAGAGCTTGAAG 120  
DB 127 AAGAAACACCCAGCGCTGGAATGGAATGGAACACAGAGCCGCGACAGAGCTTGAAG 186  
QY 121 GTCTGTCTCCAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCCAACGGC 180  
DB 187 GTCTGTCTCCAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCCAACGGC 246  
QY 181 TCCCTCTCTCCAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCCAACGGC 240  
DB 247 TCCCTCTCTCCAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCCAACGGC 306  
QY 241 AACAGGAATGCAAGAGAGCAAGTCCAACTACCGAGTCCGCTGTCTACAGATTCCTGGG 300  
DB 307 AACAGGAATGCAAGAGAGCAAGTCCAACTACCGAGTCCGCTGTCTACAGATTCCTGGG 366  
QY 301 AAGCAGAAATTTAGATTTCTGCTCTGAATCAACG 336  
DB 367 AAGCAGAAATTTAGATTTCTGCTCTGAATCAACG 402

RESULT 6  
ADM80824  
ID ADM80824 standard; cDNA; 1090 BP.  
XX ADM80824;  
XX 03-JUN-2004 (first entry)  
XX Human CADECM-11 encoding cDNA SEQ ID NO:53.  
XX human; cell adhesion and extracellular matrix protein; CADECM;  
KW neuroprotective; cytostatic; anorectic; immune disorder;  
KW neurological disorder; developmental disorder;  
KW connective tissue disorder; cell proliferative disorder; cancer; obesity;  
KW Tangier disease; gene; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 31..1008  
FT /\*tag= a  
FT /product= "CADECM-11"  
XX WO2004015396-A2.  
XX 19-FEB-2004.  
XX 12-AUG-2003; 2003WO-US025418.  
XX 13-AUG-2002; 2002US-0403781P.  
PR





CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
 CC may also be used for chromosome identification. The LP polypeptide can  
 CC also be used in manufacturing a medication. The treatment of the above  
 CC -mentioned diseases, conditions or disorders associated with aberrant  
 CC levels of the LP polypeptide.

XX Sequence 1194 BP; 268 A; 326 C; 389 G; 209 T; 0 U; 2 Other;

Query Match 100.0%; Score 336; DB 12; Length 1194;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-92;  
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCAGAGCCCGGATTGGCGACCACTGCTGCTGAAGTGTAAAGGGGCCCC 60

DB 112 GCTCAAAACATCAGAGCCCGGATTGGCGACCACTGCTGCTGAAGTGTAAAGGGGCCCC 171

QY 61 AAGAAACACCCAGCGGCTGGAATGGAATGAACACAGGCCGGACAGAGCTTGGAG 120

DB 172 AAGAAACACCCAGCGGCTGGAATGGAATGAACACAGGCCGGACAGAGCTTGGAG 231

QY 121 GTCTCTTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGCTTCTTCCCAACGCG 180

DB 232 GTCTCTTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGCTTCTTCCCAACGCG 291

QY 181 TCCCTCTTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGCTTCTTCCCAACGCG 240

DB 292 TCCCTCTTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGCTTCTTCCCAACGCG 351

QY 241 AACAGGAATGGAAGGAGACCAAGTCCACTACCGAGTCCGCTTACAGATTCTGGG 300

DB 352 AACAGGAATGGAAGGAGACCAAGTCCACTACCGAGTCCGCTTACAGATTCTGGG 411

QY 301 AAGCAGAAATTTAGATTCTGCTCTGAACTCAGC 336

DB 412 AAGCAGAAATTTAGATTCTGCTCTGAACTCAGC 447

RESULT 8

ABV73151

ID ABV73151 standard; DNA; 1223 BP.

XX AC ABV73151;

DT 08-JAN-2003 (first entry)

XX Human soluble RAGE protein encoding DNA.

DE RAGE; soluble receptor; advanced glycation endproduct; antidiabetic;  
 KW neurotropic; neuroprotective; antiarteriosclerotic; antiulcer; gene;  
 KW db.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 25..1068

FT /\*tag= a

FT /product= "soluble RAGE protein"

XX WO200274805-A1.

XX 26-SEP-2002.

XX 19-MAR-2002; 2002NO-JP002623.

XX 19-MAR-2001; 2001JP-00078409.

PR 10-AUG-2001; 2001JP-00243114.

PR 25-FEB-2002; 2002JP-00048182.

XX (UYKA-) UNIV JAPAN KANAZAWA.

XX Yamamoto H, Yonekura H, Yamamoto Y, Sakurai S, Watanabe T;

XX WPI; 2002-740851/80.

DR

DR P-PSDB; ABB82298.

XX Soluble advanced glycation endproduct receptor polypeptides and  
 PT substances modifying their activity for treatment and prevention of  
 PT disorders associated with diabetes and aging.

XX Claim 4; Page 118-120; 127pp; Japanese.

CC The invention relates to soluble receptor polypeptides for advanced  
 CC glycation endproducts (soluble RAGE) and encoding polynucleotides. The  
 CC soluble RAGE protein can be prepared by standard recombinant methodology.  
 CC The protein, polynucleotide and modulators can be used for the  
 CC prevention, treatment and diagnosis of diabetic complications, diseases  
 CC of aging, disorders of glycation of metabolic proteins, Alzheimer's  
 CC disease, arteriosclerosis and ulceration, and study of the mechanism and  
 CC pathology of these diseases. The present sequence represents the human  
 CC soluble RAGE protein encoding DNA

XX Sequence 1223 BP; 286 A; 341 C; 387 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 336; DB 6; Length 1223;

Best Local Similarity 100.0%; Pred. No. 1.5e-92;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCAGAGCCCGGATTGGCGACCACTGCTGCTGAAGTGTAAAGGGGCCCC 60

DB 91 GCTCAAAACATCAGAGCCCGGATTGGCGACCACTGCTGCTGAAGTGTAAAGGGGCCCC 150

QY 61 AAGAAACACCCAGCGGCTGGAATGGAATGAACACAGGCCGGACAGAGCTTGGAG 120

DB 151 AAGAAACACCCAGCGGCTGGAATGGAATGAACACAGGCCGGACAGAGCTTGGAG 210

QY 121 GTCCTGTCTCCCGAGGAGGCCCTGGGACAGTGTGCTGCTTCTTCCCAACGCG 180

DB 211 GTCCTGTCTCCCGAGGAGGCCCTGGGACAGTGTGCTGCTTCTTCCCAACGCG 270

QY 181 TCCCTCTTCTTCCCGGCTGTCGGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240

DB 271 TCCCTCTTCTTCCCGGCTGTCGGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 330

QY 241 AACAGGAATGGAAGGAGACCAAGTCCACTACCGAGTCCGCTTACAGATTCTGGG 300

DB 331 AACAGGAATGGAAGGAGACCAAGTCCACTACCGAGTCCGCTTACAGATTCTGGG 390

QY 301 AAGCAGAAATTTAGATTCTGCTCTGAACTCAGC 336

DB 391 AAGCAGAAATTTAGATTCTGCTCTGAACTCAGC 426

RESULT 9

ADG37043

ID ADG37043 standard; cDNA; 1223 BP.

XX AC ADG37043;

DT 26-FEB-2004 (first entry)

DE Receptor for advanced glycation endproducts (RAGE) cDNA.

XX ss; gene; receptor for advanced glycation endproducts; RAGE;  
 KW diabetic complication; glycosuria nephropathy; glycosuria retinopathy;  
 KW Alzheimer's disease; arteriosclerosis; Down's syndrome;  
 KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
 KW cancer; wound healing; human.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 25..1068

FT /\*tag= a

FT /product= "RAGE"

XX JP2003230382-A.

XX 19-AUG-2003.  
XX  
XX  
XX 08-FEB-2002; 2002JP-00032155.  
XX PF  
XX  
XX 08-FEB-2002; 2002JP-00032155.  
XX PR  
XX (KANA-) KANAZAWA DAIGAKUCHO.  
XX PA  
XX WPI; 2003-820207/77.  
XX DR P-PSDB; ADG37044.  
XX  
XX  
XX New advanced glycation endproducts-receptor for advanced glycation  
PT endproducts antagonist useful for treating or preventing diabetic  
PT complication, glycosuria nephropathy, and glycosuria retinopathy.  
XX  
XX  
XX Example 1; SEQ ID NO 1; 23pp; Japanese.  
XX  
XX  
XX The invention relates to a receptor for advanced glycation endproducts  
CC (RAGE). An AGE-RAGE antagonist composition is useful for treating or  
CC preventing diabetic complication (e.g., glycosuria nephropathy,  
CC glycosuria retinopathy), Alzheimer's disease, atherosclerosis, Down's  
CC syndrome, multiple sclerosis, amyloidosis, autoimmune disease,  
CC inflammation, cancer, wound healing, etc. The present sequence represents  
CC cDNA encoding the receptor for advanced glycation endproducts (RAGE).  
XX  
XX  
XX Sequence 1223 BP; 286 A; 341 C; 387 G; 209 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 336; DB 10; Length 1223;  
Best Local Similarity 100.0%; Pred. No. 1.5e-92;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCAAAACATCATCAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 60  
Db 91 GCTCAAAACATCATCAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 150  
QY 61 AGAAACACACCCAGCGGTGGATGGAATGGAACACACAGCCGGACAGAGCTTGGAG 120  
Db 151 AGAAACACACCCAGCGGTGGATGGAATGGAACACACAGCCGGACAGAGCTTGGAG 210  
QY 121 GTCTCTCTCCCGAGGAGGAGCCCTCGGACAGTGTCTGTCTTCCCAACGCG 180  
Db 211 GTCTCTCTCCCGAGGAGGAGCCCTCGGACAGTGTCTGTCTTCCCAACGCG 270  
QY 181 TCCTCTCTCTCCCGGTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240  
Db 271 TCCTCTCTCTCCCGGTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 330  
QY 241 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCCTGGG 300  
Db 331 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCCTGGG 390  
QY 301 AGCCAGAAATGTAGATTCTGCTCTGAATCAAG 336  
Db 391 AGCCAGAAATGTAGATTCTGCTCTGAATCAAG 426  
RESULT 10  
ADP19663  
ID ADP19663 standard; cDNA; 1239 BP.  
XX  
XX ADP19663;  
XX  
XX 12-AUG-2004 (first entry)  
XX  
XX Human LP2004 encoding cDNA SEQ ID NO:9.  
XX human; LP2004; antidiabetic; neuroprotective; nootropic;  
KW antiinflammatory; antiarthritis; antiarthritic; vulnery; cytosstatic;  
KW immunosuppressive; nephrotropic; dermatologic; gene therapy; diabetes;  
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
KW systemic lupus erythematosus; gene; ss.

XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT CDS 46..1113  
FT /\*tag= b  
FT /product= "LP2004"  
FT /note= "the present sequence only seems to encodes amino  
FT acids 1 to 356 of the LP2004 protein"  
FT 46..114  
FT /\*tag= a  
FT mat\_peptide 115..1110  
FT /\*tag= c  
XX  
XX WO2004044126-A2.  
XX  
XX 27-MAY-2004.  
XX  
XX 05-NOV-2003; 2003WO-US032734.  
XX  
XX 14-NOV-2002; 2002US-0426253P.  
XX (ELIL ) LILLY & CO ELI.  
XX  
XX Na S, Perkins DR;  
XX  
XX WPI; 2004-411705/38.  
XX P-PSDB; ADP19664.  
XX  
XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or  
PT LP2003) for diagnosing or treating disorders associated with aberrant  
PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome  
PT identification.  
XX  
XX Claim 1; SEQ ID NO 9; 111pp; English.  
XX  
XX The present sequence encodes human LP2004, which is used in the  
CC exemplification of the present invention. The present invention  
CC describes: (1) an isolated nucleic acid (I) comprising DNA having at  
CC least 95% sequence identity to a polynucleotide selected from the group  
CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown  
CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a  
CC polypeptide or mature form of a polypeptide having the amino acid  
CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide  
CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide  
CC having a nucleotide sequence which is complementary to the nucleotide  
CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector  
CC comprising (1); (3) a host cell comprising the vector; (4) producing an  
CC LP polypeptide; (5) an isolated polypeptide produced by the above method  
CC and comprising an amino acid sequence comprising about 95% sequence  
CC identity to a sequence of amino acid residues comprising LP2001, LP2003,  
CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric  
CC molecule comprising an LP polypeptide fused to a heterologous amino acid  
CC sequence; (7) an antibody which specifically binds to an LP polypeptide  
CC described above; (8) a composition (C) comprising a therapeutic amount of  
CC an active agent selected from an LP polypeptide, an agonist to an LP  
CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide  
CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a  
CC polynucleotide in combination with a pharmaceutical carrier; and (9)  
CC diagnosing or treating a mammal suffering from a disease, condition or  
CC disorder associated with aberrant levels of an LP-polypeptide. (C) has  
CC antidiabetic, neuroprotective, nootropic, cytosstatic, immunosuppressive,  
CC antirheumatic, antiarthritic, vulnery, cytosstatic, and can be used in gene  
CC nephrotropic and dermatological activities, and can be used for diagnosing or  
CC therapy. The compositions (C) and methods are useful for diagnosing or  
CC treating disorders associated with aberrant levels of an LP polypeptide,  
CC such as diabetes and its complications, Alzheimer's disease,  
CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple  
CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
CC may also be used for chromosome identification. The LP polypeptide can  
CC also be used in manufacturing a medicament for the treatment of the above  
CC mentioned diseases, conditions or disorders associated with aberrant  
CC levels of the LP polypeptide.

```
XX SQ Sequence 1239 BP; 294 A; 338 C; 391 G; 214 T; 0 U; 2 Other;
Query Match 100.0%; Score 336; DB 12; Length 1239;
Best Local Similarity 100.0%; Pred. No. 1.5e-92;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCAAAACATCAGCCCGGATTGGCGAGCCACTGTGCTGAAGTCTAAGGGGGCCCC 60
DB 112 GCTCAAAACATCAGCCCGGATTGGCGAGCCACTGTGCTGAAGTCTAAGGGGGCCCC 171
QY 61 AAGAAACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAGCTTGGAA 120
DB 172 AAGAAACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAGCTTGGAA 231
QY 121 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 232 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 291
QY 181 TCCCTCTTCTCCCGGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCCAGGCAATG 240
DB 292 TCCCTCTTCTCCCGGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCCAGGCAATG 351
QY 241 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTACAGATTCCTGG 300
DB 352 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTACAGATTCCTGG 411
QY 301 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAGC 336
DB 412 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAGC 447

RESULT 11
ADG33024
ID ADG33024 standard; DNA; 1268 BP.
AC AC
XX ADG33024;
DT 26-FEB-2004 (first entry)
DE Human DNA differentially expressed in patients with SLE SeqID348.
KW human; ds; autoimmune; chronic inflammatory disease; SLE;
KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW diverticulitis; primary biliary sclerosis.
OS Homo sapiens.
XX
XX WO2003090694-A2.
XX
XX 06-NOV-2003.
XX
XX 24-APR-2003; 2003WO-US013015.
XX
XX 24-APR-2002; 2002US-00131827.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX Wohlgemuth J, Fry K, Woodward R, Ly N;
XX WPI; 2003-877243/81.
XX
XX Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
XX such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
XX colitis, psoriasis and asthma by detecting the expression level of one or
XX more genes.
XX
XX Claim 19; SEQ ID NO 348; 877pp; English.
XX
XX This invention relates to novel methods for diagnosing and monitoring
XX autoimmune and chronic inflammatory diseases. Specifically, it refers to
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```
CC the identification of genes that have a clinical utility as diagnostic
CC tools for the management of, in particular, patients with systemic lupus
CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
CC present invention describes a method for determining the levels of
CC multiple differentially expressed genes of a patient, in a concerted
CC manner, in order to achieve an improved diagnostic assay with sensitivity
CC and specificity for the disease in question. As such, these genes are
CC useful for the diagnosis of various other inflammatory disorders
CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
CC ankylosing spondylitis, ulcerative colitis, primary sclerosing
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
CC This polynucleotide is a DNA sequence representing human mRNA that is
CC differentially expressed in patients with SLE, used in an exemplification
CC of the invention.
XX
SQ Sequence 1268 BP; 280 A; 361 C; 410 G; 217 T; 0 U; 0 Other;
Query Match 100.0%; Score 336; DB 10; Length 1268;
Best Local Similarity 100.0%; Pred. No. 1.5e-92;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCAAAACATCAGCCCGGATTGGCGAGCCACTGTGCTGAAGTCTAAGGGGGCCCC 60
DB 91 GCTCAAAACATCAGCCCGGATTGGCGAGCCACTGTGCTGAAGTCTAAGGGGGCCCC 150
QY 61 AAGAAACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAGCTTGGAA 120
DB 151 AAGAAACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAGCTTGGAA 210
QY 121 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 211 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 270
QY 181 TCCCTCTTCTCCCGGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCCAGGCAATG 240
DB 271 TCCCTCTTCTCCCGGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCCAGGCAATG 330
QY 241 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTACAGATTCCTGGG 300
DB 331 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTACAGATTCCTGGG 390
QY 301 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAGC 336
DB 391 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAGC 426

RESULT 12
ADP19655
ID ADP19655 standard; cDNA; 1291 BP.
XX
XX ADP19655;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human LP2000 encoding cDNA SEQ ID NO:1.
XX
XX human; LP2000; antidiabetic; neuroprotective; nootropic;
XX antiinflammatory; antirheumatic; antiarthritic; vulnerary; cytostatic;
XX immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
XX Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
XX autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
XX systemic lupus erythematosus; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 46..1089
XX /*tag= b
XX /product= "LP2000"
XX /note= "the present sequence only seems to encodes amino
XX acids 1 to 347 of the LP2000 protein"
XX sig_peptide 46..114
XX /*tag= a
```

FT mat\_peptide 115..1086  
 XX /\*tag= c  
 PN WO2004044126-A2.  
 XX 27-MAY-2004.  
 XX  
 PF 05-NOV-2003; 2003WO-US032734.  
 XX  
 PR 14-NOV-2002; 2002US-0426253P.  
 XX  
 XX (ELIL ) LILLY & CO ELI.  
 PA  
 XX Na S, Perkins DR;  
 PI WPI; 2004-411705/38.  
 DR P-PSDB; ADP19656.  
 XX  
 XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or  
 PT LP2003) for diagnosing or treating disorders associated with aberrant  
 PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome  
 PT identification.  
 XX  
 PS Example 2; SEQ ID NO 1; 111pp; English.  
 XX  
 CC The present sequence encodes human LP2000, which is used in the  
 CC exemplification of the present invention. The present invention  
 CC describes: (1) an isolated nucleic acid (I) comprising DNA having at  
 CC least 95% sequence identity to a polynucleotide selected from the group  
 CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown  
 CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a  
 CC polypeptide or mature form of a polypeptide having the amino acid  
 CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide  
 CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide  
 CC having a nucleotide sequence which is complementary to the nucleotide  
 CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector  
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an  
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method  
 CC and comprising an amino acid sequence comprising about 95% sequence  
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,  
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric  
 CC molecule comprising an LP polypeptide fused to a heterologous amino acid  
 CC sequence; (7) an antibody which specifically binds to an LP polypeptide  
 CC described above; (8) a composition (C) comprising a therapeutic amount of  
 CC an active agent selected from an LP polypeptide, an agonist to an LP  
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide  
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a  
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)  
 CC diagnosing or treating a mammal suffering from a disease, condition or  
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has  
 CC antidiabetic, neuroprotective, nootropic, antiinflammatory,  
 CC antirheumatic, antiarthritic, vulnerary, cytostatic, immunosuppressive,  
 CC nephrotropic and dermatological activities, and can be used in gene  
 CC therapy. The compositions (C) and methods are useful for diagnosing or  
 CC treating disorders associated with aberrant levels of an LP polypeptide,  
 CC such as diabetes and its complications, Alzheimer's disease,  
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple  
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
 CC may also be used for chromosome identification. The LP polypeptide can  
 CC also be used in manufacturing a medicament for the treatment of the above  
 CC mentioned diseases, conditions or disorders associated with aberrant  
 CC levels of the LP polypeptide.  
 XX  
 SQ Sequence 1291 BP; 299 A; 360 C; 403 G; 227 T; 0 U; 2 Other;  
 Query Match 100.0%; Score 336; DB 12; Length 1291;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-92;  
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 60  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 112 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 171

QY 61 AAGAAACACACCCAGCGGCTGGAATGGAACATGAACACAGGCGGACAGAACTTGGAG 120  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 172 AAGAAACACACCCAGCGGCTGGAATGGAACATGAACACAGGCGGACAGAACTTGGAG 231  
 QY 121 GTCTGTCTCTCCACAGGAGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGC 180  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 232 GTCTGTCTCTCCACAGGAGAGGCCCTCGGACAGTGTGGCTCGTCTCTTCCCAACGGC 291  
 QY 181 TCCCTCTTCTCTCCCGGCTGTCCGGATCCAGGATGAGGGGATTTTCCGTCGCCAGCAATG 240  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 292 TCCCTCTTCTCTCCCGGCTGTCCGGATCCAGGATGAGGGGATTTTCCGTCGCCAGCAATG 351  
 QY 241 AACAGGAATGGAAGAGAGACCAAGTCCCACTACCGAGTCCGTCGTCTACAGATTCTCTGG 300  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 352 AACAGGAATGGAAGAGAGACCAAGTCCCACTACCGAGTCCGTCGTCTACAGATTCTCTGG 411  
 QY 301 AAGCCAGAAATGTAGATTCTCGCTCTGAACCTCACG 336  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 412 AAGCCAGAAATGTAGATTCTCGCTCTGAACCTCACG 447

RESULT 13  
 ADP19665  
 ID ADP19665 standard; cDNA; 1329 BP.  
 XX  
 AC ADP19665;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human LP2005 encoding cDNA SEQ ID NO:11.  
 XX  
 KW human; LP2005; antidiabetic; neuroprotective; nootropic;  
 KW antiinflammatory; antirheumatic; antiarthritic; vulnerary; cytostatic;  
 KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;  
 KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
 KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
 KW systemic lupus erythematosus; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 46..1206  
 FT /\*tag= b  
 FT /product= "LP2005"  
 FT /note= "the present sequence only seems to encodes amino  
 FT acids 1 to 386 of the LP2005 protein"  
 FT sig\_peptide 46..114  
 FT /\*tag= a  
 FT mat\_peptide 115..1203  
 FT /\*tag= c  
 PN WO2004044126-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 PF 05-NOV-2003; 2003WO-US032734.  
 XX  
 PR 14-NOV-2002; 2002US-0426253P.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Na S, Perkins DR;  
 XX  
 DR WPI; 2004-411705/38.  
 DR P-PSDB; ADP19666.  
 XX  
 XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or  
 PT LP2003) for diagnosing or treating disorders associated with aberrant  
 PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome  
 PT identification.  
 XX  
 XX Claim 1; SEQ ID NO 11; 111pp; English.  
 XX

CC The present sequence encodes human LP2005, which is used in the  
 CC exemplification of the present invention. The present invention  
 CC describes: (1) an isolated nucleic acid (1) comprising DNA having at  
 CC least 95% sequence identity to a polynucleotide selected from the group  
 CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown  
 CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a  
 CC polypeptide or mature form of a polypeptide having the amino acid  
 CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide  
 CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide  
 CC having a nucleotide sequence which is complementary to the nucleotide  
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an  
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method  
 CC and comprising an amino acid sequence comprising about 95% sequence  
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,  
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric  
 CC molecule comprising an LP polypeptide fused to a heterologous amino acid  
 CC sequence; (7) an antibody which specifically binds to an LP polypeptide  
 CC described above; (8) a composition (C) comprising a therapeutic amount of  
 CC an active agent selected from an LP polypeptide, an agonist to an LP  
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide  
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a  
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)  
 CC diagnosing or treating a mammal suffering from a disease, condition or  
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has  
 CC anti-diabetic, neuroprotective, nootropic, anti-inflammatory,  
 CC antirheumatic, antiarthritic, vulnary, cytostatic, immunosuppressive,  
 CC nephrotropic and dermatological activities, and can be used in gene  
 CC therapy. The compositions (C) and methods are useful for diagnosing or  
 CC treating disorders associated with aberrant levels of an LP polypeptide,  
 CC such as diabetes and its complications, Alzheimer's disease,  
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple  
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
 CC may also be used for chromosome identification. The LP polypeptide can  
 CC also be used in manufacturing a medicament for the treatment of the above  
 CC mentioned diseases, conditions or disorders associated with aberrant  
 CC levels of the LP polypeptide.

XX  
 SQ Sequence 1329 BP; 289 A; 379 C; 424 G; 235 T; 0 U; 2 Other;

Query Match 100.0%; Score 336; DB 12; Length 1329;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-92;  
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGCCCC 60  
 DB 112 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGCCCC 171  
 QY 61 AGAAACACACCCAGCGCTGGAAATGGAATGGAACACAGCCGCGACAGAACTTGGGAAG 120  
 DB 172 AGAAACACACCCAGCGCTGGAAATGGAATGGAACACAGCCGCGACAGAACTTGGGAAG 231  
 QY 121 GTCCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGGCTCGTGTCTTCCCAACGCG 180  
 DB 232 GTCCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGGCTCGTGTCTTCCCAACGCG 291  
 QY 181 TCCCTTCTTCTCCGCTCTCGGATCCAGGATGAGGGGATTTCCGCTGCGAGCAATG 240  
 DB 292 TCCCTTCTTCTCCGCTCTCGGATCCAGGATGAGGGGATTTCCGCTGCGAGCAATG 351  
 QY 241 ACAGGAATGGAAGAGACCAAGTCCAACTACCACTCCGCTGTCTACAGATTCCTGGG 300  
 DB 352 ACAGGAATGGAAGAGACCAAGTCCAACTACCACTCCGCTGTCTACAGATTCCTGGG 411  
 QY 301 AAGCCAGAAATGTAGATTCTCCTCTGAATCAAG 336  
 DB 412 AAGCCAGAAATGTAGATTCTCCTCTGAATCAAG 447

RESULT 14

ADP19661

ID ADP19661 standard; cDNA; 1339 BP.

XX

AC ADP19661;  
 XX 12-AUG-2004 (first entry)  
 DT Human LP2003 encoding cDNA SEQ ID NO:7.  
 DE human; LP2003; antidiabetic; neuroprotective; nootropic;  
 KW antiinflammatory; antirheumatic; antiarthritic; vulnary; cytostatic;  
 KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;  
 KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
 KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
 KW systemic lupus erythematosus; gene; ss.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH 46..1137  
 CDS /\*tag= b  
 FT /product= "LP2003"  
 FT /note= "the present sequence only seems to encodes amino  
 FT acids 1 to 363 of the LP2003 protein"  
 FT 46..114  
 FT /\*tag= a  
 FT mat\_peptide 115..1134  
 FT /\*tag= c  
 FT sig\_peptide  
 FT 46..1134  
 FT /\*tag= c  
 XX WO2004044126-A2.  
 XX 27-MAY-2004.  
 XX 05-NOV-2003; 2003WO-US032734.  
 XX 14-NOV-2002; 2002US-0426253P.  
 XX (ELIL) LILLY & CO ELI.  
 XX Na S, Perkins DR;  
 XX WPI: 2004-411705/38.  
 DR P-PSDB; ADP19662.  
 XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or  
 LP2003) for diagnosing or treating disorders associated with aberrant  
 levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome  
 identification.  
 Claim 1; SEQ ID NO 7; 11pp; English.

The present sequence encodes human LP2003, which is used in the  
 exemplification of the present invention. The present invention  
 describes: (1) an isolated nucleic acid (1) comprising DNA having at  
 least 95% sequence identity to a polynucleotide selected from the group  
 consisting of: (a) a polynucleotide having a nucleotide sequence as shown  
 in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a  
 polypeptide or mature form of a polypeptide having the amino acid  
 sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide  
 fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide  
 having a nucleotide sequence which is complementary to the nucleotide  
 sequence of a polynucleotide as in (a), (b) or (c); (2) a vector  
 comprising (1); (3) a host cell comprising the vector; (4) producing an  
 LP polypeptide; (5) an isolated polypeptide produced by the above method  
 and comprising an amino acid sequence comprising about 95% sequence  
 identity to a sequence of amino acid residues comprising LP2001, LP2003,  
 LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric  
 molecule comprising an LP polypeptide fused to a heterologous amino acid  
 sequence; (7) an antibody which specifically binds to an LP polypeptide  
 described above; (8) a composition (C) comprising a therapeutic amount of  
 an active agent selected from an LP polypeptide, an agonist to an LP  
 polypeptide, an antagonist to an LP polypeptide, an LP polypeptide  
 antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a  
 polynucleotide in combination with a pharmaceutical carrier; and (9)  
 diagnosing or treating a mammal suffering from a disease, condition or  
 disorder associated with aberrant levels of an LP-polypeptide. (C) has

CC antidiabetic, neuroprotective, nootropic, antiinflammatory,  
CC antirheumatic, antiarthritic, vulnary, cytosatic, immunosuppressive,  
CC nephrotropic and dermatological activities, and can be used in gene  
CC therapy. The compositions (C) and methods are useful for diagnosing or  
CC treating disorders associated with aberrant levels of an LP polypeptide,  
CC such as diabetes and its complications, Alzheimer's disease,  
CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple  
CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
CC may also be used for chromosome identification. The LP polypeptide can  
CC also be used in manufacturing a medicament for the treatment of the above  
CC -mentioned diseases, conditions or disorders associated with aberrant  
CC levels of the LP polypeptide.

XX  
SQ Sequence 1339 BP; 318 A; 366 C; 421 G; 232 T; 0 U; 2 Other;  
Query Match 100.0%; Score 336; DB 12; Length 1339;  
Best Local Similarity 100.0%; Pred. No. 1.6e-92;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCC 60  
DB 112 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCC 171

QY 61 AAGAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCCGGACAGAGCTTGGAG 120  
DB 172 AAGAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCCGGACAGAGCTTGGAG 231

QY 121 GTCCTGTCTCCCGAGGAGGAGCCCTCGGACAGTGTGCTGTCTCTCCCAACGCG 180  
DB 232 GTCCTGTCTCCCGAGGAGGAGCCCTCGGACAGTGTGCTGTCTCTCCCAACGCG 291

QY 181 TCCTCTTCTCCCGCTGTGGGATTCAGGATTCAGGAGGATTCCTGGTCCAGCAATG 240  
DB 292 TCCTCTTCTCCCGCTGTGGGATTCAGGATTCAGGAGGATTCCTGGTCCAGCAATG 351

QY 241 ACAGAGATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTACAGATTCCTGG 300  
DB 352 AACAGAGATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTACAGATTCCTGG 411

QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCAACG 336  
DB 412 AAGCCAGAAATGTAGATTCTGCTCTGAATCAACG 447

RESULT 15  
ADP19659  
ID ADP19659 standard; cDNA; 1384 BP.  
AC ADP19659;  
XX  
XX 12-AUG-2004 (first entry)  
DE Human LP2002 encoding cDNA SEQ ID NO:5.  
XX  
XX human; LP2002; antidiabetic; neuroprotective; nootropic;  
KW antinflammatory; antirheumatic; antiarthritic; vulnary; cytosatic;  
KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;  
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;  
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;  
KW systemic lupus erythematosus; gene; ss.  
XX  
OS Homo sapiens.

PH Key Location/Qualifiers  
FT CDS 46..1308  
FT /\*tag= b  
FT /product= "LP2002"  
FT /note= "the present sequence only seems to encodes amino  
FT acids 1 to 420 of the LP2002 protein"  
FT 46..114  
FT sig\_peptide /\*tag= a  
FT mat\_peptide 115..1305 /\*tag= c  
FT

XX WO2004044126-A2.  
XX 27-MAY-2004.  
XX 05-NOV-2003; 2003WO-US032734.  
XX 14-NOV-2002; 2002US-0426253P.  
XX (ELIL ) LILLY & CO ELI.  
XX Na S, Perkins DR;  
XX WPI; 2004-411705/38.  
XX P-PSDB; ADP19660.  
XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or  
XX LP2003) for diagnosing or treating disorders associated with aberrant  
XX levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome  
XX identification.  
XX Example 2; SEQ ID NO 5; 111pp; English.  
XX The present sequence encodes human LP2002, which is used in the  
XX exemplification of the present invention. The present invention  
XX describes: (1) an isolated nucleic acid (1) comprising DNA having at  
XX least 95% sequence identity to a polynucleotide selected from the group  
XX consisting of: (a) a polynucleotide having a nucleotide sequence as shown  
XX in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a  
XX polypeptide or mature form of a polypeptide having the amino acid  
XX sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide  
XX fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide  
XX having a nucleotide sequence which is complementary to the nucleotide  
XX sequence of a polynucleotide as in (a), (b) or (c); (2) a vector  
XX comprising (1); (3) a host cell comprising the vector; (4) producing an  
XX LP polypeptide; (5) an isolated polypeptide produced by the above method  
XX and comprising an amino acid sequence comprising about 95% sequence  
XX identity to a sequence of amino acid residues comprising LP2001, LP2003,  
XX LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric  
XX molecule comprising an LP polypeptide fused to a heterologous amino acid  
XX sequence; (7) an antibody which specifically binds to an LP polypeptide  
XX described above; (8) a composition (C) comprising a therapeutic amount of  
XX an active agent selected from an LP polypeptide, an agonist to an LP  
XX polypeptide, an antagonist to an LP polypeptide, an LP polypeptide  
XX antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a  
XX polynucleotide in combination with a pharmaceutical carrier; and (9)  
XX diagnosing or treating a mammal suffering from a disease, condition or  
XX disorder associated with aberrant levels of an LP-polypeptide. (C) has  
XX antidiabetic, neuroprotective, nootropic, antiinflammatory,  
XX antirheumatic, antiarthritic, vulnary, cytosatic, immunosuppressive,  
XX nephrotropic and dermatological activities, and can be used in gene  
XX therapy. The compositions (C) and methods are useful for diagnosing or  
XX treating disorders associated with aberrant levels of an LP polypeptide,  
XX such as diabetes and its complications, Alzheimer's disease,  
XX inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple  
XX sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They  
XX may also be used for chromosome identification. The LP polypeptide can  
XX also be used in manufacturing a medicament for the treatment of the above  
XX -mentioned diseases, conditions or disorders associated with aberrant  
XX levels of the LP polypeptide.

XX  
SQ Sequence 1384 BP; 312 A; 386 C; 444 G; 240 T; 0 U; 2 Other;  
Query Match 100.0%; Score 336; DB 12; Length 1384;  
Best Local Similarity 100.0%; Pred. No. 1.6e-92;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCC 60  
DB 112 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCC 171

QY 61 AAGAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCCGGACAGAGCTTGGAG 120





GenCore version 5.1.6  
Copyright (c) 1993 - 2005, CompuGen Ltd.  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	336	100.0	336	16	US-10-091-019-4
2	336	100.0	1020	19	US-10-091-019-2
3	336	100.0	1223	19	US-10-472-507A-1
4	336	100.0	1391	16	US-10-091-019-1
5	336	100.0	1415	18	US-10-115-635-351
6	336	100.0	1463	18	US-10-115-635-352
7	334.4	99.5	1217	17	US-10-309-290-95
8	332.8	99.0	1405	8	US-08-905-709-3
9	332.8	99.0	1405	8	US-08-755-235-3
10	332.8	99.0	1405	18	US-10-850-861-3
11	270.6	80.5	1438	8	US-08-905-709-1

12	270.6	80.5	1438	8	US-08-755-235-1
13	270.6	80.5	1438	18	US-10-850-861-1
14	242	72.0	1173	17	US-10-309-290-99
15	242	72.0	1226	17	US-10-309-290-97
16	197	58.6	203	16	US-10-029-386-16362
17	197	58.6	485	13	US-10-027-632-257559
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36	35.4	10.5	755	18	US-10-653-047-4384
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38	34	10.1	274	16	US-10-029-386-13779
39	34	10.1	328	9	US-09-815-343-540
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c	34	10.1	5874	18	US-10-719-993-370
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c	34	10.1	74648	18	US-10-719-993-6875
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ALIGNMENTS

RESULT 1  
US-10-091-019-4  
; Sequence 4, Application US/10091019  
; Publication NO. US20030166063A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Robert B.  
; APPLICANT: Shen, Jane M.  
; APPLICANT: Shabbaz, Manouchehr M.  
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins  
; FILE REFERENCE: 41305-270555  
; CURRENT APPLICATION NUMBER: US/10/091,019  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/273,418  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 336  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-091-019-4

Query Match	100.0%;	Score 336;	DB 16;	Length 336;
Best Local Similarity	100.0%;	Pred. No. 2.9e-99;		
Matches 336;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	GCTCAAAACATCACAGCCCGGATTGCGAGCCACCTGGTCTCAAGTGTAAAGGGGGCCCC	60	
Db	1	GCTCAAAACATCACAGCCCGGATTGCGAGCCACCTGGTCTCAAGTGTAAAGGGGGCCCC	60	
Qy	61	AAGAAACACCCACCGCGCTGGAATGGAATCTGAACACAGCCGGACAGAGCTTGGAG	120	
Db	61	AAGAAACACCCACCGCGCTGGAATGGAATCTGAACACAGCCGGACAGAGCTTGGAG	120	

QY 121 GTCCTGTCTCCAGGAGGAGGCGCTGAGCAGTGTGCTGCTGCTTCCCAACGGC 180  
Db 121 GTCTGTCTCTCCAGGAGGAGGCGCTGAGCAGTGTGCTGCTGCTTCCCAACGGC 180  
QY 181 TCCCTCTTCTCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 240  
Db 181 TCCCTCTTCTCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 240  
QY 241 AACAGGAATGGAAGGAGACCAAGTCAACTACGAGTCCGTGTCTACGAGTTCCTGGG 300  
Db 241 AACAGGAATGGAAGGAGACCAAGTCAACTACGAGTCCGTGTCTACGAGTTCCTGGG 300  
QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336  
Db 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336

## RESULT 2

US-10-091-019-2  
; Sequence 2, Application US/10091019  
; Publication No. US20030166063A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Robert B.  
; APPLICANT: Shen, Jane M.  
; APPLICANT: Shahbaz, Manouchehr M.  
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins  
; FILE REFERENCE: 41305-270555  
; CURRENT APPLICATION NUMBER: US/10/091,019  
; CURRENT FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/273,418  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 1020  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1020)  
; OTHER INFORMATION:

US-10-091-019-2

Query Match 100.0%; Score 336; DB 16; Length 1020;  
Best Local Similarity 100.0%; Pred. No. 3.7e-99;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGCTGCTGAAGTGAAGGGGCCCCC 60  
Db 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGCTGCTGAAGTGAAGGGGCCCCC 126  
QY 61 AAGAAACCAACCCAGCGGCTGGAATGGAACCTGAACACAGCGCCGACAGAGCTTGGAG 120  
Db 127 AAGAAACCAACCCAGCGGCTGGAATGGAACCTGAACACAGCGCCGACAGAGCTTGGAG 186  
QY 121 GTCCTGTCTCCAGGAGAGGCGCCCTGGGACAGTGTGCTGCTCTCCCAACGGC 180  
Db 187 GTCCTGTCTCCAGGAGAGGCGCCCTGGGACAGTGTGCTGCTCTCCCAACGGC 246  
QY 181 TCCCTCTTCTTCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240  
Db 247 TCCCTCTTCTTCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 306  
QY 241 AACAGGAATGGAAGGAGACCAAGTCAACTACGAGTCCGTGTCTACGAGTTCCTGGG 300  
Db 307 AACAGGAATGGAAGGAGACCAAGTCAACTACGAGTCCGTGTCTACGAGTTCCTGGG 366  
QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336  
Db 367 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 402

## RESULT 3

US-10-472-507A-1  
; Sequence 1, Application US/10472507A  
; Publication No. US2005003017A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamamoto, Hiroshi  
; APPLICANT: Yonekura, Hideto  
; APPLICANT: Yamamoto, Yasuhiko  
; APPLICANT: Sakurai, Shigeru  
; APPLICANT: Watanabe, Takuo  
; TITLE OF INVENTION: Soluble RAGE Protein  
; FILE REFERENCE: 026350-089  
; CURRENT APPLICATION NUMBER: US/10/472,507A  
; CURRENT FILING DATE: 2003-09-22  
; PRIOR APPLICATION NUMBER: PCT/JP02,02623  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: JP 2001-78409  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: JP 2001-243114  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: JP 2002-48182  
; PRIOR FILING DATE: 2002-02-25  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1223  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)....(1068)  
; OTHER INFORMATION:

US-10-472-507A-1

Query Match 100.0%; Score 336; DB 19; Length 1223;  
Best Local Similarity 100.0%; Pred. No. 3.8e-99;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGCTGCTGAAGTGAAGGGGCCCCC 60  
Db 91 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGCTGCTGAAGTGAAGGGGCCCCC 150  
QY 61 AAGAAACCAACCCAGCGGCTGGAATGGAACCTGAACACAGCGCCGACAGAGCTTGGAG 120  
Db 151 AAGAAACCAACCCAGCGGCTGGAATGGAACCTGAACACAGCGCCGACAGAGCTTGGAG 210  
QY 121 GTCCTGTCTCCAGGAGAGGCGCCCTGGGACAGTGTGCTGCTCTCCCAACGGC 180  
Db 211 GTCCTGTCTCCAGGAGAGGCGCCCTGGGACAGTGTGCTGCTCTCCCAACGGC 270  
QY 181 TCCCTCTTCTTCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240  
Db 271 TCCCTCTTCTTCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 330  
QY 241 AACAGGAATGGAAGGAGACCAAGTCAACTACGAGTCCGTGTCTACGAGTTCCTGGG 300  
Db 331 AACAGGAATGGAAGGAGACCAAGTCAACTACGAGTCCGTGTCTACGAGTTCCTGGG 390  
QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336  
Db 391 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 426

## RESULT 4

US-10-091-019-1  
; Sequence 1, Application US/10091019  
; Publication No. US20030166063A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Robert B.  
; APPLICANT: Shen, Jane M.  
; APPLICANT: Shahbaz, Manouchehr M.  
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins  
; FILE REFERENCE: 41305-270555  
; CURRENT APPLICATION NUMBER: US/10/091,019  
; CURRENT FILING DATE: 2002-03-05

;; PRIOR APPLICATION NUMBER: US 60/273,418  
;; PRIOR FILING DATE: 2001-03-05  
;; NUMBER OF SEQ ID NOS: 10  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 1  
;; LENGTH: 1391  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-091-019-1

Query Match 100.0%; Score 336; DB 16; Length 1391;  
Best Local Similarity 100.0%; Pred. No. 3.9e-99;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60  
DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 126  
QY 61 AAGAAACACCCAGCGCTGGAATGGAATGGAACACAGCCCGGACAGAACTTGGGAAG 120  
DB 127 AAGAAACACCCAGCGCTGGAATGGAATGGAACACAGCCCGGACAGAACTTGGGAAG 186  
QY 121 GTCCTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTCCCAACGGC 180  
DB 187 GTCCTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTCTCTCCCAACGGC 246  
QY 181 TCCCTCTTCTCCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240  
DB 247 TCCCTCTTCTCCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 306  
QY 241 AACAGAAATGGAAGAGAGCCAAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTTCTGGG 300  
DB 307 AACAGAAATGGAAGAGAGCCAAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTTCTGGG 366  
QY 301 AAGCCAGAAATTTAGATTCTGCCTCTGAATCAAG 336  
DB 367 AAGCCAGAAATTTAGATTCTGCCTCTGAATCAAG 402

RESULT 5  
US-10-115-635-351  
; Sequence 351, Application US/10115635  
; Publication No. US20040137434A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and  
; FILE REFERENCE: 797CON  
; CURRENT APPLICATION NUMBER: US/10/115,635  
; PRIOR FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: 09/714,936  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 362  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 351  
; LENGTH: 1415  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(1239)  
US-10-115-635-351

Query Match 100.0%; Score 336; DB 18; Length 1415;  
Best Local Similarity 100.0%; Pred. No. 3.9e-99;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60  
DB 91 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 150  
QY 61 AAGAAACACCCAGCGCTGGAATGGAATGGAACACAGCCCGGACAGAACTTGGGAAG 120  
DB 151 AAGAAACACCCAGCGCTGGAATGGAATGGAACACAGCCCGGACAGAACTTGGGAAG 210  
QY 121 GTCCTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTGTCTTCCCAACGGC 180  
DB 211 GTCCTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGCTCGTGTCTTCCCAACGGC 270  
QY 181 TCCCTCTTCTCCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240  
DB 271 TCCCTCTTCTCCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 330  
QY 241 AACAGAAATGGAAGAGAGCCAAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTTCTGGG 300  
DB 331 AACAGAAATGGAAGAGAGCCAAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTTCTGGG 390  
QY 301 AAGCCAGAAATTTAGATTCTGCCTCTGAATCAAG 336  
DB 391 AAGCCAGAAATTTAGATTCTGCCTCTGAATCAAG 426

RESULT 6  
US-10-115-635-352  
; Sequence 352, Application US/10115635  
; Publication No. US20040137434A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and  
; FILE REFERENCE: 797CON  
; CURRENT APPLICATION NUMBER: US/10/115,635  
; PRIOR FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: 09/714,936  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 362  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 352  
; LENGTH: 1463  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(1287)  
US-10-115-635-352

Query Match 100.0%; Score 336; DB 18; Length 1463;  
Best Local Similarity 100.0%; Pred. No. 3.9e-99;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60  
DB 91 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 150

61	Qy	AGAAACACACCCACGGGCTGGATGGAACCTGAACACAGGCCGGACAGAAGCTTCGAAAG	120
151	Db	AGAAACACACCCACGGGCTGGATGGAACCTGAACACAGGCCGGACAGAAGCTTCGAAAG	210
121	Qy	GTCTGTCTCTCCACAGGAGAGGCCCTGGGACAGTGTGGCTGTGTCTTCCCAACGCG	180
211	Db	GTCTGTCTCTCCACAGGAGAGGCCCTGGGACAGTGTGGCTGTGTCTTCCCAACGCG	270
181	Qy	TGCTCTTCTCTCCGGCTGTGGGATCCAGGATGAGGGGATTTTCGGTGCCAGGCAATG	240
271	Db	TCTCTTCTCTCTCCGGCTGTGGGATCCAGGATGAGGGGATTTTCGGTGCCAGGCAATG	330
241	Qy	AACAGGAATGGAAGAGACCAAGTCCAATCACCAGTCCGTGTCTACACAGATTCTCTGGG	300
331	Db	AACAGGAATGGAAGAGACCAAGTCCAATCACCAGTCCGTGTCTACACAGATTCTCTGGG	390
301	Qy	AAGCAGAAATTTGATATTTGCCTCTGAACTCAG	336
391	Db	AAGCAGAAATTTGATATTTGCCTCTGAACTCAG	426

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RESULT 7
US-10-309-290-95
/ Sequence 95, Application US/10309290
/ Publication No. US20040023241A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Anderson, David W.
/ APPLICANT: Boldson, Ferenc L.
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Chillakuru, Rajeev A.
/ APPLICANT: Edinger, Shlomit R.
/ APPLICANT: Gerlach, Valerie L.
/ APPLICANT: Gorman, Linda
/ APPLICANT: Gould-Rothberg, Bonnie E.
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Jeffers, Michael E.
/ APPLICANT: Ji, Weizhen
/ APPLICANT: Li, Li
/ APPLICANT: Malyankar, Uriel M.
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Murphey, Ryan
/ APPLICANT: Paturdjian, Meera
/ APPLICANT: Peyman, John A.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Rieser, Daniel K.
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Smithson, Glenna
/ APPLICANT: Starling, Gary
/ APPLICANT: Taupier, Raymond J.
/ APPLICANT: Voss, Edward Z.
/ APPLICANT: Zhong, Hailong
/ APPLICANT: Zhong, Mei
/ TITLE OF INVENTION: THERAPEUTIC POLYPP
/ FILE REFERENCE: 21402-502A
/ CURRENT APPLICATION NUMBER: US/10/309
/ CURRENT FILING DATE: 2002-12-02
/ PRIOR APPLICATION NUMBER: 60/336,600
/ PRIOR FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: 60/338,285
/ PRIOR FILING DATE: 2001-12-07
/ PRIOR APPLICATION NUMBER: 60/341,346
/ PRIOR FILING DATE: 2001-12-12
/ PRIOR APPLICATION NUMBER: 60/341,477
/ PRIOR FILING DATE: 2001-12-17
/ PRIOR APPLICATION NUMBER: 60/341,540
/ PRIOR FILING DATE: 2001-12-17
/ PRIOR APPLICATION NUMBER: 60/342,592
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/344,297
/ PRIOR FILING DATE: 2001-12-27
/ PRIOR APPLICATION NUMBER: 60/344,903
/ PRIOR FILING DATE: 2001-12-31

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; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 95
; LENGTH: 1217
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(1214)
US-10-309-290-95

Query Match          99.5%; Score 334.4; DB 17; Length 1217;
Best Local Similarity 99.7%; Pred. No. 1.3e-99;
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1 GCTAAACATCACAGCCCGGATTGGCAGCCACTGCTGCTGAAGTGTGAAGGGGCCCC 60
Db 69 GCTCAAAACATCACAGCTCGGATTTGGGAGCCACTGGTGTGAAGTGTGAAGGGGCCCC 128
Qy 61 AGAAACACACCCAGCGGCTCGAATGAAACTGAACACAGCCGCGACAGAGCTTGGAG 120
Db 129 AGAAACACACCCAGCGGCTCGAATGAAACTGAACACAGCCGCGACAGAGCTTGGAG 188
Qy 121 GTCTGTGTCTCCAGGAGGAGGCCCTTGGGACAGTGTGGCTCGTGTCTTCCACAGCG 180
Db 189 GTCTGTGTCTCCAGGAGGAGGCCCTTGGGACAGTGTGGCTCGTGTCTTCCACAGCG 248
Qy 181 TCCTCTTCTCTTTCGCGCTGTCCGATCCAGGATGAGGGGATTTTCGCTGCCAGGCAATG 240
Db 249 TCCTCTTCTTTCGCGCTGTCCGATCCAGGATGAGGGGATTTTCGCTGCCAGGCAATG 308
Qy 241 ACAGGAATGGAAGGAGACCAAGTCCAATACCGAGTCCGTGTCTACAGATTTCTGGG 300
Db 309 ACACGAATGGAAGGAGACCAAGTCCAATACCGAGTCCGTGTCTACAGATTTCTGGG 368
Qy 301 AAGCCAGAAATTTAGATTTCTGCCTCTGAACCTCACG 336
Db 369 AAGCCAGAAATTTAGATTTCTGCCTCTGAACCTCACG 404

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RESULT 8  
 US-08-905-709-3  
 ; Sequence 3, Application US/08905709  
 ; Publication No. US20010039256A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stern, David  
 ; APPLICANT: Schmidt, Ann M.  
 ; TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED  
 ; TITLE OF INVENTION: ATHEROSCLEROSIS USING (SRAGE) SOLUBLE RECEPTOR FOR  
 ; TITLE OF INVENTION: ADVANCED GLYCATION ENDPRODUCTS  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/905,709  
 ; FILING DATE: 05-AUG-1997  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:

```
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/52876
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-905-709-3

Query Match          99.0%; Score 332.8; DB 8; Length 1405;
Best Local Similarity 99.4%; Pred. No. 4.3e-98;
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCAACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 60
DB 67 GCTCAAAACATCAACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 126
QY 61 AAGAACACACCCAGCGGCTGGAATGGAATGAACTGAACACAGCGCGGACAGAGCTTGGAG 120
DB 127 AAGAACACACCCAGCGGCTGGAATGGAATGGAATGAACTGAACACAGCGCGGACAGAGCTTGGAG 186
QY 121 GTCTCTCTCTCCCGGAGGAGGCCCTGGGACAGTGTGGTCTGTCTTCCCAACGGC 180
DB 187 GTCTCTCTCTCCCGGAGGAGGCCCTGGGACAGTGTGGTCTGTCTTCCCAACGGC 246
QY 181 TCCTCTCTCTCCCGGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240
DB 247 TCCTCTCTCTCCCGGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 306
QY 241 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 300
DB 307 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 366
QY 301 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAGC 336
DB 367 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAGC 402

RESULT 9
US-08-755-235-3
; Sequence 3, Application US/08755235
; Publication No. US20030059423A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Human
; US-08-755-235-3

Query Match          99.0%; Score 332.8; DB 8; Length 1405;
Best Local Similarity 99.4%; Pred. No. 4.3e-98;
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCAACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 60
DB 67 GCTCAAAACATCAACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 126
QY 61 AAGAACACACCCAGCGGCTGGAATGGAATGGAATGAACTGAACACAGCGCGGACAGAGCTTGGAG 120
DB 127 AAGAACACACCCAGCGGCTGGAATGGAATGGAATGAACTGAACACAGCGCGGACAGAGCTTGGAG 186
QY 121 GTCTCTCTCTCCCGGAGGAGGCCCTGGGACAGTGTGGTCTGTCTTCCCAACGGC 180
DB 187 GTCTCTCTCTCCCGGAGGAGGCCCTGGGACAGTGTGGTCTGTCTTCCCAACGGC 246
QY 181 TCCTCTCTCTCCCGGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240
DB 247 TCCTCTCTCTCCCGGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 306
QY 241 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 300
DB 307 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 366
QY 301 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAGC 336
DB 367 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAGC 402

RESULT 10
US-10-850-861-3
; Sequence 3, Application US/10850861
; Publication No. US20040228855A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/10/850,861
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/08/755,235
; PRIOR FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Human
; US-10-850-861-3

Query Match          99.0%; Score 332.8; DB 18; Length 1405;
Best Local Similarity 99.4%; Pred. No. 4.3e-98;
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCAACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 60
DB 67 GCTCAAAACATCAACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 126
QY 61 AAGAACACACCCAGCGGCTGGAATGGAATGGAATGAACTGAACACAGCGCGGACAGAGCTTGGAG 120
DB 127 AAGAACACACCCAGCGGCTGGAATGGAATGGAATGAACTGAACACAGCGCGGACAGAGCTTGGAG 186
QY 121 GTCTCTCTCTCCCGGAGGAGGCCCTGGGACAGTGTGGTCTGTCTTCCCAACGGC 180
DB 187 GTCTCTCTCTCCCGGAGGAGGCCCTGGGACAGTGTGGTCTGTCTTCCCAACGGC 246
QY 181 TCCTCTCTCTCCCGGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240
DB 247 TCCTCTCTCTCCCGGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 306
QY 241 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 300
DB 307 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 366
QY 301 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAGC 336
DB 367 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAGC 402

RESULT 11
US-08-905-709-1
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Sequence 1, Application US/08905709  
 Publication No. US20010039256A1  
 GENERAL INFORMATION:  
 APPLICANT: Stern, David  
 APPLICANT: Schmidt, Ann Marie  
 APPLICANT: Wu, Jun  
 TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED  
 TITLE OF INVENTION: ATHEROSCLEROSIS USING (sRAGE) SOLUBLE RECEPTOR FOR  
 TITLE OF INVENTION: ADVANCED GLYCAN ENDPRODUCTS  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/905,709  
 FILING DATE: 05-AUG-1997  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 0575/52876  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-278-0400  
 TELEFAX: 212-391-0526  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1438 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-905-709-1

Query Match 80.5%; Score 270.6; DB 8; Length 1438;  
 Best Local Similarity 90.4%; Pred. No. 8.2e-78;  
 Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;  
 QY 4 CAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAACTGTAAAGGGGCCCCCAAG 63  
 DB 79 CAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAACTGTAAAGGGGCCCCCAAG 138  
 QY 64 AAACACCCCGAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGAGCTTGGAAAGTC 123  
 DB 139 AAACACCCCGAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGAGCTTGGAAAGTC 198  
 QY 124 CTGTCTCCCGAGGAGGAGCCCTCGGACAGTGTGGCTCGTCTCCCAACGGCTCC 183  
 DB 199 CTGTCTCCCGAG--GGAGACCCCTGGATAGCGTGGTCTCGGCTCCCAACGGCTCC 255  
 QY 184 CTCTTCTTCGGCTGTGGATCCAGGATGAGGAGATTTCCGTGCGAGCAATGAAC 243  
 DB 256 CTCTTCTTCGGCTGTGGATCCAGGATGAGGAGATTTCCGTGCGGCAACGAGC 315  
 QY 244 AGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGCTCTACAGATTCCTGGGAAG 303  
 DB 316 CGGAGCGGAAGAGAGACCAAGTCTAACTACCGAGTCCGAGTCTATCAGATTCCTGGGAAG 375  
 QY 304 CAGAAATTTGATTTCTGCCTCTGAACCTCAGC 336  
 DB 376 CCAGAAATTTGATTTCTGCCTCTGAACCTCAGC 408

RESULT 12  
 US-08-755-235-1  
 Sequence 1, Application US/08755235

Publication No. US20030059423A1  
 GENERAL INFORMATION:  
 APPLICANT: Stern, David M.  
 APPLICANT: Schmidt, Ann Marie  
 APPLICANT: Wu, Jun  
 TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES  
 FILE REFERENCES: 0575/50159  
 CURRENT APPLICATION NUMBER: US/08/755,235  
 CURRENT FILING DATE: 1996-11-22  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 1438  
 TYPE: DNA  
 ORGANISM: Bovine  
 US-08-755-235-1

Query Match 80.5%; Score 270.6; DB 8; Length 1438;  
 Best Local Similarity 90.4%; Pred. No. 8.2e-78;  
 Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;  
 QY 4 CAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAACTGTAAAGGGGCCCCCAAG 63  
 DB 79 CAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAACTGTAAAGGGGCCCCCAAG 138  
 QY 64 AAACACCCCGAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTGGAAAGTC 123  
 DB 139 AAACACCCCGAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTGGAAAGTC 198  
 QY 124 CTGTCTCCCGAGGAGGAGCCCTCGGACAGTGTGGCTCGTCTCCCAACGGCTCC 183  
 DB 199 CTGTCTCCCGAG--GGAGACCCCTGGATAGCGTGGTCTCGGCTCCCAACGGCTCC 255  
 QY 184 CTCTTCTTCGGCTGTGGATCCAGGATGAGGAGATTTCCGTGCGAGCAATGAAC 243  
 DB 256 CTCTTCTTCGGCTGTGGATCCAGGATGAGGAGATTTCCGTGCGGCAACGAGC 315  
 QY 244 AGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGCTCTACAGATTCCTGGGAAG 303  
 DB 316 CGGAGCGGAAGAGAGACCAAGTCTAACTACCGAGTCCGAGTCTATCAGATTCCTGGGAAG 375  
 QY 304 CAGAAATTTGATTTCTGCCTCTGAACCTCAGC 336  
 DB 376 CCAGAAATTTGATTTCTGCCTCTGAACCTCAGC 408

RESULT 13  
 US-10-850-861-1  
 Sequence 1, Application US/10850861  
 Publication No. US2004022885A1  
 GENERAL INFORMATION:  
 APPLICANT: Stern, David M.  
 APPLICANT: Wu, Jun  
 TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES  
 FILE REFERENCES: 0575/50159  
 CURRENT APPLICATION NUMBER: US/10/850,861  
 CURRENT FILING DATE: 2004-05-20  
 PRIOR APPLICATION NUMBER: US/08/755,235  
 PRIOR FILING DATE: 1996-11-22  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 1438  
 TYPE: DNA  
 ORGANISM: Bovine  
 US-10-850-861-1

Query Match 80.5%; Score 270.6; DB 18; Length 1438;  
 Best Local Similarity 90.4%; Pred. No. 8.2e-78;  
 Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;  
 QY 4 CAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAACTGTAAAGGGGCCCCCAAG 63

Db 79 CAAAACATCACAGCCGGATCGGAGCCACTGGTGTGAATGCAAGGGAGCCGCCCAAG 138  
Qy 64 AAACACACCCAGCGGTGGAATGGAATCTGAACACAGGCGCGGACAGAACTTTGGAGGTC 123  
Db 139 AAACACACCCAGCGGTGGAATGGAATCTGAACACAGGCGCGGACAGAACTTTGGAGGTC 198  
Qy 124 CTGTCTCCCGAGGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGCTCC 183  
Db 199 CTGTCTCCCGAGGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGCTCC 255  
Qy 184 CTCTTCTCTCCCGGTCTCGGGATCCAGGATGAGGGATTTCCGGTGGCCAGCAATGAAC 243  
Db 256 CTCTTCTCTCCCGGTCTCGGGATCCAGGATGAGGGATTTCCGGTGGCCAGCAATGAAC 315  
Qy 244 AGGAATGGAAGGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACCAAGATTTCTGGGAAG 303  
Db 316 CGGAGCGGAAGGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACCAAGATTTCTGGGAAG 375  
Qy 304 CCAGAAATGTAGATTCCTGCTTGAACCTCAGC 336  
Db 376 CCAGAAATGTAGATTCCTGCTTGAACCTCAGC 408

RESULT 14  
US-10-309-290-99  
; Sequence 99, Application US/10309290  
; Publication No. US20040023241A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsbrook II, John P.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Chillakuru, Rajeev A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Gould-Rothberg, Bonnie E.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Jeffers, Michael E.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Li, Li  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Murphey, Ryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Peyman, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Starling, Gary  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Voss, Edward Z.  
; APPLICANT: Zhong, Hailong  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-502A  
; CURRENT APPLICATION NUMBER: US/10/309,290  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: 60/336,600  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,285  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/341,346  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/341,477  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/341,540  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/342,592  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 60/344,297

; PRIOR FILING DATE: 2001-12-27  
; PRIOR APPLICATION NUMBER: 60/344,903  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/373,288  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 60/380,981  
; PRIOR FILING DATE: 2002-05-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 99  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1170)  
US-10-309-290-99  
  
Query Match 72.0%; Score 242; DB 17; Length 1173;  
Best Local Similarity 87.5%; Pred. No. 1.7e-68;  
Matches 294; Conservative 0; Mismatches 0; Indels 42; Gaps 1;  
  
Qy 1 GCTCAAAACATCACAGCCGGATTCGGCGAGCCACCTGGTGTGAATGGAAGTGGAGGCGCCGCC 60  
Db 67 GCTCAAAACATCACAGCCGGATTCGGCGAGCCACCTGGTGTGAATGGAAGTGGAGGCGCCGCC 126  
Qy 61 AAGAAACCAACCCAGCGGTGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 120  
Db 127 AAGAAACCAACCCAGCGGTGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 158  
Qy 121 GTCTGTCTTCCCGAGGAGGCGCCCTGGGACAGTGTGGTGTCTTCCCAACGGCTCC 180  
Db 159 -----GGGAGGAGGCGCCCTGGGACAGTGTGGTGTCTTCCCAACGGCTCC 204  
Qy 181 TCCCTTCTCTCCCGGTCTCGGGATCCAGGATGAGGGATTTCCGGTGGCCAGGCAATG 240  
Db 205 TCCCTTCT 264  
Qy 241 AACAGGAATGGAAGGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACCAAGATTTCTGGG 300  
Db 265 AACAGGAATGGAAGGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACCAAGATTTCTGGG 324  
Qy 301 AAGCCAGAAATGTAGATTCGCTTGAACCTCAGC 336  
Db 325 AAGCCAGAAATGTAGATTCGCTTGAACCTCAGC 360  
  
RESULT 15  
US-10-309-290-97  
; Sequence 97, Application US/10309290  
; Publication No. US20040023241A1  
; GENERAL INFORMATION:  
; APPLICANT: Alsbrook II, John P.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Chillakuru, Rajeev A.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Gould-Rothberg, Bonnie E.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Jeffers, Michael E.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Li, Li  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Murphey, Ryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Peyman, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Rieger, Daniel K.

Job time : 232.363 secs

APPLICANT: Shenoy, Suresh G.  
APPLICANT: Smithson, Glenda  
APPLICANT: Starling, Gary  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Voss, Edward Z.  
APPLICANT: Zhong, Haihong  
APPLICANT: Zhong, Mei  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-502A  
CURRENT APPLICATION NUMBER: US/10/309,290  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/336,600  
PRIOR FILING DATE: 2001-12-05  
PRIOR APPLICATION NUMBER: 60/338,285  
PRIOR FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: 60/341,346  
PRIOR FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: 60/341,477  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 60/341,540  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 60/342,592  
PRIOR FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: 60/344,297  
PRIOR FILING DATE: 2001-12-27  
PRIOR APPLICATION NUMBER: 60/344,903  
PRIOR FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: 60/373,288  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: 60/380,981  
PRIOR FILING DATE: 2002-05-15  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 274  
SOFTWARE: CuraseqList version 0.1  
SEQ ID NO 97  
LENGTH: 1226  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (25)..(1194)  
US-10-309-290-97

Query Match 72.0%; Score 242; DB 17; Length 1226;  
Best Local Similarity 87.5%; Pred. No. 1.7e-68;  
Matches 294; Conservative 0; Mismatches 0; Indels 42; Gaps 1;  
QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAGTGTAAAGGGGGCCCCC 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 91 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAGTGTAAAGGGGGCCCCC 150  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 AGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAG 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 151 AGAAACACACCCAGCGGCTGGAATGGAACCTGGAATGGAACCTGGAATGGAACCTGGA 182  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 GTCTGTCTCTCCCGAGGAGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 183 -----GGGAGGAGCCCTCGGACAGTGTGGTCTGTCCTTCCCAACGGC 228  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 TCCTCTTCTTCCGGCTCTCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 229 TCCCTCTTCTTCCGGCTCTCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 288  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 AACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCCTGGG 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 289 AACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCCTGGG 348  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 301 AAGCCAGAAATTTGATTTCTGCTCTGAACCTCAG 336  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 349 AAGCCAGAAATTTGATTTCTGCTCTGAACCTCAG 384  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: March 14, 2005, 22:23:15



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 18:01:28 ; Search time 1333.11 Seconds

(without alignments)  
9593.774 Million cell updates/sec

Title: US-10-091-019-4

Perfect score: 336

Sequence: 1 gctcaaacatcacagccgcg.....attctgcctctgaactcacg 336

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336	100.0	553	4	BI772105 603059188
2	336	100.0	715	4	BG529831 602558918
3	336	100.0	724	4	BG536369 602564760
4	336	100.0	729	4	BG545652 602572917
5	336	100.0	730	4	BG539104 602568478
6	336	100.0	750	4	BG548202 602575359
7	336	100.0	755	4	BG529866 602558957
8	336	100.0	841	9	BI771266 603054610
9	336	100.0	1163	9	AY421474 Pan trogl
10	336	100.0	1194	5	BQ067161 AGENCOURT
11	336	100.0	1215	9	AY421473 Homo sapi
12	334.4	99.5	774	4	BG506672 601861271
13	332.8	99.0	549	4	BG546024 602573327
14	331.2	98.6	538	4	BG484869 602505568
15	325	96.7	692	4	BG483796 602503447
16	325	96.7	822	4	BG540530 602569259
17	325	96.7	832	4	BG548148 602575303
18	324	96.4	613	4	BG570489 602591356
19	324	96.4	724	4	BI772019 603058871
20	324	96.4	894	4	BG538911 602568563
21	323.4	96.2	810	4	BG569848 602590474
22	322.4	96.0	736	4	BG540452 602568768
23	321.8	95.8	605	4	BG570394 602590833
24	314	93.5	599	4	BG538906 602568558

25	314	93.5	835	4	BG548514	602576507
26	310.4	92.4	698	4	BG537129	602565523
27	307.2	91.4	770	4	BG547990	602575902
28	286.8	85.4	876	4	BG535844	602563978
29	270.6	80.5	585	1	AV612348	AV612348
30	270.6	80.5	644	1	AV610398	AV610398
31	270.6	80.5	650	1	AV611162	AV611162
32	269.2	80.1	633	1	AV611204	AV611204
33	269	80.1	659	1	AV609932	AV609932
34	265	78.9	723	4	BG534930	602554119
35	264.4	78.7	549	4	BG538294	602566764
36	261	77.7	742	4	BG533975	602553076
37	250	74.4	399	4	BM721731	BM721731
38	247.8	73.8	656	4	BG537945	602563624
39	244	72.6	777	4	BG545464	602572696
40	242.2	72.1	537	6	CB598482	AGENCOURT
41	242.2	72.1	718	7	CK366081	AGENCOURT
42	242.2	72.1	719	7	CK366019	AGENCOURT
43	242.2	72.1	720	7	CK366743	AGENCOURT
44	242.2	72.1	742	7	CK364097	AGENCOURT
45	242.2	72.1	743	7	CK364561	AGENCOURT

#### ALIGNMENTS

RESULT 1  
LOCUS BI772105 553 bp mRNA linear EST 25-SBP-2001  
DEFINITION 603059188F1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5208812 5', mRNA sequence.  
ACCESSION BI772105  
VERSION BI772105.1 GI:15763683  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 553)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
cDNA Library Preparation: Life Technologies, Inc.  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM11523 row: o column: 21  
High quality sequence stop: 553.  
Location/Qualifiers  
1..553  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5208812"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_122"  
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH\_MGC Library."

#### ORIGIN

Query Match 100.0%; Score 336; DB 4; Length 553;									
Best Local Similarity 100.0%; Pred. No. 4.8e-83;									
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GCTCAAAACATCAGCCCGGATTGGCGACCACTGGTGTGAAGTGTAAAGGGGGCCCC	60						
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QY	61	AAGAAACACCCAGCGGCTGGAATGGAATCAACACAGCCGGACAGAGCTTGGAG	120						
Db	129	AAGAAACACCCAGCGGCTGGAATGGAATCAACACAGCCGGACAGAGCTTGGAG	188						
QY	121	GTCTGTCTCCAGGAGAGGCCCTCGTGGACAGTGTGGCTCGTCTCCCAACGGC	180						
Db	189	GTCTGTCTCCAGGAGAGGCCCTCGTGGACAGTGTGGCTCGTCTCCCAACGGC	248						
QY	181	TCCCTCTTCTCCGCTGTGCGGATCCAGGATGAGGGATTTTCGGTGCAGGCAATG	240						
Db	249	TCCCTCTTCTCCGCTGTGCGGATCCAGGATGAGGGATTTTCGGTGCAGGCAATG	308						
QY	241	AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTACCAAGTCTCTGGG	300						
Db	309	AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTACCAAGTCTCTGGG	368						
QY	301	AAGCCAGAAATTTAGATTCTGCTCTGAATCAAG	336						
Db	369	AAGCCAGAAATTTAGATTCTGCTCTGAATCAAG	404						
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BG529831									
LOCUS									
DEFINITION 602558918F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:469660 5', mRNA linear EST 03-APR-2001									
mRNA sequence.									
ACCESSION BG529831									
VERSION BG529831.1 GI:13521368									
KEYWORDS EST.									
SOURCE Homo sapiens (human)									
ORGANISM Homo sapiens									
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
1 (bases 1 to 715)									
NIH-MGC http://mgi.nci.nih.gov/.									
National Institutes of Health, Mammalian Gene Collection (MGC)									
Unpublished (1999)									
Contact: Robert Strausberg, Ph.D.									
Email: cgabbs-remail.nih.gov									
Tissue Procurement: ATCC									
CDNA Library Preparation: CLONTECH Laboratories, Inc.									
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)									
DNA Sequencing by: Incyte Genomics, Inc.									
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:									
http://image.llnl.gov									
Plate: LLCMI524 row: d column: 05									
High quality sequence stop: 713.									
Location/Qualifiers									
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/clone="IMAGE:469660"									
/tissue_type="embryonal carcinoma"									
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/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgtggcc); Site_2: SfiI (ggccattggcc); SfiII (ggccgtggcc); and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTAGAGCCGAGGCGGACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies									
FEATURES									
source									
1. 724									
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/db_xref="taxon:9606"									
/clone="IMAGE:4689447"									
/lab_host="DH10B (T1 phage-resistant)"									
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/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgtggcc); Site_2: SfiI (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor									

contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."									
Query Match 100.0%; Score 336; DB 4; Length 715;									
Best Local Similarity 100.0%; Pred. No. 5.1e-83;									
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GCTCAAAACATCAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCC	60						
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QY	61	AAGAAACACCCAGCGGCTGGAATGGAATCAACACAGCCGGACAGAGCTTGGAG	120						
Db	158	AAGAAACACCCAGCGGCTGGAATGGAATCAACACAGCCGGACAGAGCTTGGAG	217						
QY	121	GTCTGTCTCCAGGAGAGGCCCTCGGACAGTGTGGCTCGTCTCCCAACGGC	180						
Db	218	GTCTGTCTCCAGGAGAGGCCCTCGGACAGTGTGGCTCGTCTCCCAACGGC	277						
QY	181	TCCCTCTTCTCCGCTGTGCGGATCCAGGATGAGGGATTTTCGGTGCAGGCAATG	240						
Db	278	TCCCTCTTCTCCGCTGTGCGGATCCAGGATGAGGGATTTTCGGTGCAGGCAATG	337						
QY	241	AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTACCAAGTCTCTGGG	300						
Db	338	AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTACCAAGTCTCTGGG	397						
QY	301	AAGCCAGAAATTTAGATTCTGCTCTGAATCAAG	336						
Db	398	AAGCCAGAAATTTAGATTCTGCTCTGAATCAAG	433						
RESULT 3									
BG536369									
LOCUS									
DEFINITION 602564760F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4689447 5', mRNA linear EST 03-APR-2001									
mRNA sequence.									
ACCESSION BG536369									
VERSION BG536369.1 GI:13527915									
KEYWORDS EST.									
SOURCE Homo sapiens (human)									
ORGANISM Homo sapiens									
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
1 (bases 1 to 724)									
NIH-MGC http://mgi.nci.nih.gov/.									
National Institutes of Health, Mammalian Gene Collection (MGC)									
Unpublished (1999)									
Contact: Robert Strausberg, Ph.D.									
Email: cgabbs-remail.nih.gov									
Tissue Procurement: CLONTECH Laboratories, Inc.									
CDNA Library Preparation: CLONTECH Laboratories, Inc.									
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)									
DNA Sequencing by: Incyte Genomics, Inc.									
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:									
http://image.llnl.gov									
Plate: LLCMI505 row: g column: 16									
High quality sequence stop: 724.									
Location/Qualifiers									
1. 724									
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/clone="IMAGE:4689447"									
/lab_host="DH10B (T1 phage-resistant)"									
/clone_lib="NIH MGC 77"									
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgtggcc); Site_2: SfiI (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor									

contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

Query Match 100.0%; Score 336; DB 4; Length 715;  
Best Local Similarity 100.0%; Pred. No. 5.1e-83;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCAGCCCGGATTGGCGACCACTGGTGTGAAGTGTAAAGGGGGCCCC 60  
Db 98 GCTCAAAACATCAGCCCGGATTGGCGACCACTGGTGTGAAGTGTAAAGGGGGCCCC 157  
QY 61 AAGAAACACCCAGCGGCTGGAATGGAATCAACACAGCCGGACAGAGCTTGGAG 120  
Db 158 AAGAAACACCCAGCGGCTGGAATGGAATCAACACAGCCGGACAGAGCTTGGAG 217  
QY 121 GTCTGTCTCCAGGAGAGGCCCTCGTGGACAGTGTGGCTCGTCTCCCAACGGC 180  
Db 218 GTCTGTCTCCAGGAGAGGCCCTCGTGGACAGTGTGGCTCGTCTCCCAACGGC 277  
QY 181 TCCTCTCTCTCCGCTGTGCGGATCCAGGATGAGGGATTTTCGGTGCAGGCAATG 240  
Db 278 TCCTCTCTCTCCGCTGTGCGGATCCAGGATGAGGGATTTTCGGTGCAGGCAATG 337  
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTACCAAGTCTCTGGG 300  
Db 338 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTACCAAGTCTCTGGG 397  
QY 301 AAGCCAGAAATTTAGATTCTGCTCTGAATCAAG 336  
Db 398 AAGCCAGAAATTTAGATTCTGCTCTGAATCAAG 433

RESULT 3  
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LOCUS 602564760F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:469447 5', mRNA linear EST 03-APR-2001  
DEFINITION mRNA sequence.  
ACCESSION BG536369  
VERSION BG536369.1 GI:13527915  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 724)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCMI505 row: g column: 16  
High quality sequence stop: 724.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:469447"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH MGC 77"  
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggccgtggcc); Site\_2: SfiI (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CACGCCCATTTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

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ORIGIN
Query Match      100.0%; Score 336; DB 4; Length 724;
Best Local Similarity 100.0%; Pred. No. 5.1e-83;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACATGCTGCTCAAGTGTAAAGGGGGCCCC 60
DB 79 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACATGCTGCTCAAGTGTAAAGGGGGCCCC 138

QY 61 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAACTTGGAG 120
DB 139 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAACTTGGAG 198

QY 121 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGC 180
DB 199 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGC 258

QY 181 TCCCTCTTCTCCCGCTGTGGGATCCAGAGTGGGAGTTCCTGGTGCAGGCAATG 240
DB 259 TCCCTCTTCTCCCGCTGTGGGATCCAGAGTGGGAGTTCCTGGTGCAGGCAATG 318

QY 241 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTTACCAGATTCTCTGG 300
DB 319 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTTACCAGATTCTCTGG 378

QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336
DB 379 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 414

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RESULT 4
BG545652      729 bp mRNA linear EST 04-APR-2001
LOCUS        602572917F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4700836 5',
DEFINITION   mRNA sequence.
ACCESSION    BG545652
VERSION      BG545652.1 GI:13544317
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: CLONTECH Laboratories, Inc.
              CDNA Library Preparation: CLONTECH Laboratories, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
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              High quality sequence stop: 701.
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                  /clone="IMAGE:4700836"
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                  /clone_lib="NIH_MGC_77"

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FEATURES  
source

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccctcgccc); Site 2: SfiI (ggccattagccc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATTTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

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ORIGIN
Query Match      100.0%; Score 336; DB 4; Length 729;
Best Local Similarity 100.0%; Pred. No. 5.1e-83;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACATGCTGCTCAAGTGTAAAGGGGGCCCC 60
DB 99 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACATGCTGCTCAAGTGTAAAGGGGGCCCC 158

QY 61 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAACTTGGAG 120
DB 159 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAACTTGGAG 218

QY 121 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGC 180
DB 219 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGC 278

QY 181 TCCCTCTTCTCCCGCTGTGGGATCCAGAGTGGGAGTTCCTGGTGCAGGCAATG 240
DB 279 TCCCTCTTCTCCCGCTGTGGGATCCAGAGTGGGAGTTCCTGGTGCAGGCAATG 338

QY 241 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTTACCAGATTCTCTGG 300
DB 339 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCTTACCAGATTCTCTGG 398

QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336
DB 399 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 434

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RESULT 5
BG539104      730 bp mRNA linear EST 03-APR-2001
LOCUS        602568478F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4693027 5',
DEFINITION   mRNA sequence.
ACCESSION    BG539104
VERSION      BG539104.1 GI:13531337
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: CLONTECH Laboratories, Inc.
              CDNA Library Preparation: CLONTECH Laboratories, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
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FEATURES  
source

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/clones="IMAGE:4693027"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH_MGC_77"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCAGAGCGCGAGCGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

```

```

ORIGIN
Query Match 100.0%; Score 336; DB 4; Length 730;
Best Local Similarity 100.0%; Pred. No. 5.1e-83;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGATTGGCGAGCCACTGGTGTGAAGTGAAGGGGCCCC 60
DB 104 GCTCAAAACATCACAGCCCGATTGGCGAGCCACTGGTGTGAAGTGAAGGGGCCCC 163
QY 61 AGAAACACCCAGCGCGGTGGAATGGAATGAACACACAGCCCGGACAGAGCTTGAAG 120
DB 164 AGAAACACCCAGCGCGGTGGAATGGAATGAACACACAGCCCGGACAGAGCTTGAAG 223
QY 121 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 224 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 283
QY 181 TCCTCTTCTTCCTCCGCTGTCGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 240
DB 284 TCCTCTTCTTCCTCCGCTGTCGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 343
QY 241 ACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTTCACAGATTCTCTGG 300
DB 344 ACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTTCACAGATTCTCTGG 403
QY 301 AGCCAGAAATTTAGATTCTGCTCTGAACTCAGC 336
DB 404 AGCCAGAAATTTAGATTCTGCTCTGAACTCAGC 439

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RESULT 6
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LOCUS 60257359F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703246 5',
DEFINITION mRNA sequence.
ACCESSION BG548202
VERSION BG548202.1 GI:13546867
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 750)
NIH-MGC http://imgc.ncbi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1541 row: f column: 15
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Location/Qualifiers
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/organism="Homo sapiens"
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/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH_MGC_77"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCAGAGCGCGAGCGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

```

```

ORIGIN
Query Match 100.0%; Score 336; DB 4; Length 750;
Best Local Similarity 100.0%; Pred. No. 5.1e-83;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGATTGGCGAGCCACTGGTGTGAAGTGAAGGGGCCCC 60
DB 80 GCTCAAAACATCACAGCCCGATTGGCGAGCCACTGGTGTGAAGTGAAGGGGCCCC 139
QY 61 AGAAACACCCAGCGCGGTGGAATGGAATGAACACAGCCCGGACAGAGCTTGAAG 120
DB 140 AGAAACACCCAGCGCGGTGGAATGGAATGAACACAGCCCGGACAGAGCTTGAAG 199
QY 121 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 200 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 259
QY 181 TCCTCTTCTTCCTCCGCTGTCGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 240
DB 260 TCCTCTTCTTCCTCCGCTGTCGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 319
QY 241 AACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTTCACAGATTCTCTGG 300
DB 320 AACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTTCACAGATTCTCTGG 379
QY 301 AGCCAGAAATTTAGATTCTGCTCTGAACTCAGC 336
DB 380 AGCCAGAAATTTAGATTCTGCTCTGAACTCAGC 415

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RESULT 7
BG529866 755 bp mRNA linear EST 03-APR-2001
LOCUS 60255895F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4696622 5',
DEFINITION mRNA sequence.
ACCESSION BG529866
VERSION BG529866.1 GI:13521403
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 755)
NIH-MGC http://imgc.ncbi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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**TITLE**  
**JOURNAL**  
**PUBMED**  
**REFERENCE**  
**AUTHORS**  
 2 (bases 1 to 1163)  
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
**Direct Submission**  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
**COMMENT**  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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 QY 61 AAGAAACCAACCCAGCGGCTGGAAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAA 120  
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 QY 121 GTCTCTCTCCAGGAGAGAGCCCTGGACAGTGTGCTGTCTTCCCAACGCG 180  
 Db 135 GTCTCTCTCCAGGAGAGAGCCCTGGACAGTGTGCTGTCTTCCCAACGCG 194  
 QY 181 TCCTCTCTCTCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGCTGCGAGCAATG 240  
 Db 195 TCCTCTCTCTCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGCTGCGAGCAATG 254  
 QY 241 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 300  
 Db 255 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 314  
 QY 301 AAGCCAGAAATTTAGATTCTGCTCTGAATCAGC 336  
 Db 315 AAGCCAGAAATTTAGATTCTGCTCTGAATCAGC 350  
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 BQ067161  
**VERSION**  
 BQ067161.1 GI:19896207  
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**ORGANISM**  
 Homo sapiens  
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**TITLE**  
 NIH-MGC http://mgi.nci.nih.gov/  
**AUTHORS**  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL**  
 Unpublished (1999)  
**COMMENT**  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
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 High quality sequence stop: 630.  
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 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_115"  
 /note="Organ: pooled brain, lung, testis; Vector:  
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 6 male brains, age range 23-27; 1  
 male lung, age 27; and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH\_MGC Library."  
**ORIGIN**  
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 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 101 GCTCAAAACATACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGCCCC 160  
 QY 61 AAGAAACCAACCCAGCGGCTGGAAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAA 120  
 Db 161 AAGAAACCAACCCAGCGGCTGGAAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAA 220  
 QY 121 GTCTCTCTCCAGGAGAGAGCCCTGGACAGTGTGCTGTCTTCCCAACGCG 180  
 Db 221 GTCTCTCTCCAGGAGAGAGCCCTGGACAGTGTGCTGTCTTCCCAACGCG 280  
 QY 181 TCCTCTCTCTCCGCTGTGCGGATCCAGGATCAGGGGATTTCCGCTGCGAGCAATG 240  
 Db 281 TCCTCTCTCTCCGCTGTGCGGATCCAGGATCAGGGGATTTCCGCTGCGAGCAATG 340  
 QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCTCTGG 300  
 Db 341 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCTCTGG 400  
 QY 301 AAGCCAGAAATTTAGATTCTGCTCTGAATCAGC 336  
 Db 401 AAGCCAGAAATTTAGATTCTGCTCTGAATCAGC 436

**RESULT 11**  
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**DEFINITION**  
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 AY421473  
**VERSION**  
 AY421473.1 GI:39748335  
**KEYWORDS**  
 GSS.  
**SOURCE**  
 Homo sapiens (human)  
**ORGANISM**  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1215)  
**TITLE**  
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
**AUTHORS**

Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 14671302  
 2 (bases 1 to 1215)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 Location/Qualifiers  
 1..1215  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
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**ORIGIN**

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 Best Local Similarity 100.0%; Pred. No. 5.7e-83;  
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTCAAGTGAAGGGGCCCC 60  
 DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTCAAGTGAAGGGGCCCC 126  
 QY 61 AAGAAACACACCCAGCGGCTGGAATGGAACTGAACACAGGCGGACAGAACTTGGAG 120  
 DB 127 AAGAAACACACCCAGCGGCTGGAATGGAACTGAACACAGGCGGACAGAACTTGGAG 186  
 QY 121 GTCTGTCTTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGCG 180  
 DB 187 GTCTGTCTTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGCG 246  
 QY 181 TCCCTCTTCTTCCCGTGTCCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 240  
 DB 247 TCCCTCTTCTTCCCGTGTCCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 306  
 QY 241 AACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGATTCCTGGG 300  
 DB 307 AACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGATTCCTGGG 366  
 QY 301 AAGCCAGAAATGTAGATTCTGCCTCTGAATCAAGC 336  
 DB 367 AAGCCAGAAATGTAGATTCTGCCTCTGAATCAAGC 402

**RESULT 12**  
 BG506672  
 LOCUS 601861271F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4070993 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG506672  
 VERSION BG506672.1 GI:13468189  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 774)  
**REFERENCE**  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLC915 row: n column: 18  
 High quality sequence stop: 723.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4070993"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_77"  
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:  
 SfiI (ggccgctcgcc); Site 2: SfiI (ggccattagcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGGCGGCGGACATG-TT(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.9  
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

**FEATURES**  
 source

**ORIGIN**

Query Match 99.5%; Score 334.4; DB 4; Length 774;  
 Best Local Similarity 99.7%; Pred. No. 1.5e-82;  
 Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTCAAGTGAAGGGGCCCC 60  
 DB 98 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTCAAGTGAAGGGGCCCC 157  
 QY 61 AAGAAACACACCCAGCGGCTGGAATGGAACTGAACACAGGCGGACAGAACTTGGAG 120  
 DB 158 AAGAAACACACCCAGCGGCTGGAATGGAACTGAACACAGGCGGACAGAACTTGGAG 217  
 QY 121 GTCTGTCTTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGCG 180  
 DB 218 GTCTGTCTTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGCG 277  
 QY 181 TCCCTCTTCTTCCCGTGTCCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 240  
 DB 278 TCCCTCTTCTTCCCGTGTCCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 337  
 QY 241 AACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGATTCCTGGG 300  
 DB 338 AACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGATTCCTGGG 397  
 QY 301 AAGCCAGAAATGTAGATTCTGCCTCTGAATCAAGC 336  
 DB 398 AAGCCAGAAATGTAGATTCTGCCTCTGAATCAAGC 433

**RESULT 13**  
 BG546024  
 LOCUS 602573327F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4701318 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG546024  
 VERSION BG546024.1 GI:13544689  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 549)  
**REFERENCE**  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1CM1536 row: f column: 07  
 High quality sequence stop: 544.

## FEATURES

Location/Qualifiers

source

1..549

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4701318"

/lab\_host="DH10B (TI phage-resistant)"

/clone\_lib="NIH\_MGC\_77"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 99.0%; Score 332.8; DB 4; Length 549;  
 Best Local Similarity 99.4%; Pred. No. 3.8e-82;  
 Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60  
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 QY 95 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 154  
 DB |||||  
 QY 61 AAGAAACACACCCAGCGGCTGGAAATGGAATGAACTGAACACAGCGCGGACAGAAAGCTTGGAG 120  
 DB |||||  
 QY 155 AAGAAACACACCCAGCGGCTGGAAATGGAATGGAATGGAACAGACAGCGCGGACAGAAAGCTTGGAG 214  
 DB |||||  
 QY 121 GTCTGTCTCCCGAGGAGAGCCCTGGGACAGTGTGGCTGTCTTCCCAACGGC 180  
 DB |||||  
 QY 215 GTCTGTCTCCCGAGGAGAGCCCTGGGACAGTGTGGCTGTCTTCCCAACGGC 274  
 DB |||||  
 QY 181 TCCTCTCTCTCCCGCTGTGGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 240  
 DB |||||  
 QY 275 TCCTCTCTCTCCCGCTGTGGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 334  
 DB |||||  
 QY 241 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGGG 300  
 DB |||||  
 QY 335 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGGG 394  
 DB |||||  
 QY 301 AAGCCAGAAATGTAGATTCTGCTGTGAATCAAGTCAAG 336  
 DB |||||  
 QY 395 AAGCCAGAAATGTAGATTCTGCTGTGAATCAAGTCAAG 430  
 DB |||||

## RESULT 14

BG484869

LOCUS

DEFINITION BG484869 538 bp mRNA linear EST 21-MAR-2001  
 602505568F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4618816 5',  
 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 538)

## AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1CM1377 row: h column: 17  
 High quality sequence stop: 534.

## FEATURES

Location/Qualifiers

source

1..538

/organism="Homo sapiens"

/mol\_type="mRNA"

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/clone="IMAGE:4618816"

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/clone\_lib="NIH\_MGC\_77"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 98.6%; Score 331.2; DB 4; Length 538;  
 Best Local Similarity 99.1%; Pred. No. 1.1e-81;  
 Matches 333; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60  
 DB |||||  
 QY 99 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 158  
 DB |||||  
 QY 61 AAGAAACACACCCAGCGGCTGGAAATGGAATGGAACAGACAGCGCGGACAGAAAGCTTGGAG 120  
 DB |||||  
 QY 159 AAGAAACACACCCAGCGGCTGGAAATGGAATGGAACAGACAGCGCGGACAGAAAGCTTGGAG 218  
 DB |||||  
 QY 121 GTCTGTCTCCCGAGGAGAGCCCTGGGACAGTGTGGCTGTCTTCCCAACGGC 180  
 DB |||||  
 QY 219 GTCTGTCTCCCGAGGAGAGCCCTGGGACAGTGTGGCTGTCTTCCCAACGGC 278  
 DB |||||  
 QY 181 TCCTCTCTCTCCCGCTGTGGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 240  
 DB |||||  
 QY 279 TCCTCTCTCTCCCGCTGTGGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 338  
 DB |||||  
 QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGGG 300  
 DB |||||  
 QY 339 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGGG 398  
 DB |||||  
 QY 301 AAGCCAGAAATGTAGATTCTGCTGTGAATCAAGTCAAG 336  
 DB |||||  
 QY 399 AAGCCAGAAATGTAGATTCTGCTGTGAATCAAGTCAAG 434  
 DB |||||

## RESULT 15

BG483796

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BG483796 692 bp mRNA linear EST 21-MAR-2001  
 602503447F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4617035 5',  
 mRNA sequence.  
 BG483796  
 BG483796.1 GI:13415985  
 Homo sapiens (human)  
 Homo sapiens



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence stop: 622.

FEATURES

Location/Qualifiers

source

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4617035"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH\_MGC\_77"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:  
SfiI (ggcgctggcc); Site 2: SfiI (ggccattggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGCGCCGACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.9  
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match	96.7%	Score 325;	DB 4;	Length 692;
Best Local Similarity	99.7%	Pred. No. 6.1e-80;		
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QY	61	AAGAAACCAACCCAGCGGCTGGAATGGAATGAACACACAGCGCGGACAGAGCTTGGAG	120	
Db	139	AAGAAACCAACCCAGCGGCTGGAATGGAATGAACACACAGCGCGGACAGAGCTTGGAG	198	
QY	121	GTCTGTCTCTCCAGGAGGAGGCCCTGGGACAGTGTGGTCTGTCTTCCCAACGGC	180	
Db	199	GTCTGTCTCTCCAGGAGGAGGCCCTGGGACAGTGTGGTCTGTCTTCCCAACGGC	258	
QY	181	TCCTCTCTCTCCAGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG	240	
Db	259	TCCTCTCTCTCCAGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG	318	
QY	241	AACAGGAATGG-AAAGGAGACCAAGTCCAACTACGAGTCCGTGTCTACAGATTCTCTGG	299	
Db	319	AACAGGAATGGAAAGGAGACCAAGTCCAACTACGAGTCCGTGTCTACAGATTCTCTGG	378	
QY	300	GAAGCCAGAAATTGTAGATTTCGCTCTGAACTCAG	336	
Db	379	GAAGCCAGAAATTGTAGATTTCGCTCTGAACTCAG	415	

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